

Shears, Beverly

From: Devi, Sarvamangala
 Sent: Wednesday, July 06, 2005 8:49 AM
 To: Shears, Beverly
 Subject: 10/606,618

Beverly:

In application 10/606,618, please perform a search for SEQ ID NO: 4 and an at least eight amino acid-long fragment thereof; a polypeptide comprising amino acids 1-178 of SEQ ID NO: 4; and a polypeptide comprising amino acids 720 to 745 of SEQ ID NO: 4 in commercial and pending databases.

Please include an inventors' name search for: Ralph C. Judd and Scott D. Manning.

Thanx.

S. DEVI, Ph.D.
 AU 1645
 Rems - 3C18

1

Date completed: _____

Searcher: Beverly e 2523

Terminal time: _____

Elapsed time: _____

CPU time: _____

Total time: _____

Number of Searches: _____

Number of Databases: _____

Search Site

_____ STIC

_____ CM-1

_____ Pre-S

Type of Search

_____ N.A. Sequence

_____ A.A. Sequence

_____ Structure

_____ Bibliographic

Vendors

_____ IG

_____ STN

_____ Dialog

_____ APS

_____ Geninfo

_____ SDC

_____ DARC/Questel

_____ Other CGN

THIS PAGE BLANK (USPTO)



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number 158556

TO: Sarvamangala Devi
Art Unit: 1645
Location: REM 3C18
Serial Number: 10/606618

Monday, July 11, 2005

From: Beverly Shears
Location: Biotech-Chem Library
REM 1A54
Phone: 571-272-2528
beverly.shears@uspto.gov

Search Notes

Protein Sequence Searches – February 2005

All of the sequence databases on ABSS have recently been updated.

- Please note that the curators of the UniProt database have purged some temporary accession numbers from the most recent version of UniProt. These sequences have been assigned new permanent accession numbers. The new UniProt record may not contain the previous temporary accession number.
- If you encounter an accession number from an older search run against UniProt (results file extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein Archive database (uniPARC) at:

<http://www.pir.uniprot.org/database/archive.shtml>

If you have any questions regarding this information or your results, please contact any STIC searcher.



THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:37:49 ; Search time 175 Seconds
(without alignments)
2332.155 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLMIGISPLAF.....LKKKPEDEIQRFQGLGTTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1612378 seqs, 512079187 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Uniprot 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	2	O30912
2	752	94.4	797	2	Q9JX31
3	752	94.4	797	2	Q9KIH0
4	157	19.7	792	2	P95359
5	13	1.6	771	2	Q7NVY6
6	13	1.6	786	2	Q8MH2
7	13	1.6	787	2	Q88H14
8	10	1.3	765	2	Q8XZ13
9	9	1.1	328	2	Q9SMN7
10	9	1.1	361	2	Q6LS43
11	9	1.1	435	2	Q9LXP7
12	9	1.1	713	2	Q9ZAE1
13	9	1.1	713	2	Q72J08
14	9	1.1	769	2	Q62JD2
15	9	1.1	769	2	Q63T20
16	9	1.1	778	2	Q7VYC2
17	9	1.1	778	2	Q7WA52
18	9	1.1	778	2	Q7WJ86
19	9	1.1	797	2	Q9S341
20	9	1.1	797	2	Q7N8N9
21	9	1.1	952	2	Q8COX4
22	9	1.1	1035	2	Q9M7J0
23	8	1.0	55	2	Q8MT28
24	8	1.0	82	1	VIM3_BPPH1
25	8	1.0	129	2	Q97L79
26	8	1.0	186	2	Q9ATW3
27	8	1.0	225	2	Q6B441
28	8	1.0	225	2	Q9ZU33
29	8	1.0	241	2	Q8H308
30	8	1.0	277	2	Q87P36
31	8	1.0	290	2	Q6FRT4

32	8	1.0	299	2	Q8NSK6	Q8nsk6 corynebacte
33	8	1.0	321	2	Q86GZ0	Q86gz0 rhipicephal
34	8	1.0	334	1	GYAR_PYRHO	O58320 pyrococcus
35	8	1.0	334	2	Q8MTY1	Q8myt1 rhipicephal
36	8	1.0	335	1	GYAR_PYRAB	Q9uyr1 pyrococcus
37	8	1.0	337	2	Q9KRW5	Q9krw5 vibrio chol
38	8	1.0	341	2	Q9SE52	Q9se52 eriosema ps
39	8	1.0	426	2	O81885	O81885 arabidopsis
40	8	1.0	428	2	O81885	O81885 arabidopsis
41	8	1.0	428	2	Q75JR2	Q75jr2 dictyosteli
42	8	1.0	429	1	FLIK_BACSU	P23451 bacillus su
43	8	1.0	439	2	Q8S7B4	Q8s7b4 oryza sativ
44	8	1.0	439	2	Q7XFL9	Q7xf19 oryza sativ
45	8	1.0	441	2	Q6SEY9	Q6set9 bacillus 11
46	8	1.0	461	2	Q93ZN9	Q93zn9 arabidopsis
47	8	1.0	474	2	Q9T200	Q9t200 bacterioph
48	8	1.0	529	2	Q67NE9	Q67ne9 symbiobacte
49	8	1.0	558	2	Q7F9Z5	Q7f9z5 oryza sativ
50	8	1.0	558	2	Q7XK07	Q7xk07 oryza sativ
51	8	1.0	583	2	Q911V1	Q911v1 pseudomonas
52	8	1.0	758	2	Q82U03	Q82u03 nitrosomona
53	8	1.0	825	2	Q6FCG7	Q6fcg7 acinetobact
54	8	1.0	826	2	Q8EGG7	Q8eg7 shevanella
55	8	1.0	903	1	MSPI_SCHPO	P87320 schizosacch
56	8	1.0	1066	2	Q6NP12	Q6np12 drosophila
57	8	1.0	1085	2	Q8FQ0	Q8fq0 corynebacte
58	8	1.0	1363	1	ILPR_BRALA	O02466 branchiosto
59	8	1.0	1459	2	Q75G47	Q75g47 oryza sativ
60	8	1.0	1475	2	Q9LQU6	Q9lqu6 arabidopsis
61	8	1.0	1577	1	HLVA_PROMI	P16466 proteus mir
62	8	1.0	2408	2	Q9V549	Q9v549 drosophila
63	8	1.0	2903	2	Q9N8R7	Q9n8r7 trypanosoma
64	8	1.0	4919	2	Q9ZHL0	Q9zhl0 haemophilus
65	7	0.9	6199	2	Q6JAN0	Q6jan0 brachydanio
66	7	0.9	63	2	Q8TE37	Q8te37 homo sapien
67	7	0.9	65	2	Q82UE9	Q82ue9 nitrosomona
68	7	0.9	67	2	Q6TMQ2	Q6tmq2 streptomyce
69	7	0.9	71	2	Q8XMZ3	Q8xmz3 clostridium
70	7	0.9	75	2	Q8X5D6	Q8x5d6 escherichia
71	7	0.9	75	2	Q83LQ3	Q83lq3 shigella fl
72	7	0.9	85	2	Q6D0U7	P06965 escherichia
73	7	0.9	85	2	Q726R5	Q726r5 erwinia car
74	7	0.9	93	2	Q9XXG0	Q9xxg0 caenorhabdi
75	7	0.9	95	2	Q6G599	Q6g599 bartonella
76	7	0.9	98	2	P8S_STRCO	O86722 streptomyce
77	7	0.9	101	2	Q76445	O76445 caenorhabdi
78	7	0.9	102	1	RL21_METKA	O8tuu3 methanopyru
79	7	0.9	104	2	Q9IN54	Q9in54 citrus psor
80	7	0.9	104	2	Q9IN56	Q9in56 citrus psor
81	7	0.9	104	2	Q9IN57	Q9in57 citrus psor
82	7	0.9	104	2	Q9IN58	Q9in58 citrus psor
83	7	0.9	104	2	Q9IN59	Q9in59 citrus psor
84	7	0.9	104	2	Q9IN60	Q9in60 citrus psor
85	7	0.9	109	2	Q9Y9U5	Q9y9u5 aeropyrum p
86	7	0.9	115	2	Q7S7S3	Q7s7s3 neurospora
87	7	0.9	115	2	Q8RSN6	Q8rsn6 uncultured
88	7	0.9	120	2	Q6CQL2	Q6cql2 kluyveromyc
89	7	0.9	123	1	KNG_GADMO	P83856 gadus morhu
90	7	0.9	124	1	CRCB_PHOLL	Q7n768 photorhabdu
91	7	0.9	126	2	Q9VM79	Q9vm79 drosophila
92	7	0.9	127	2	Q0C096	O06096 methanococc
93	7	0.9	128	2	Q0C266	Q0c266 neurospora
94	7	0.9	130	2	Q76CY7	Q76cy7 conger myri
95	7	0.9	130	2	Q9PV14	Q9pv14 mola mola (
96	7	0.9	131	2	Q93773	O93773 uncultured
97	7	0.9	131	2	Q9A7L3	Q9a7l3 caulobacter
98	7	0.9	134	2	Q8PN27	O8pn27 xanthomonas
99	7	0.9	135	2	Q45783	O45783 caenorhabdi
100	7	0.9	138	2	Q7X116	Q7xi16 leptospiril
101	7	0.9	139	2	Q7RZ14	Q7rz14 arabidopsis
102	7	0.9	140	2	Q9EMS9	Q9ems9 amsacta moo
103	7	0.9	145	2	Q91110	Q91110 morone saxa
104	7	0.9	148	2	O50574	O50574 bacillus ps

105	7	0.9	150	1	SSRP_CAMJIE	Q9pni9 campylobact	178	7	0.9	243	2	Q89DF6	Q89df6 bradyrhizob
106	7	0.9	150	2	Q6D5B1	Q6d5b1 erwinnia car	179	7	0.9	246	2	Q98FG4	Q98fg4 rhizobium l
107	7	0.9	156	2	Q70T64	Q70t64 ciona intes	180	7	0.9	248	2	Q8PUT8	Q8put8 methanosarc
108	7	0.9	157	2	Q8ETJ7	Q8etj7 oceanobacil	181	7	0.9	248	2	Q98K42	Q98k42 rhizobium l
109	7	0.9	163	2	Q8GV17	Q8gv17 arabidopsis	182	7	0.9	249	2	Q8TJK1	Q8tjk1 methanosarc
110	7	0.9	164	2	Q7RG61	Q7rg61 giardia lam	183	7	0.9	249	2	Q81AW6	Q81aw6 bacillus ce
111	7	0.9	164	2	Q6EPF5	Q6epf5 oryza sativ	184	7	0.9	254	2	Q7SAF5	Q7saf5 neurospora
112	7	0.9	168	2	Q9DKM2	Q9dkm2 spodoptera	185	7	0.9	254	2	Q946T1	Q946t1 sorghum bic
113	7	0.9	169	1	YLZ6_CABEL	P34419 caenorhabdi	186	7	0.9	255	2	Q97NR2	Q97nr2 streptococc
114	7	0.9	171	2	Q9ZAL7	Q9zal7 listeria iv	187	7	0.9	255	2	Q8CY97	Q8cy97 streptococc
115	7	0.9	171	2	Q97QH7	Q97qh7 streptococc	188	7	0.9	257	1	HADD_RHISP	Q8k1s9 rhizobium s
116	7	0.9	172	2	Q9JGT9	Q9jgt9 northern ce	189	7	0.9	260	2	Q8VST1	Q8vst1 vibrio para
117	7	0.9	173	2	Q9SVE4	Q9sve4 arabidopsis	190	7	0.9	264	2	Q8MSS7	Q8ms7 drosophila
118	7	0.9	176	2	Q8SRN5	Q8srn5 encephalito	191	7	0.9	264	2	Q84Y78	Q84y78 chlamydia t
119	7	0.9	177	2	Q676Z8	Q676z8 hyacinthus	192	7	0.9	264	2	Q824J5	Q824j5 chlamydomphi
120	7	0.9	177	2	Q9R8W8	Q9r8w8 rhizobium s	193	7	0.9	264	2	Q9PJS1	Q9pjs1 chlamydia m
121	7	0.9	177	2	Q9R8X0	Q9r8x0 rhizobium s	194	7	0.9	266	2	Q8CES7	Q8ces7 mus muscula
122	7	0.9	177	2	Q9R8X1	Q9r8x1 rhizobium s	195	7	0.9	267	2	Q61I73	Q61i73 drosophila
123	7	0.9	177	2	Q9R8X2	Q9r8x2 rhizobium s	196	7	0.9	267	2	Q74C45	Q74c45 geobacter s
124	7	0.9	177	2	Q9Z3N0	Q9z3n0 rhizobium s	197	7	0.9	267	2	Q7NGC2	Q7ngc2 geobacter s
125	7	0.9	178	2	Q9Z3N4	Q9z3n4 rhizobium s	198	7	0.9	267	2	Q893R1	Q893r1 clostridium
126	7	0.9	179	2	Q6H0X9	Q6h0x9 sulfolobus	199	7	0.9	267	2	Q893R1	Q893r1 thermoplasm
127	7	0.9	180	2	Q84IV2	Q84iv2 mycobacteri	200	7	0.9	268	2	Q86780	Q86780 streptomyc
128	7	0.9	184	2	Q264Z9	Q264z9 methanobact	201	7	0.9	269	2	Q81IU2	Q81iu2 plasmodium
129	7	0.9	184	2	Q6NEZ6	Q6nez6 leptospira	202	7	0.9	269	2	Q9XAC7	Q9xac7 streptomyc
130	7	0.9	184	2	Q6FCT9	Q6fct9 acinetobact	203	7	0.9	270	2	Q6BTI8	Q6bti8 debaryomyce
131	7	0.9	185	2	Q62LFP2	Q62lfp2 burkholderi	204	7	0.9	272	2	Q64ZK6	Q64zk6 bacteroides
132	7	0.9	185	2	Q63WA2	Q63wa2 burkholderi	205	7	0.9	273	2	Q6Z0W7	Q6z0w7 oryza sativ
133	7	0.9	187	2	Q83NG0	Q83ng0 tropheryma	206	7	0.9	274	2	Q87KK2	Q87kk2 vibrio para
134	7	0.9	190	2	Q782U6	Q782u6 galid herp	207	7	0.9	277	2	Q7IZT2	Q7izt2 trypanosoma
135	7	0.9	190	2	Q9QTE3	Q9qte3 marek's dis	208	7	0.9	279	2	Q758X7	Q758x7 ashbya goss
136	7	0.9	193	2	Q8VUA8	Q8vua8 lactococcus	209	7	0.9	279	2	Q6P3A1	Q6p3a1 mus musculu
137	7	0.9	194	2	Q6CY36	Q6cy36 kluyveromyc	210	7	0.9	280	2	Q99X12	Q99xi2 streptococc
138	7	0.9	194	2	Q7XVA3	Q7xva3 griffithsia	211	7	0.9	280	2	Q7CWM8	Q7cm8 streptococc
139	7	0.9	196	2	Q8LMY9	Q8lmy9 oryza sativ	212	7	0.9	280	2	Q9A8A2	Q9a8a2 caulobacter
140	7	0.9	196	2	Q7THD4	Q7thd4 aichi virus	213	7	0.9	280	2	Q8KSH2	Q8ksh2 streptococc
141	7	0.9	196	2	Q7THD5	Q7thd5 aichi virus	214	7	0.9	281	2	Q8DUM0	Q8dum0 streptococc
142	7	0.9	196	2	Q7THD6	Q7thd6 aichi virus	215	7	0.9	282	2	Q96NE7	Q96ne7 homo sapien
143	7	0.9	197	2	Q83N11	Q83n11 tropheryma	216	7	0.9	283	2	Q9R9F9	Q9rf9 streptomyc
144	7	0.9	199	2	Q62M56	Q62m56 burkholderi	217	7	0.9	287	1	PSA3_YEAST	P21242 saccharomyc
145	7	0.9	202	1	HIS7_RHIME	Q92tb0 rhizobium m	218	7	0.9	288	2	Q8W190	Q8w190 euglena gra
146	7	0.9	205	2	Q6CVD5	Q6cvd5 kluyveromyc	219	7	0.9	288	2	Q823B6	Q823b6 chlamydomphi
147	7	0.9	207	1	THIE_CHRVO	Q7plr3 chromobacte	220	7	0.9	289	2	Q743L1	Q743l1 mycobacteri
148	7	0.9	207	1	Q7PXX3	Q7pxh3 anopheles g	221	7	0.9	290	2	Q749Y5	Q749y5 geobacter s
149	7	0.9	214	1	NODB_RHIGA	P50354 rhizobium g	222	7	0.9	291	2	Q30441	O30441 bordetella
150	7	0.9	214	2	Q9CD65	Q9cd65 mycobacteri	223	7	0.9	291	2	Q7W3M9	Q7w3m9 bordetella
151	7	0.9	216	2	Q6FXH5	Q6fxh5 candida gla	224	7	0.9	291	2	Q7WF05	Q7wf05 bordetella
152	7	0.9	216	2	Q7NFC9	Q7nfc9 geobacter	225	7	0.9	292	2	Q9REA4	Q9rea4 enterococcu
153	7	0.9	218	2	Q9Z5F9	Q9z5f9 mycobacteri	226	7	0.9	295	2	Q9GL75	Q9gl75 bos taurus
154	7	0.9	218	2	Q6ZEU7	Q6zeu7 burkholderi	227	7	0.9	295	2	Q9ERF5	Q9erf5 mesocricetu
155	7	0.9	218	2	Q63YC9	Q63yc9 burkholderi	228	7	0.9	297	2	Q7SG71	Q7sg71 neurospora
156	7	0.9	221	2	Q8KK26	Q8kk26 proteus vul	229	7	0.9	298	2	Q9GL74	Q9gl74 cercopithe
157	7	0.9	221	2	Q6DAJ2	Q6daj2 erwinnia car	230	7	0.9	298	2	Q7M9T0	Q7m9t0 wolinnella s
158	7	0.9	223	2	Q82ID5	Q82td5 nitrosomona	231	7	0.9	299	2	Q7QPM1	Q7qpm1 giardia lam
159	7	0.9	225	2	Q8KT67	Q8kt67 photorhabdu	232	7	0.9	299	2	Q7MGD6	Q7mgd6 vibrio vuln
160	7	0.9	225	2	Q7N0Z5	Q7n0z5 photorhabdu	233	7	0.9	299	2	Q8D4T3	Q8d4t3 vibrio vuln
161	7	0.9	226	2	Q965W3	Q965w3 caenorhabdi	234	7	0.9	301	2	Q8PXU9	Q8pxu9 methanosarc
162	7	0.9	226	2	Q9VLK7	Q9vlk7 drosophila	235	7	0.9	301	2	Q82B65	Q82b65 streptomyc
163	7	0.9	227	2	Q63S36	Q63s36 burkholderi	236	7	0.9	304	2	Q8FRS6	Q8frs6 corynebacte
164	7	0.9	228	2	Q9EMK6	Q9emk6 ansacta moo	237	7	0.9	305	2	P90872	P90872 caenorhabdi
165	7	0.9	232	2	Q7QBH1	Q7qbh1 anopheles g	238	7	0.9	305	2	Q90RT24	Q9rt24 deinococcus
166	7	0.9	233	2	Q7U5M9	Q7u5m9 synecococc	239	7	0.9	305	2	Q6APE9	Q6ape9 desulfotale
167	7	0.9	233	2	Q9RJ1	Q9rjp1 streptomyc	240	7	0.9	306	2	Q7RUI7	Q7ru17 neurospora
168	7	0.9	234	2	Q253Z7	Q253z7 helicobacte	241	7	0.9	306	2	Q8UCH5	Q8uch5 agrobacteri
169	7	0.9	234	2	Q9ZLM6	Q9zlm6 helicobacte	242	7	0.9	307	2	Q8LCA2	Q8lca2 arabidopsis
170	7	0.9	235	2	Q7NMY8	Q7nmy8 chromobacte	243	7	0.9	308	2	Q84L58	Q84l58 ciccr ariet
171	7	0.9	238	2	Q7XBL0	Q7xb10 pachysandra	244	7	0.9	308	2	Q828C9	Q828c9 streptomyc
172	7	0.9	238	2	Q882R1	Q882r1 pseudomonas	245	7	0.9	308	2	Q8FCP5	Q8fcp5 escherichia
173	7	0.9	238	2	Q9HYM6	Q9hym6 pseudomonas	246	7	0.9	311	2	Q8U9T2	Q8u9t2 agrobacteri
174	7	0.9	241	2	Q68961	Q68961 helicobacte	247	7	0.9	314	2	Q8LG78	Q8lg78 arabidopsis
175	7	0.9	242	2	Q6GMV5	Q6gmv5 akebia trif	248	7	0.9	314	2	Q9LPG2	Q9lpg2 arabidopsis
176	7	0.9	242	2	Q7U774	Q7u774 synecococc	249	7	0.9	315	2	Q9FXV5	Q9fxv5 arabidopsis
177	7	0.9	243	2	Q7N9U3	Q7n9u3 photorhabdu	250	7	0.9	316	2	Q82W49	Q82w49 nitrosomona

251	7	0.9	316	2	065566	Q65566 bovine herp	324	7	0.9	361	2	082WK0	Q82wk0 nitrosomona
252	7	0.9	316	2	Q77CC0	Q77cc0 bovine herp	325	7	0.9	362	1	LDOX_VITVI	P51093 vitis vinif
253	7	0.9	317	2	Q6N9N0	Q6n9n0 rhodopseudo	326	7	0.9	362	1	RECA_BRAJA	Q89184 bradyrhizob
254	7	0.9	317	2	Q7N4V6	Q7n4v6 photorhabdu	327	7	0.9	362	2	Q8T114	Q9ax57 oryza sativ
255	7	0.9	320	2	FLAI_TREHY	P32520 treponema h	328	7	0.9	362	2	Q9AX57	Q73v31 mycobacteri
256	7	0.9	322	2	Q6H4W3	Q6h4w3 oryza sativ	329	7	0.9	362	2	Q73V31	Q6gn23 xenopus lae
257	7	0.9	324	2	Q8XGHO	Q8xgh0 salmonella	330	7	0.9	362	2	Q6GN23	P87256 aspergillus
258	7	0.9	324	2	Q7CR48	Q7cr48 salmonella	331	7	0.9	363	1	LE3A_ASPNG	Q877a3 aspergillus
259	7	0.9	325	2	Q9P753	Q9p753 neovispora	332	7	0.9	364	2	Q877A9	Q98g12 rhizobium l
260	7	0.9	325	2	Q9FAA4	Q9faa4 brevbacter	333	7	0.9	367	2	Q98G12	Q72wm8 xenopus lae
261	7	0.9	325	2	Q6NHT0	Q6nht0 corynebacte	334	7	0.9	369	2	Q7ZWM8	Q27855 tetrahymena
262	7	0.9	325	2	Q79VG6	Q79vg6 corynebacte	335	7	0.9	371	2	Q27855	Q73rv5 mycobacteri
263	7	0.9	326	2	Q8FQ21	Q8fq21 corynebacte	336	7	0.9	371	2	Q73RV5	Q8fr78 corynebacte
264	7	0.9	328	2	Q6NQ23	Q6ngc3 arabidopsis	337	7	0.9	371	2	Q6FR78	Q6r796 ostrleid her
265	7	0.9	328	2	Q9RB11	Q9rb11 pectobacter	338	7	0.9	371	2	Q6R796	P40316 saccharomyc
266	7	0.9	328	2	Q7USN3	Q7usn3 rhodopirell	339	7	0.9	373	1	SECU YEAST	Q7ujj0 rhodopirell
267	7	0.9	330	2	Q7U9S8	Q7u9s8 synechococc	340	7	0.9	373	1	RECA_RHOBA	Q70812 bacterioph
268	7	0.9	331	2	Q71118	Q71118 human immun	341	7	0.9	375	2	Q70812	Q76101 dileptus ma
269	7	0.9	333	2	Q88VL6	Q88vl6 lactobacill	342	7	0.9	376	2	Q76101	Q7wzcs lactobacill
270	7	0.9	335	2	Q9ZPW3	Q9zpw3 arabidopsis	343	7	0.9	376	2	Q7WZC5	Q741b2 lactobacill
271	7	0.9	335	2	Q71115	Q71115 human immun	344	7	0.9	377	2	Q74LB2	Q06587 homo sapien
272	7	0.9	335	2	Q71116	Q71116 human immun	345	7	0.9	377	1	RNG1_HUMAN	Q8wm5 macaca mula
273	7	0.9	335	2	Q71117	Q71117 human immun	346	7	0.9	377	2	Q8WMN5	Q35730 mus musculu
274	7	0.9	335	2	Q71120	Q71120 human immun	347	7	0.9	377	2	Q35730	Q6mg96 rattus norv
275	7	0.9	335	2	Q71320	Q71320 human immun	348	7	0.9	377	2	Q6MGB6	Q92128 mus musculu
276	7	0.9	336	1	C1W1_MOUSE	Q08581 mus musculu	349	7	0.9	377	2	Q921Z8	Q8av27 gallus gall
277	7	0.9	336	1	OTCC_STRP3	P65609 streptococc	350	7	0.9	377	2	Q8AV27	Q8g3e1 brucella su
278	7	0.9	336	1	OTCC_STRP8	P65610 streptococc	351	7	0.9	379	2	Q8G3E1	Q8yeel bruceila me
279	7	0.9	336	1	OTCC_STRP4	P16964 streptococc	352	7	0.9	380	2	Q8YEE1	Q9kyw7 streptomyce
280	7	0.9	336	2	Q99199	Q99199 mus musculu	353	7	0.9	380	2	Q9KYW7	Q96q15 homo sapien
281	7	0.9	337	1	IMP2_HUMAN	Q9ug22 homo sapien	354	7	0.9	381	2	Q96Q15	Q7mt14 porphyronon
282	7	0.9	337	1	OTC2_STRP3	P65605 streptococc	355	7	0.9	382	2	Q7MT14	Q6nw44 brachydanio
283	7	0.9	337	1	OTC2_STRP5	P65606 streptococc	356	7	0.9	382	2	Q6NWD4	Q8kwi1 bacillus st
284	7	0.9	337	1	OTCC_STRAG	Q8rp83 streptococc	357	7	0.9	383	2	Q8KWF1	Q6ud50 uncultured
285	7	0.9	339	2	Q8C9Y2	Q8c9y2 mus musculu	358	7	0.9	383	2	Q6UD24	Q63in7 burkholderi
286	7	0.9	340	2	Q9G644	Q9g644 calotes cal	359	7	0.9	383	2	Q6UD50	Q8nr26 corynebacte
287	7	0.9	341	2	Q98CD7	Q98cd7 rhizobium l	360	7	0.9	383	2	Q63IN7	Q40492 nicotiana t
288	7	0.9	341	2	Q7UJB2	Q7ujb2 rhodopirell	361	7	0.9	384	2	Q8NR26	Q9fgq3 oryza sativ
289	7	0.9	344	2	Q9X606	Q9x6q6 actinobacil	362	7	0.9	384	2	Q40492	Q921j4 rhizobium m
290	7	0.9	344	2	Q630X0	Q630x0 bacillus ce	363	7	0.9	384	2	Q9FSQ3	Q8tr21 methanosarc
291	7	0.9	344	2	Q66J69	Q66j69 xenopus lae	364	7	0.9	384	2	Q921J4	Q7vs16 bordetella
292	7	0.9	345	2	Q6P164	Q6p164 homo sapien	365	7	0.9	385	2	Q8TR21	Q7we88 bordetella
293	7	0.9	345	2	Q8J0W1	Q8j0w1 cryptococcu	366	7	0.9	386	2	Q7VS16	P48290 leptospira
294	7	0.9	346	2	Q8J0X2	Q8j0x2 cryptococcu	367	7	0.9	386	2	Q7WEB8	Q6pfk0 brachydanio
295	7	0.9	347	2	Q7PGU5	Q7pgu5 anopheles g	368	7	0.9	387	1	RECA_LEPBI	Q9s3z4 streptomyce
296	7	0.9	347	2	Q8SH97	Q8sh97 brookesia p	369	7	0.9	387	2	Q6PFK0	Q8pv83 methanosarc
297	7	0.9	347	2	Q8SHA3	Q8sha3 brookesia b	370	7	0.9	388	1	XYLA_STRCK	Q9ltv7 arabidopsis
298	7	0.9	347	2	Q9SU74	Q9su74 arabidopsis	371	7	0.9	390	2	Q8PV83	Q8t3j1 drosophila
299	7	0.9	348	2	Q6REG8	Q6reg8 rhodococcus	372	7	0.9	390	2	Q9LTV7	Q7rst8 plasmodium
300	7	0.9	348	2	Q70PA6	Q70pa6 mellittangiu	373	7	0.9	391	2	Q8T3J1	Q65fq4 bacillus li
301	7	0.9	348	2	Q64RZ1	Q64rz1 bacteroides	374	7	0.9	393	2	Q7RST8	Q81k92 plasmodium
302	7	0.9	349	1	ISPG_CLOAB	Q97156 clostridium	375	7	0.9	393	2	Q65FQ4	Q6hxx4 bacillus an
303	7	0.9	349	2	Q8CFE7	Q8cfef mus musculu	376	7	0.9	394	2	Q8IK92	Q9r6t2 synechococc
304	7	0.9	351	2	Q66K46	Q66k46 homo sapien	377	7	0.9	394	2	Q6HXX4	Q89e17 bradyrhizob
305	7	0.9	351	2	Q70AX1	Q70ax1 actinoplane	378	7	0.9	398	2	Q9R6T2	Q29133 archaeoglob
306	7	0.9	351	2	Q6AL26	Q6al26 desulfotale	379	7	0.9	398	2	Q89E17	Q91lp8 pseudomonas
307	7	0.9	351	2	Q6NSS5	Q6nss5 mus musculu	380	7	0.9	399	1	ENO_ARCFU	Q8et06 oceanobacil
308	7	0.9	353	2	Q6ZZG5	Q6zzg5 actinoplane	381	7	0.9	401	2	Q91LP8	Q6bgi7 paramecium
309	7	0.9	354	2	Q99XC6	Q99xc6 staphylococ	382	7	0.9	402	2	Q8ET06	Q6sh30 uncultured
310	7	0.9	354	2	Q99XC6	P45370 c poly-beta	383	7	0.9	404	2	Q6BGI7	Q9nv04 homo sapien
311	7	0.9	355	1	PHBC_CHRVI	Q9c778 arabidopsis	384	7	0.9	405	2	Q6SH30	Q7pnq3 anopheles g
312	7	0.9	355	2	Q9C778	Q9c778 arabidopsis	385	7	0.9	405	2	Q9NV04	Q86v19 homo sapien
313	7	0.9	355	2	Q8NVY5	Q8nyv5 staphylococ	386	7	0.9	406	2	Q7PNQ3	Q6ype8 oryza sativ
314	7	0.9	355	2	Q8YYA1	Q8yya1 anabaena sp	387	7	0.9	407	2	Q6VPE8	Q6cmj5 kluyveromyc
315	7	0.9	355	2	Q7NK07	Q7nk07 gloeobacter	388	7	0.9	408	2	Q6CMJ5	Q01961 picchia past
316	7	0.9	355	2	Q6GD41	Q6gd41 staphylococ	389	7	0.9	409	1	PEXC_PICPA	Q6ab18 propionibac
317	7	0.9	357	2	Q7NZU9	Q7nzu9 chromobacte	390	7	0.9	410	2	Q6AB18	Q8e2r6 streptococc
318	7	0.9	358	1	REC2_MYXXA	P48292 myxococcus	391	7	0.9	410	2	Q6AB18	Q9z5t5 zymomonas m
319	7	0.9	358	2	Q81PE1	Q81pe1 bacillus an	392	7	0.9	412	2	Q8E2R6	Q961z5 homo sapien
320	7	0.9	358	2	Q7S255	Q7s255 brachydanio	393	7	0.9	413	2	Q9Z5T5	Q7qbw1 anopheles g
321	7	0.9	360	2	Q7ME25	Q7mez5 vibrio vuln	394	7	0.9	413	2	Q961Z5	Q7qbw2 anopheles g
322	7	0.9	360	2	Q8D7X9	Q8d7x9 vibrio vuln	395	7	0.9	413	2	Q7QBW1	
323	7	0.9	361	2	Q6L1J2	Q6l1j2 picrophilus	396	7	0.9	413	2	Q7QBW2	

397	7	0.9	413	2	Q8JZV4	Q8jzv4 m riken cdn	470	7	0.9	476	2	Q8U552	Q8u552 agrobacteri
398	7	0.9	414	1	CD61_METAC	Q8tur2 methanosarc	471	7	0.9	476	2	Q7V9V6	Q7v9v6 prochloroco
399	7	0.9	414	1	CD61_METAC	Q8pxa8 methanosarc	472	7	0.9	477	2	Q87HT2	Q87ht2 vibrio para
400	7	0.9	415	1	PGK_ASHGO	Q757G0 ashbya goss	473	7	0.9	480	2	Q6R2R8	Q6r2r8 hyposoter d
401	7	0.9	416	2	Q99X43	Q99x43 staphylococ	474	7	0.9	482	2	Q892C7	Q892c7 clostridium
402	7	0.9	416	2	Q7AIY3	Q7aly3 staphylococ	475	7	0.9	485	2	Q6W1U7	Q6w1u7 rhizobium s
403	7	0.9	416	2	Q7AB14	Q7ab14 staphylococ	476	7	0.9	485	2	Q73LL4	Q73ll4 treponema d
404	7	0.9	416	2	Q6GCU8	Q6gcu8 staphylococ	477	7	0.9	486	2	Q6ZP84	Q6zpa4 homo sapien
405	7	0.9	416	2	Q6GK8	Q6gk8 staphylococ	478	7	0.9	487	2	Q8U0H5	Q8u0h5 pyrococcus
406	7	0.9	417	1	PGK_CANNA	P41757 candida mal	479	7	0.9	487	2	Q7SXF3	Q7sxf3 brachydanio
407	7	0.9	418	2	Q8DW5	Q8dw5 streptococc	480	7	0.9	488	2	Q6PIJ6	Q6pij6 homo sapien
408	7	0.9	419	1	Y4ML_RHLSN	P55571 rhizobium s	481	7	0.9	488	2	Q8SB18	Q8sb18 oryza sativ
409	7	0.9	420	1	CDC6_PYRFU	P81413 pyrococcus	482	7	0.9	488	2	Q89H76	Q89h76 bradyrhizob
410	7	0.9	420	1	YF41_METJA	Q58936 methanococc	483	7	0.9	489	1	C128_MYCBO	P63714 mycobacteri
411	7	0.9	420	2	Q9RJQ6	Q9rjq6 streptomyc	484	7	0.9	489	1	C128_MYCTU	P63713 mycobacteri
412	7	0.9	421	2	Q95V69	Q95v69 tetrahymena	485	7	0.9	489	1	OCLN_POTTR	Q28793 potorous tr
413	7	0.9	422	1	LACE_AGRD	P29822 agrobacteri	486	7	0.9	493	2	Q761Y0	Q761y0 oryza sativ
414	7	0.9	422	2	Q8ZNC0	Q8znc0 salmonella	487	7	0.9	497	2	Q97RD6	Q97rd6 streptococc
415	7	0.9	423	2	Q93256	Q93256 gallus gall	488	7	0.9	497	2	Q8DQ91	Q8dq91 streptococc
416	7	0.9	424	2	Q89R42	Q89r42 bradyrhizob	489	7	0.9	498	2	Q97V40	Q97v40 sulfolobus
417	7	0.9	427	2	Q7Q6T1	Q7q6t1 anopheles g	490	7	0.9	498	2	Q6X195	Q6x195 bacterioph
418	7	0.9	428	2	Q6O947	Q6o947 trypanosoma	491	7	0.9	499	2	Q6X1A1	Q6x1a1 bacterioph
419	7	0.9	428	2	P74349	P74349 synechocyst	492	7	0.9	500	2	Q6X1A2	Q6x1a2 bacterioph
420	7	0.9	428	2	Q747R9	Q747r9 geobacter s	493	7	0.9	501	2	Q6X1A3	Q6x1a3 bacterioph
421	7	0.9	429	1	SYS_PHOLL	Q7n6e7 photorhabdu	494	7	0.9	502	1	DNAA_MYCLE	P46388 mycobacteri
422	7	0.9	430	2	Q8YCL3	Q8ycl3 brucella me	495	7	0.9	503	2	Q8MQF7	Q8mqf7 caenorhabdi
423	7	0.9	432	2	Q7RAW2	Q7raw2 plasmodium	496	7	0.9	503	2	Q8EK00	Q8ek00 shewanella
424	7	0.9	431	2	Q21194	Q21194 caenorhabdi	497	7	0.9	506	2	Q17537	Q17537 caenorhabdi
425	7	0.9	431	2	Q8HT85	Q8ht85 selaginella	498	7	0.9	507	2	Q6C8B4	Q6c8b4 varrowia li
426	7	0.9	431	2	Q73M29	Q73m29 treponema d	499	7	0.9	508	2	P90790	P90790 caenorhabdi
427	7	0.9	432	2	Q66H32	Q66h32 rattus norv	500	7	0.9	509	2	Q9VBP7	Q9vbp7 drosophila
428	7	0.9	432	1	CDC6_PYRAB	Q9v2f2 pyrococcus	501	7	0.9	509	2	Q8D0L7	Q8d0l7 yersinia pe
429	7	0.9	432	2	Q6NWF0	Q6nwf0 brachydanio	502	7	0.9	514	2	Q9DF59	Q9df59 brachydanio
430	7	0.9	435	2	Q9TXJ4	Q9txj4 leishmania	503	7	0.9	515	1	PVR1_MOUSE	Q9jkt6 mus musculu
431	7	0.9	435	2	Q6G2S5	Q6g2s5 bartonella	504	7	0.9	515	1	PVR1_PIG	Q9gl76 sus scrofa
432	7	0.9	436	2	Q836C0	Q836c0 enterococcu	505	7	0.9	515	2	Q97Y93	Q97y93 sulfolobus
433	7	0.9	437	1	CDC6_PYRHO	O57864 pyrococcus	506	7	0.9	515	2	Q6P9M9	Q6p9m9 mus musculu
434	7	0.9	437	2	Q7NHM7	Q7nhm7 glieobacter	507	7	0.9	516	2	Q7MQB5	Q7mqb5 vibrio vuln
435	7	0.9	437	2	Q6D216	Q6d216 erwinia car	508	7	0.9	517	1	PVR1_HUMAN	Q12223 homo sapien
436	7	0.9	438	2	Q6BC08	Q6bc08 edwardsiell	509	7	0.9	518	1	CD63_HALN1	Q9hms3 halobacteri
437	7	0.9	444	2	Q23497	Q23497 caenorhabdi	510	7	0.9	518	2	Q747N5	Q747n5 geobacter s
438	7	0.9	444	2	Q89M95	Q89m95 bradyrhizob	511	7	0.9	519	2	Q7S8P0	Q7s8p0 neurospora
439	7	0.9	444	2	Q89NM0	Q89nm0 bradyrhizob	512	7	0.9	526	1	K1CU_BOVIN	F06394 bos taurus
440	7	0.9	445	2	Q6N715	Q6n715 rhodopseudo	513	7	0.9	526	2	Q8RME3	Q8rme3 alcaligenes
441	7	0.9	446	2	Q6BU59	Q6bu59 debaryomyc	514	7	0.9	527	2	Q63A80	Q63a80 bacillus ce
442	7	0.9	446	2	Q7SB26	Q7sb26 neurospora	515	7	0.9	527	2	Q6HHM4	Q6hhm4 bacillus th
443	7	0.9	447	2	Q7QKE9	Q7qke9 anopheles g	516	7	0.9	529	2	Q9FD13	Q9fdi3 brevibacter
444	7	0.9	448	2	Q8Y1V0	Q8y1v0 ralstonia s	517	7	0.9	532	2	Q7NYE6	Q7nye6 chromobacte
445	7	0.9	451	1	VPS9_YEAST	P54787 saccharomyc	518	7	0.9	537	1	YDU2_SCHPO	O13863 schizosacch
446	7	0.9	453	2	Q6A855	Q6a855 propionibac	519	7	0.9	537	2	Q6MD44	Q6md44 parachlamyd
447	7	0.9	456	2	Q57794	Q57794 pyrococcus	520	7	0.9	537	2	Q8QQ94	Q8qq94 avian infec
448	7	0.9	456	2	Q8R9H8	Q8r9h8 thermoanaer	521	7	0.9	543	2	Q6D418	Q6d418 erwinia car
449	7	0.9	459	2	Q881M9	Q881m9 pseudomonas	522	7	0.9	545	2	Q7QY12	Q7qy12 giardia lam
450	7	0.9	460	2	Q98R23	Q98r23 guillardia	523	7	0.9	545	2	Q66A41	Q66a41 yersinia ps
451	7	0.9	460	2	Q74GQ7	Q74gq7 geobacter s	524	7	0.9	545	2	Q8ZE13	Q8zel3 yersinia pe
452	7	0.9	461	2	Q6JKE9	Q6jke9 neodiprion	525	7	0.9	545	2	Q6NJCS	Q6njcs corynebacte
453	7	0.9	463	2	Q6SY98	Q6sy98 photorhabdu	526	7	0.9	546	2	Q7UT65	Q7ut65 rhodopirell
454	7	0.9	464	2	Q7Z3Y7	Q7z3y7 homo sapien	527	7	0.9	547	2	Q75AW8	Q75aw8 ashbya goss
455	7	0.9	464	2	Q7ACN3	Q7acn3 escherichia	528	7	0.9	547	2	Q73J78	Q73j78 treponema d
456	7	0.9	464	2	Q8X7J5	Q8x7j5 escherichia	529	7	0.9	547	2	Q8AJJ6	Q8alj6 bacteroides
457	7	0.9	464	2	Q8CVX8	Q8cvx8 escherichia	530	7	0.9	550	2	Q9RBI1	Q9rb11 acinetobact
458	7	0.9	466	2	Q8FVD7	Q8fvd7 brucella su	531	7	0.9	550	2	Q6FCC3	Q6fcc3 acinetobact
459	7	0.9	469	2	Q51997	Q51997 halobacteri	532	7	0.9	551	2	Q6J9V5	Q6j9v5 zea mays (m
460	7	0.9	469	2	Q6CSM6	Q6csm6 kluyveromyc	533	7	0.9	556	2	Q810A1	Q810a1 mus musculu
461	7	0.9	470	2	Q6AF02	Q6af02 leifsonia x	534	7	0.9	556	2	Q9D972	Q9d972 mus musculu
462	7	0.9	471	2	Q9EZF8	Q9ezf8 streptococc	535	7	0.9	562	1	CH60_TRYCR	Q95046 trypanosoma
463	7	0.9	471	2	Q9RCK6	Q9rck6 streptomyc	536	7	0.9	562	2	Q8NK91	Q8nk91 aspergillus
464	7	0.9	471	2	Q92CE1	Q92ce1 listeria in	537	7	0.9	562	2	Q75AY9	Q75ay9 ashbya goss
465	7	0.9	472	2	Q9F2B6	Q9f2b6 thauera aro	538	7	0.9	562	2	Q9V725	Q9v725 drosophila
466	7	0.9	473	2	Q712I1	Q712i1 streptomyc	539	7	0.9	564	2	Q9POT6	Q9pt6 ureaplasma
467	7	0.9	473	2	Q84I42	Q84i42 streptomyc	540	7	0.9	567	2	Q9HGH9	Q9hgh9 aspergillus
468	7	0.9	473	2	Q7MXZ1	Q7mxz1 porphyronon	541	7	0.9	572	2	Q6ZH86	Q6zh86 oryza sativ
469	7	0.9	475	2	Q6Y636	Q6y636 mus musculu	542	7	0.9	573	2	Q9VDS0	Q9vds0 drosophila

543	7	0.9	575	2	065IP7	Q65ip7 bacillus li	616	7	0.9	728	1	KDGL ARATH	Q39017 arabidopsis
544	7	0.9	580	2	Q89YL8	Q89yl8 bacteroides	617	7	0.9	728	2	Q9YOY0	Q9yoY0 ranid herpe
545	7	0.9	581	2	Q6TBO7	Q6tbo7 manheimia	618	7	0.9	733	2	Q9UBZ1	Q9ubz1 homo sapien
546	7	0.9	583	1	ARSA_ECOLI	P52145 escherichia	619	7	0.9	733	2	Q8PIV9	Q8piv9 xanthomonas
547	7	0.9	583	1	ARSA_ACIMU	O50593 acidiophilu	620	7	0.9	734	2	Q7NPF4	Q7npf4 gloeobacter
548	7	0.9	584	2	Q79SA6	Q79sa6 incn plaemi	621	7	0.9	741	2	HGL2 ARATH	Q87uf7 pseudomonas
549	7	0.9	584	2	Q98N7	Q98nt7 rhizobium l	622	7	0.9	741	2	Q87UF7	P46607 arabidopsis
550	7	0.9	585	2	Q9KJ73	Q9kji3 klebsiella	623	7	0.9	747	2	Q9CSF1	Q9c5f1 arabidopsis
551	7	0.9	587	1	RGPI_HUMAN	P46050 homo sapien	624	7	0.9	747	2	Q7P2X4	Q7p2x4 fusbacteri
552	7	0.9	588	2	Q6LLI2	Q6lll2 picrophilus	625	7	0.9	750	2	Q8PHT0	Q8pht0 xanthomon
553	7	0.9	589	1	RGPI_MOUSE	P46061 mus musculu	626	7	0.9	755	2	Q6K624	Q6k624 oryza sativ
554	7	0.9	589	2	Q91YS2	Q91ys2 mus musculu	627	7	0.9	756	2	Q751Y0	Q751y0 ashbya goss
555	7	0.9	589	2	Q7TWM1	Q7tmw1 mus musculu	628	7	0.9	758	2	Q6FSM0	Q6fsw0 candida gla
556	7	0.9	589	2	Q8C2E3	Q8c2e3 mus musculu	629	7	0.9	761	2	Q9H2G6	Q9h2g6 homo sapien
557	7	0.9	589	2	Q6NZB5	Q6nzb5 mus musculu	630	7	0.9	763	2	Q64Z23	Q64z23 bacteroides
558	7	0.9	594	2	Q86JK0	Q86jk0 dictyosteli	631	7	0.9	771	2	Q81298	O81298 arabidopsis
559	7	0.9	596	2	Q6X194	Q6x194 bacterioph	632	7	0.9	773	2	Q33541	O33541 endosymbion
560	7	0.9	596	2	Q6X197	Q6x197 bacterioph	633	7	0.9	774	2	Q6FN99	Q6fn99 candida gla
561	7	0.9	596	2	Q6X198	Q6x198 bacterioph	634	7	0.9	778	2	Q73G77	Q73g77 wolbachia p
562	7	0.9	596	2	Q6X199	Q6x199 bacterioph	635	7	0.9	784	2	Q87E11	Q87e11 xylella fas
563	7	0.9	596	2	Q6X1A0	Q6x1a0 bacterioph	636	7	0.9	784	2	Q9PEI2	Q9pei2 xylella fas
564	7	0.9	596	2	Q6X1A4	Q6x1a4 bacterioph	637	7	0.9	786	2	Q86L03	Q86l03 dictyosteli
565	7	0.9	596	2	Q6T811	Q6t811 manheimia	638	7	0.9	788	2	Q8PML3	Q8pml3 xanthomonas
566	7	0.9	604	2	O04098	O04098 arabidopsis	639	7	0.9	794	2	Q8P569	Q8p569 xanthomonas
567	7	0.9	605	1	NRDD_BPT4	P07071 bacterioph	640	7	0.9	795	2	Q886N5	Q886n5 pseudomonas
568	7	0.9	605	2	Q6BB07	Q6bp07 debaryomyce	641	7	0.9	796	2	Q8PEN2	Q8ppn2 xanthomonas
569	7	0.9	605	2	Q7Y558	Q7y558 bacterioph	642	7	0.9	797	2	Q9HXI4	Q9hxy4 pseudomonas
570	7	0.9	610	2	Q8W6J7	Q8w6j7 sinorhizobi	643	7	0.9	798	2	Q7PMI8	Q7pmi8 anopheles g
571	7	0.9	610	2	Q62J44	Q62j44 burkholderi	644	7	0.9	799	1	Y231 BUCAP	Q8k9s5 buchnera ap
572	7	0.9	610	2	Q63ST4	Q63st4 burkholderi	645	7	0.9	807	2	Q94HV9	Q94hv9 arabidopsis
573	7	0.9	612	2	Q912F4	Q91zf4 cereal yell	646	7	0.9	808	2	Q8BIB8	Q8biv8 mus musculu
574	7	0.9	614	2	Q7Q2A3	Q7q2a3 anopheles g	647	7	0.9	809	2	Q96JS3	Q96ja3 homo sapien
575	7	0.9	616	1	GLMS_AERPE	Q9ycq6 a glucosami	648	7	0.9	811	2	Q6K7R9	Q6k7r9 oryza sativ
576	7	0.9	619	1	CALX_CABEL	P34652 caenorhabdi	649	7	0.9	811	2	Q80T97	Q80t97 mus musculu
577	7	0.9	620	1	ORC2_YEAST	P32833 saccharomyc	650	7	0.9	812	2	Q8XF68	Q8xf68 salmonella
578	7	0.9	623	2	Q96J32	Q96j32 homo sapien	651	7	0.9	812	2	Q7CP94	Q7cp94 salmonella
579	7	0.9	623	2	Q8YQ88	Q8yq88 anabaena sp	652	7	0.9	813	1	RNR_ECOLI	P21499 escherichia
580	7	0.9	626	2	Q65N18	Q65n18 bacillus li	653	7	0.9	813	1	RNR_SHIFL	P30851 shigella fl
581	7	0.9	628	2	Q82HQ5	Q82hd5 streptomyce	654	7	0.9	818	2	O8NM59	Q8nm59 corynebacte
582	7	0.9	632	1	HI14_HUMAN	Q8ihu5 homo sapien	655	7	0.9	818	2	Q8PAW1	Q8paw1 xanthomonas
583	7	0.9	632	1	HI14_MOUSE	Q80tn5 mus musculu	656	7	0.9	821	2	Q69DS5	Q69ds5 oryza sativ
584	7	0.9	632	2	Q7U778	Q7u778 synchococc	657	7	0.9	822	2	Q6H6R9	Q6h6r9 oryza sativ
585	7	0.9	641	2	Q9KWU1	Q9kwu1 sphingomona	658	7	0.9	823	2	Q9S7P3	Q9s7p3 arabidopsis
586	7	0.9	646	2	Q6ZPH4	Q6zph4 mus musculu	659	7	0.9	827	2	Q8FAK5	Q8fak5 escherichia
587	7	0.9	647	2	Q73NK7	Q73nk7 treponema d	660	7	0.9	827	2	Q8XDL9	Q8xdl9 escherichia
588	7	0.9	649	1	LONH_METJA	Q58812 methanococc	661	7	0.9	838	2	Q7QNU7	Q7qnu7 giardia lam
589	7	0.9	651	2	Q6TKP9	Q6tkp9 homo sapien	662	7	0.9	841	2	Q7NMS8	Q7nms8 gloeobacter
590	7	0.9	654	2	Q62L07	Q62l07 burkholderi	663	7	0.9	845	2	Q6VAL8	Q6val8 arsenite-ox
591	7	0.9	656	2	Q9SLA7	Q9sls1 photobacter	664	7	0.9	849	2	Q6DB45	Q6dba5 erwinia car
592	7	0.9	659	2	Q6LLS1	Q6lls1 arabidopsis	665	7	0.9	850	2	Q8FC25	Q8fc25 escherichia
593	7	0.9	661	2	Q7MC29	Q7mc29 vibrio vuln	666	7	0.9	856	2	Q97KW5	Q97kw5 clostridium
594	7	0.9	661	2	Q8D582	Q8d582 vibrio vuln	667	7	0.9	857	2	Q6AJQ8	Q6ajq8 desulfotale
595	7	0.9	662	2	Q6XB70	Q6xbj0 mycobacteri	668	7	0.9	859	2	Q6UDK3	Q6udk3 psittacid h
596	7	0.9	663	2	Q6BNA8	Q6bna8 debaryomyce	669	7	0.9	868	2	Q75BV7	Q75bv7 ashbya goss
597	7	0.9	663	2	Q8RWP2	Q8rwp2 arabidopsis	670	7	0.9	870	2	Q6ATA6	Q6ata6 oryza sativ
598	7	0.9	663	2	Q940B9	Q940b9 arabidopsis	671	7	0.9	873	2	Q74A79	Q74a79 geobacter s
599	7	0.9	663	2	Q67ZT9	Q67zt9 arabidopsis	672	7	0.9	883	2	Q6CRS9	Q6crs9 kluyveromyc
600	7	0.9	665	1	MTRI_HUMAN	Q13613 homo sapien	673	7	0.9	885	2	Q8A1E1	Q8a1e1 bacteroides
601	7	0.9	666	2	Q89DT9	Q89dt9 bradyrhizob	674	7	0.9	887	2	Q8XV49	Q8xv49 ralatonia s
602	7	0.9	666	2	Q9KKR7	Q9kk7 vibrio chol	675	7	0.9	888	2	Q9LQ62	Q9lq62 arabidopsis
603	7	0.9	674	2	Q7QB46	Q7qb46 anopheles g	676	7	0.9	893	2	Q6C3K8	Q6c3k8 yarrowia li
604	7	0.9	680	2	Q8IMW5	Q8imes drosophila	677	7	0.9	897	2	Q7KN84	Q7kn84 drosophila
605	7	0.9	684	2	Q7S840	Q7s840 neurospora	678	7	0.9	897	2	Q9UIK2	Q9ulk2 drosophila
606	7	0.9	684	2	Q7X7M2	Q7x7m2 oryza sativ	679	7	0.9	897	2	Q9VGZ6	Q9vgz6 drosophila
607	7	0.9	685	2	Q6S001	Q6s001 dictyosteli	680	7	0.9	916	2	Q9W354	Q9w354 drosophila
608	7	0.9	693	2	Q63TE4	Q63te4 burkholderi	681	7	0.9	942	2	Q18298	Q18298 caenorhabdi
609	7	0.9	695	2	Q8RPS4	Q8rps4 pseudomonas	682	7	0.9	944	2	Q7Q0U5	Q7q0u5 anopheles g
610	7	0.9	697	2	Q7QNS2	Q7qns2 giardia lam	683	7	0.9	946	2	Q9EV24	Q9ev24 manheimia
611	7	0.9	697	2	Q9VEP8	Q9vep8 drosophila	684	7	0.9	946	2	Q89GU0	Q89gu0 bradyrhizob
612	7	0.9	699	2	Q82E12	Q82e12 streptomyce	685	7	0.9	946	2	Q89XV1	Q89xv1 bradyrhizob
613	7	0.9	702	2	Q8G6C8	Q8g6c8 bifidobacte	686	7	0.9	947	1	LKTA_PASSP	P55123 pasteurella
614	7	0.9	717	2	Q9VAY0	Q9vay0 drosophila	687	7	0.9	947	2	Q6FKI5	Q6fki5 candida gla
615	7	0.9	718	2	Q7RPJ6	Q7rpj6 plasmodium	688	7	0.9	948	2	Q7XTP3	Q7xtp3 oryza sativ

689	7	0.9	949	2	057149	057149 human herpe	762	0.9	1187	2	Q94CJ9	Q94cj9 arabidopsis
690	7	0.9	950	1	P4R1_HUMAN	Q8tf05 homo sapien	763	0.9	1222	2	Q868R4	Q868r4 anopheles g
691	7	0.9	951	1	P4R1_MOUSE	Q8k2v1 mus musculu	764	0.9	1222	2	Q98PR9	Q98pr9 mycoplasma
692	7	0.9	951	1	P4R1_RAT	Q8vi02 rattus norv	765	0.9	1239	2	Q9DEF4	Q9def4 xenopus lae
693	7	0.9	952	2	Q6BKU6	Q6bk16 debaryomyce	766	0.9	1259	2	Q44971	Q44971 caenorhabdi
694	7	0.9	952	2	Q6H911	Q6h911 botrytis ci	767	0.9	1260	2	Q804R3	Q804r3 brachydanio
695	7	0.9	953	1	LKAI_PASHA	P16535 pasteurella	768	0.9	1277	2	Q7UKG2	Q7ukg2 rhodopirell
696	7	0.9	953	1	LKAB_PASHA	P55118 pasteurella	769	0.9	1276	2	Q6BFB2	Q6bfb2 paramecium
697	7	0.9	953	2	Q6TB03	Q6tb03 manheimia	770	0.9	1285	2	Q6UNF4	Q6unf4 ictalurus p
698	7	0.9	953	2	Q9ETG5	Q9etg5 pasteurella	771	0.9	1301	2	Q7XB17	Q7xb17 drosophila
699	7	0.9	953	2	Q9ETX2	Q9etx2 manheimia	772	0.9	1301	2	Q9U982	Q9u982 drosophila
700	7	0.9	953	2	Q9EV23	Q9ev23 manheimia	773	0.9	1322	2	Q6CKZ5	Q6ckz5 kluyveromyc
701	7	0.9	953	2	Q9EV25	Q9ev25 manheimia	774	0.9	1336	2	Q73550	Q73550 semliki for
702	7	0.9	953	2	Q9EV26	Q9ev26 manheimia	775	0.9	1349	2	Q9L096	Q9l096 streptomyce
703	7	0.9	953	2	Q9EV29	Q9ev29 pasteurella	776	0.9	1350	2	Q9VWB0	Q9vwb0 drosophila
704	7	0.9	953	2	Q9EV30	Q9ev30 pasteurella	777	0.9	1361	2	Q8QZ08	Q8qzg8 chilo iride
705	7	0.9	953	2	Q9EV31	Q9ev31 pasteurella	778	0.9	1366	2	Q9ZFG3	Q9zpg3 arabidopsis
706	7	0.9	953	2	Q9EV32	Q9ev32 pasteurella	779	0.9	1370	2	Q6A078	Q6a078 mus musculu
707	7	0.9	953	2	Q9EV33	Q9ev33 pasteurella	780	0.9	1382	2	Q7P330	Q7p330 fusbacteri
708	7	0.9	953	2	Q9EV34	Q9ev34 pasteurella	781	0.9	1390	2	Q6PL18	Q6pl18 homo sapien
709	7	0.9	963	1	KINH_HUMAN	P33176 homo sapien	782	0.9	1415	2	Q6FVI3	Q6fvi3 candida gla
710	7	0.9	963	1	KINH_MOUSE	Q61768 mus musculu	783	0.9	1418	2	Q98SW6	Q98sw6 xenopus lae
711	7	0.9	967	2	Q8TDL2	Q8tdl2 homo sapien	784	0.9	1422	2	Q8IBL9	Q8ibl9 plasmodium
712	7	0.9	976	2	Q9UI58	Q9ui58 leishmania	785	0.9	1434	1	PTC1_MOUSE	Q61115 mus musculu
713	7	0.9	978	2	Q8N890	Q8n890 homo sapien	786	0.9	1434	2	Q6UY90	Q6uy90 rattus norv
714	7	0.9	983	1	GCSP_ANASP	Q7ynf9 anabaena sp	787	0.9	1442	1	PTC1_CHICK	Q90693 gallus gall
715	7	0.9	985	2	Q7Q8G8	Q7q8g8 anopheles g	788	0.9	1444	2	Q7WUL1	Q7wul1 neisseria m
716	7	0.9	988	2	Q63LC1	Q63lc1 burkholderi	789	0.9	1447	1	PTC1_HUMAN	Q13635 homo sapien
717	7	0.9	988	2	Q63VP1	Q63vp1 burkholderi	790	0.9	1449	2	Q9F3Z5	Q9f3z5 neisseria m
718	7	0.9	992	2	Q9UV08	Q9uv08 emericella	791	0.9	1449	2	Q9JWB4	Q9jwb4 neisseria m
719	7	0.9	996	2	Q924M9	Q924m9 rattus norv	792	0.9	1453	1	CE29_BOVIN	Q9t423 bos taurus
720	7	0.9	996	2	Q6JTV1	Q6jtv1 mus musculu	793	0.9	1454	2	Q9F3Z4	Q9f3z4 neisseria m
721	7	0.9	996	2	Q6P730	Q6p730 rattus norv	794	0.9	1457	2	Q8GKS4	Q8gks4 neisseria m
722	7	0.9	997	2	Q76BA8	Q76ba8 callorhinch	795	0.9	1457	2	Q9X7H1	Q9x7h1 neisseria m
723	7	0.9	997	2	Q76BB4	Q76bb4 potamoxygo	796	0.9	1457	2	Q9UXL6	Q9jxl6 neisseria m
724	7	0.9	1004	2	Q8TUS3	Q8tj53 methanosarc	797	0.9	1463	2	Q69298	Q69298 gallid herp
725	7	0.9	1014	2	Q96PY4	Q96py4 homo sapien	798	0.9	1468	2	Q6SLD4	Q6sl44 cochllobolu
726	7	0.9	1016	2	Q8NSA4	Q8nsa4 corynebacte	799	0.9	1479	2	Q7KQT5	Q7kqt5 drosophila
727	7	0.9	1016	2	Q888X2	Q888x2 pseudomonas	800	0.9	1482	2	Q9V4Y0	Q9v4y0 drosophila
728	7	0.9	1018	2	Q7RRF9	Q7rrf9 plasmodium	801	0.9	1487	2	Q8RHT9	Q8rht9 fusbacteri
729	7	0.9	1021	2	Q6FS37	Q6fs37 candida gla	802	0.9	1508	1	BCSC_XANAC	P58938 xanthomonas
730	7	0.9	1025	2	Q7R6E6	Q7r6e6 giardia lam	803	0.9	1513	2	Q9WSZ8	Q9wsz8 human herpe
731	7	0.9	1031	2	Q6Y293	Q6y293 oryza sativ	804	0.9	1520	2	Q9QJ16	Q9qj16 human herpe
732	7	0.9	1036	2	Q9C0C0	Q9c0c0 homo sapien	805	0.9	1539	1	CE29_HUMAN	Q15078 homo sapien
733	7	0.9	1045	2	Q6CQ79	Q6cq79 kluyveromyc	806	0.9	1572	2	Q7SGQ7	Q7sgq7 neurospora
734	7	0.9	1054	2	Q67430	Q67430 aquifex aeo	807	0.9	1584	2	Q8Q0G8	Q8q0g8 methanosarc
735	7	0.9	1057	2	Q9V9G1	Q9v9g1 drosophila	808	0.9	1608	2	Q6FX52	Q6fx52 candida gla
736	7	0.9	1065	2	Q96SE1	Q96sei homo sapien	809	0.9	1618	2	Q9KKB1	Q9kxb1 rickettsia
737	7	0.9	1071	2	Q9VBA3	Q9vba3 drosophila	810	0.9	1632	2	Q8QHS2	Q8qhs2 human herpe
738	7	0.9	1087	2	Q6C117	Q6c117 yarrowia li	811	0.9	1656	1	QMPB_RICJA	Q06653 r outer mem
739	7	0.9	1088	1	DP2L_THEVO	Q97cr6 thermoplasm	812	0.9	1658	2	Q9RWI1	Q9rwi1 deinococcus
740	7	0.9	1088	2	Q28333	Q28333 archaeoglob	813	0.9	1686	2	Q00443	Q00443 homo sapien
741	7	0.9	1092	2	Q6J4U7	Q6j4u7 drosophila	814	0.9	1708	2	Q7XWZ9	Q7xwz9 oryza sativ
742	7	0.9	1095	2	Q6C4Q2	Q6c4q2 yarrowia li	815	0.9	1724	2	Q70TF5	Q70tf5 oncorhynch
743	7	0.9	1098	2	Q6CPF5	Q6cpf5 kluyveromyc	816	0.9	1766	2	Q6XHA8	Q6xha8 dictyosteli
744	7	0.9	1098	2	Q7QUN5	Q7qun5 giardia lam	817	0.9	1804	2	Q809B7	Q809b7 semliki for
745	7	0.9	1107	2	Q7Q7N3	Q7q7n3 anopheles g	818	0.9	1896	2	Q84MR5	Q84mr5 oryza sativ
746	7	0.9	1107	2	Q7WMS5	Q7wm5 porphyromon	819	0.9	1928	2	Q8D674	Q8d674 vibrio vuln
747	7	0.9	1121	1	WDR6_HUMAN	Q9nnw5 homo sapien	820	0.9	1943	2	Q25331	Q25331 helicobacte
748	7	0.9	1125	2	Q6BM05	Q6bm05 debaryomyce	821	0.9	1956	2	Q9Y2K3	Q9y2k3 homo sapien
749	7	0.9	1125	2	Q99ME2	Q99me2 mus musculu	822	0.9	1989	2	Q9ERT7	Q9ert7 mus musculu
750	7	0.9	1128	2	Q6AMN5	Q6amn5 desulfotale	823	0.9	2134	2	Q7QAT6	Q7qat6 anopheles g
751	7	0.9	1130	2	Q7PXL7	Q7pxl7 anopheles g	824	0.9	2174	2	Q92UU8	Q92u8 rhizobium m
752	7	0.9	1132	2	Q6P0N0	Q6p0n0 homo sapien	825	0.9	2215	2	Q7WBN0	Q7wb0 bordetella
753	7	0.9	1132	2	Q7RAI4	Q7rai4 plasmodium	826	0.9	2223	2	Q7WTF4	Q7wtf4 streptomyce
754	7	0.9	1139	2	Q54073	Q54073 synecococc	827	0.9	2274	2	Q9Z1K7	Q9z1k7 mus musculu
755	7	0.9	1139	2	Q8DGF2	Q8dgt2 synecococc	828	0.9	2303	2	Q95996	Q95996 homo sapien
756	7	0.9	1156	2	Q93209	Q93209 feline foam	829	0.9	2431	1	POLN_SFV	P08411 semliki for
757	7	0.9	1156	2	P90458	P90458 feline sync	830	0.9	2431	2	Q8JMP6	Q8jmp6 semliki for
758	7	0.9	1156	2	Q70LW4	Q70lw4 feline foam	831	0.9	2432	2	Q815I9	Q815i9 plasmodium
759	7	0.9	1156	2	Q70LW8	Q70lw8 feline foam	832	0.9	2432	2	Q9QBM1	Q9qbm1 semliki for
760	7	0.9	1158	2	Q6GM32	Q6gm32 xenopus lae	833	0.9	2478	2	Q8YTN5	Q8ytn5 anabaena sp
761	7	0.9	1165	2	Q7PKP8	Q7pkp8 anopheles g	834	0.9	2479	2	Q66GS8	Q66gs8 homo sapien

835	7	0.9	2838	2	08VHJ9	Q8vhi9 rattus norv	908	6	0.8	53	2	Q6PMW3	O6pmw3 bos taurus
836	7	0.9	2909	2	Q8MV78	Q8my78 aterina pe	909	6	0.8	54	2	Q8RT38	Q8rt38 lactobacill
837	7	0.9	3122	2	R89459	R89459 human herpe	910	6	0.8	55	2	Q85VES	Q85ves manheimia
838	7	0.9	3194	2	Q8ZLM3	Q8zlm3 helicobacte	911	6	0.8	56	2	Q8VJH5	Q8vjh5 mycobacteri
839	7	0.9	3216	2	Q8FLK3	Q8flk3 escherichia	912	6	0.8	57	2	Q7S794	Q7s794 neurospora
840	7	0.9	3242	2	Q8G9X9	Q8g9x9 escherichia	913	6	0.8	57	2	Q85257	Q85257 streptococc
841	7	0.9	3346	2	Q7WN54	Q7wn54 bordetella	914	6	0.8	57	2	Q868F2	Q868f2 vercinia ps
842	7	0.9	3455	2	Q7WTD6	Q7wt6 streptomyc	915	6	0.8	57	2	Q64QM5	Q64qm5 bacteroides
843	7	0.9	3836	2	Q6TW53	Q6ty53 hirudo medi	916	6	0.8	57	2	Q82CC5	Q82cc5 yersinia pe
844	7	0.9	3956	2	Q7WTF2	Q7wtf2 streptomyc	917	6	0.8	58	2	Q9S4C7	Q9s4c7 porphyromon
845	7	0.9	4106	2	Q846X2	Q846x2 streptomyc	918	6	0.8	58	2	Q7TL98	Q7tl98 tomato leaf
846	7	0.9	4485	1	DYHG CHLRE	Q39575 chlamydomon	919	6	0.8	58	2	Q88540	Q88540 tomato leaf
847	7	0.9	5369	2	Q9R9J0	Q9r9j0 bacillus su	920	6	0.8	58	2	Q88550	Q88550 tomato leaf
848	6	0.8	18	2	Q6LEN9	Q6len9 homo sapien	921	6	0.8	58	2	Q8B5S8	Q8b5s8 tomato leaf
849	6	0.8	23	2	Q96708	Q96708 ilyanassa o	922	6	0.8	58	2	Q8B5T2	Q8b5t2 tomato leaf
850	6	0.8	23	2	Q25138	Q25138 halictotis ru	923	6	0.8	58	2	Q9QD89	Q9qd89 human immun
851	6	0.8	23	2	Q25161	Q25161 halictotis s	924	6	0.8	59	2	Q6EB62	Q6eb62 campylobact
852	6	0.8	23	2	Q86MM9	Q86mm9 pecten maxi	925	6	0.8	59	2	Q8KCM6	Q8kcm6 chlorobium
853	6	0.8	25	1	Q8X1 MOUSE	R82976 mus musculu	926	6	0.8	60	2	Q81TF7	Q81tf7 bacillus an
854	6	0.8	25	2	Q8MT1	Q8mt1 eisenia and	927	6	0.8	60	2	Q9RT52	Q9rt52 deinococcus
855	6	0.8	26	2	Q8NTR0	Q8njr0 euryymna sc	928	6	0.8	62	2	Q8IF77	Q8if77 trypanosoma
856	6	0.8	27	2	Q02601	Q02601 berce ovata	929	6	0.8	62	2	Q7P310	Q7p310 fusobacteri
857	6	0.8	27	2	Q97457	Q97457 tryptetesa l	930	6	0.8	62	2	Q8G8G5	Q8g8g5 mycoplasma
858	6	0.8	27	2	Q17148	Q17148 branchiosto	931	6	0.8	62	2	Q72UB4	Q72ub4 leptospira
859	6	0.8	27	2	Q26396	Q26396 ctenodrilus	932	6	0.8	62	2	Q8TOR6	Q8tor6 leptospira
860	6	0.8	27	2	Q26533	Q26533 saccoglossu	933	6	0.8	63	2	Q8GWT9	Q8gwt9 arabidopsis
861	6	0.8	27	2	Q7KQNS	Q7kqs tryptetesa l	934	6	0.8	63	2	Q6T2C0	Q6t2c0 streptomyc
862	6	0.8	27	2	Q90299	Q90299 carassius a	935	6	0.8	63	2	Q71J91	Q71j91 lactobacill
863	6	0.8	27	2	Q91272	Q91272 petromyzon	936	6	0.8	63	2	Q9EW93	Q9ew93 streptomyc
864	6	0.8	27	2	Q91273	Q91273 petromyzon	937	6	0.8	63	2	Q8NQG0	Q8nqg0 corynebacte
865	6	0.8	28	2	Q17074	Q17074 antheraea p	938	6	0.8	63	2	Q73794	Q73794 xenopus lae
866	6	0.8	29	2	Q17073	Q17073 antheraea p	939	6	0.8	64	2	Q633Q4	Q633q4 bacillus ce
867	6	0.8	30	2	Q96707	Q96707 lithobius f	940	6	0.8	64	2	Q72V64	Q72v64 leptospira
868	6	0.8	31	2	Q86LM4	Q86lm4 lumbricus s	941	6	0.8	64	2	Q722K4	Q722k4 bacillus ce
869	6	0.8	32	2	Q86LM5	Q86lm5 urechis cau	942	6	0.8	64	2	Q817K2	Q817k2 bacillus ce
870	6	0.8	32	2	Q86LM6	Q86lm6 loligo opal	943	6	0.8	64	2	Q81L53	Q81l53 bacillus an
871	6	0.8	32	2	Q65V69	Q65v69 manheimia	944	6	0.8	64	2	Q8SZP2	Q8szp2 leptospira
872	6	0.8	33	2	Q9XS29	Q9xs29 sus scrofa	945	6	0.8	64	2	Q71714	Q71714 human immun
873	6	0.8	33	2	Q8V9C6	Q8v9c6 cotton leaf	946	6	0.8	65	2	Q7NAX6	Q7nxa6 chromobacte
874	6	0.8	33	2	Q9IEV0	Q9iev0 cotton leaf	947	6	0.8	65	2	Q9PFF3	Q9pff3 xylella fas
875	6	0.8	34	2	Q7PD47	Q7pd47 giardia lam	948	6	0.8	66	2	Q9NQP6	Q9nqp6 homo sapien
876	6	0.8	35	2	Q79471	Q79471 human immun	949	6	0.8	66	2	R87463	R87463 hemidactylu
877	6	0.8	36	2	Q748T1	Q748t1 geobacter s	950	6	0.8	66	2	Q8U809	Q8u809 agrobacteri
878	6	0.8	36	2	Q91144	Q91144 notophthalm	951	6	0.8	66	2	Q9DQ45	Q9dq45 human immun
879	6	0.8	38	2	Q91XM7	Q91xm7 rattus norv	952	6	0.8	66	2	Q9DQ48	Q9dq48 human immun
880	6	0.8	38	2	Q9JL01	Q9j101 rattus norv	953	6	0.8	66	2	Q9DQ49	Q9dq49 human immun
881	6	0.8	39	2	Q9UD61	Q9ud61 homo sapien	954	6	0.8	66	2	Q9DQ50	Q9dq50 human immun
882	6	0.8	39	2	Q6SXQ4	Q6sxq4 eptaretus	955	6	0.8	66	2	Q9DQ51	Q9dq51 human immun
883	6	0.8	39	2	Q6M7D0	Q6m7d0 corynebacte	956	6	0.8	66	2	Q9DQ52	Q9dq52 human immun
884	6	0.8	40	2	Q25534	Q25534 mytilus tro	957	6	0.8	67	2	Q61698	Q61698 hydra atten
885	6	0.8	42	2	Q61336	Q61336 panulirus i	958	6	0.8	67	2	Q61698	Q61698 hydra atten
886	6	0.8	42	2	Q8F264	Q8f264 leptospira	959	6	0.8	67	2	Q7D2H8	Q7d2h8 agrobacteri
887	6	0.8	43	2	Q8EF80	Q8ef80 shewanella	960	6	0.8	67	2	Q8X443	Q8x443 escherichia
888	6	0.8	43	2	Q91F98	Q91f98 chilo iride	961	6	0.8	67	2	Q7UE29	Q7ue29 rhodopirell
889	6	0.8	44	2	Q7R8B6	Q7r8b6 plasmodium	962	6	0.8	67	2	Q82Q11	Q82q11 streptomyc
890	6	0.8	44	2	Q87W23	Q87w23 pseudomonas	963	6	0.8	68	2	Q8PUD4	Q8pud4 methanosa
891	6	0.8	45	2	Q7YJ33	Q7y733 nicotiana s	964	6	0.8	68	2	Q7SMZ6	Q7smz6 homo sapien
892	6	0.8	45	2	Q7XL87	Q7xl87 oryza sativ	965	6	0.8	68	2	Q98RX3	Q98rx3 quillardia
893	6	0.8	45	2	Q6UMM0	Q6umm0 hepatitis c	966	6	0.8	68	2	Q9K928	Q9k928 bacillus ha
894	6	0.8	45	2	Q6UMM1	Q6umm1 hepatitis c	967	6	0.8	68	2	Q11613	Q11613 human immun
895	6	0.8	47	2	Q7PFT7	Q7pft7 anopheles g	968	6	0.8	69	1	RL38 LYCES	RL38 lycopersico
896	6	0.8	47	2	Q95W96	Q95w96 equus cabal	969	6	0.8	69	2	Q6KZ16	Q6kz16 picophilus
897	6	0.8	48	2	Q6F5J0	Q6f5j0 bovine vira	970	6	0.8	69	2	Q71HS8	Q71hs8 lactobacill
898	6	0.8	49	2	Q6CSL8	Q6cal8 kluyveromyc	971	6	0.8	69	2	Q9R3Q4	Q9r3q4 streptococc
899	6	0.8	49	2	Q7YUJ0	Q7yu10 trypanosoma	972	6	0.8	69	2	Q9RCM3	Q9rcm3 streptococc
900	6	0.8	50	2	Q6QW42	Q6qw42 azospirillu	973	6	0.8	69	2	Q9RCM7	Q9rcm7 streptococc
901	6	0.8	50	2	Q7YJ13	Q7yj13 nicotiana t	974	6	0.8	69	2	Q65GZ4	Q65gz4 bacillus l1
902	6	0.8	51	2	Q8NSN4	Q8nsn4 corynebacte	975	6	0.8	69	2	Q9WCQ3	Q9wcq3 human immun
903	6	0.8	51	2	Q73TU2	Q73tu2 mycobacteri	976	6	0.8	70	1	RL31 ECOLI	RL31 escherichia
904	6	0.8	51	2	Q7UMC6	Q7umc6 rhodopirell	977	6	0.8	70	2	Q8Q7F8	Q8q78 methanosa
905	6	0.8	52	2	Q8MRT2	Q8mrt2 drosophila	978	6	0.8	70	2	Q8H5L7	Q8h5l7 oryza sativ
906	6	0.8	52	2	Q8YX17	Q8yn17 anabaena sp	979	6	0.8	70	2	Q83PD4	Q83pd4 shigella fl
907	6	0.8	52	2	Q87259	Q87259 chimpanzee	980	6	0.8	70	2	Q8BMZ8	Q8bmz8 mus musculu

981 6 0.8 71 1 RL31_PSPK Q88cu3 pseudomonas
 982 6 0.8 71 1 RS28_ARCFU O29493 archaeoglob
 983 6 0.8 71 2 Q8WMH0 Q8wmh0 sus scrofa
 984 6 0.8 71 2 Q9GJ62 Q9gj62 salmo trutt
 985 6 0.8 71 2 Q9GJ63 Q9gj63 salmo trutt
 986 6 0.8 71 2 Q9GJ65 Q9gj65 salmo trutt
 987 6 0.8 71 2 Q9GJ66 Q9gj66 salmo trutt
 988 6 0.8 71 2 Q9GJ67 Q9gj67 salmo trutt
 989 6 0.8 71 2 Q9GJ68 Q9gj68 salmo trutt
 990 6 0.8 71 2 Q9GJ71 Q9gj71 salmo trutt
 991 6 0.8 71 2 Q9GJ72 Q9gj72 salmo trutt
 992 6 0.8 71 2 Q62C83 Q62c83 burkholderi
 993 6 0.8 71 2 Q7MYC6 Q7myc6 photorhabdu
 994 6 0.8 71 2 Q7VM76 Q7vm76 haemophilus
 995 6 0.8 72 2 O15172 O15172 homo sapien
 996 6 0.8 72 2 Q9WC08 Q9wcc8 human immu
 997 6 0.8 73 1 RL29_AQUAE P56613 aquifex aeo
 998 6 0.8 73 1 SAS2_BACME F10571 bacillus me
 999 6 0.8 73 2 Q47834 Q47834 enterococcu
 1000 6 0.8 73 2 Q83AD2 Q83ad2 coxiella bu

ALIGNMENTS

RESULT 1

O30912 ID O30912 PRELIMINARY; PRT; 797 AA.
 AC O30912;
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Outer membrane protein Omp85.
 GN Name=omp85;
 OS Neisseria meningitidis.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=487;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HH;
 RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
 RA Manning D.S.; Reschke D.K.; Judd R.C.;
 RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
 RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
 RT multocida Oma87.";
 RL Microb. Pathog. 25:11-21(1998).
 DR EMBL; AF021245; AAC17599.1; -;
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac surface Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 SQ SEQUENCE 797 AA; 89539 MW; CF911B5F70B999CF CRC64;

Query Match 100.0%; Score 797; DB 2; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVENYLPVKVGDTYNDTHGSA 60
 DB 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVENYLPVKVGDTYNDTHGSA 60
 QY 61 IISLKYATGFFDVRVETADQQLLTIVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
 DB 61 IISLKYATGFFDVRVETADQQLLTIVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
 QY 121 SQVFNQATLNAQVAGLKEEYLGKGLNIQTTPVKTKLARNRVIDITIDEGKSAKITDIE 180
 DB 121 SQVFNQATLNAQVAGLKEEYLGKGLNIQTTPVKTKLARNRVIDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRLKRMQMSLTGGITWLTTRSNQFNEQKFAQDMKVTDYFQNNGVDFPRIL 240
 DB 181 FEGNOVYSDRLKRMQMSLTGGITWLTTRSNQFNEQKFAQDMKVTDYFQNNGVDFPRIL 240

RESULT 2

Q9JX31 ID Q9JX31 PRELIMINARY; PRT; 797 AA.
 AC Q9JX31;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Outer membrane protein OMP85.
 GN Name=omp85; OrderedLocusNames=NMA0085;
 OS Neisseria meningitidis (serogroup A).
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Neisseria.
 OX NCBI_TaxID=65699;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=22491 / Serogroup A / Serotype 4A;
 RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
 RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
 RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
 RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
 RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
 RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
 RA Whitehead S., Spratt B.G., Barrall B.G.;
 RT "Complete DNA sequence of a serogroup A strain of Neisseria
 RT meningitidis Z2491.";
 RL Nature 404:502-506(2000).
 DR EMBL; AL162752; CAB83401.1; -;
 DR PIR; D82000; D82000.
 DR InterPro; IPR000184; Bac_surfAg_D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac surface Ag; 1.


```
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DE47E00C9E1D1F CRC64;

Query Match
Best Local Similarity 94.4%; Score 752; DB 2; Length 797;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEY 140
QY 141 LGRGKLNIIQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLRQMSLTE 200
DB 141 LGRGKLNIIQTPKVTKLARNRVDITIDEGSKAKITDIEFEGNQVYSRDKLRQMSLTE 200
QY 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYDFDRIILDTDIQTNEDKTKQTIKIVH 260
DB 201 GGIWTLTRSNQFNEQKFAQDMKVTDFYQNGYDFDRIILDTDIQTNEDKTKQTIKIVH 260
QY 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSGAGYAS 320
DB 261 EGGFRFGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSGAGYAS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRELQMESAPYDTS 380
QY 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGVQDTGLVM 440
DB 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGVQDTGLVM 440
QY 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSPDTPYFTADGVSGLGVYGVKAFDPRKAS 500
DB 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSPDTPYFTADGVSGLGVYGVKAFDPRKAS 500
QY 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKPKHYADFICKYKGTG 560
DB 501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKPKHYADFICKYKGTG 560
QY 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620
DB 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLQYYSATHNQWTFPP 620
QY 621 LSKTFTMLGGEVGIAGGYGRTEKIEIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKIS 680
DB 621 LSKTFTMLGGEVGIAGGYGRTEKIEIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKIS 680
QY 681 YGNGKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
DB 681 YGNGKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
QY 741 AGNTHKSTFTNELRYSAGGAVTWSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSAGGAVTWSPLGPMKF 772

RESULT 3
Q9K1H0 PRELIMINARY; PRT; 797 AA.
AC Q9K1H0;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE Outer membrane protein Omp85.
GN OrderedLocusNames=NB0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
```

```

Db 621 LSKTFTLMLGGEVGIAGGYGRTKIPFPENFYGGGLGSRVGYESGTLGPVKYDYEYGEKIS 680
Qy 681 YGKNKANVSAELLFPMPGKADARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGKNKANVSAELLFPMPGKADARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 4
P95359
ID P95359 PRELIMINARY; PRT; 792 AA.
AC P95359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA19;
RA MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S.; Reschke D.K.; Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
RT multocida Oms87.";
RL Microb. Pathog. 25:111-21(1998).
RL EMBL; U81959; AAC17600.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 19.7%; Score 157; DB 2; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.le-150;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQWESAPYDTSKLQSKERVEL 391
Db 332 TKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQWESAPYDTSKLQSKERVEL 391
Qy 392 LGYFDNVQFQDAVPLAGTPDKVDLNLSTERTSGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFQDAVPLAGTPDKVDLNLSTERTSGSLDLSAGVQDTGLVMSAGVSQDNLFG 451
Qy 452 TGKSAALRASRKTTLINGSLSFTDPYPTAGVSLGYD 488
Db 452 TGKSAALRASRKTTLINGSLSFTDPYPTAGVSLGYD 488

RESULT 5
Q7NY6
ID Q7NY6 PRELIMINARY; PRT; 771 AA.
AC Q7NY6;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
[1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 12472 / DSM 30191;

```

```

RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.L.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grisard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.O., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunarez H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RT "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability.";
RL PROC. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL; AE016917; AAQ59877.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 771;
Best Local Similarity 100.0%; Pred. No. 0.0013;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TVFNYPVVKVGD 52
Db 42 TVFNYPVVKVGD 54

RESULT 6
Q88MH2
ID Q88MH2 PRELIMINARY; PRT; 786 AA.
AC Q88MH2;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein, bacterial surface antigen family.
GN OrderedLocusNames=PP1599;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
[1]
RP SEQUENCE FROM N.A.
RC MEDLINE=22423060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzaz A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hohelsel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.W.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";

```

```

RL Environ. Microbiol. 4:799-808 (2002).
DR ENBL; AE016779; AAN67220.1; -.
DR TIGR; PP1599; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 786 AA; 86513 MW; D88E288A938D9E98 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 786;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 DPYFTADGVSLGY 487
DB 474 DPYFTADGVSLGY 486

RESULT 7
Q88H14 PRELIMINARY; PRT; 787 AA.
AC Q88H14;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacterial surface antigen family protein.
GN OrderedLocusNames=PP3373;
OS Pseudomonas putida (strain KT2440).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=160488;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2243060; PubMed=12534463;
RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,
RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,
RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,
RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,
RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,
RA Moazzes A., Utterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,
RA Wedler H., Lauber J., Stjepandic D., Hoheisel J., Straetz M., Heim S.,
RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,
RA Fraser C.M.;
RT "Complete genome sequence and comparative analysis of the
RT metabolically versatile Pseudomonas putida KT2440.";
RL Environ. Microbiol. 4:799-808 (2002).
DR ENBL; AE016786; AAN68977.1; -.
DR TIGR; PP3373; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 787 AA; 86513 MW; 41F90C4E311A6A97 CRC64;

Query Match 1.6%; Score 13; DB 2; Length 787;
Best Local Similarity 100.0%; Pred. No. 0.0014;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 475 DPYFTADGVSLGY 487
DB 474 DPYFTADGVSLGY 486

RESULT 8
Q8XZ13 PRELIMINARY; PRT; 765 AA.
AC Q8XZ13;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.

```

```

GN Names=RS05280; OrderedLocusNames=RS041412;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangelot S.,
RA Ariat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502 (2002).
DR ENBL; AL646064; CAD15114.1; -.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00061; ADP_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 1.3%; Score 10; DB 2; Length 765;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 359 KTRDEVVRRE 368
DB 365 KTRDEVVRRE 374

RESULT 9
Q9SNM7 PRELIMINARY; PRT; 328 AA.
AC Q9SNM7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein T8P19.130.
GN Names=T8P19.130;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Choine N., Robert C., Brottier P., Wincker P., Cattolico L.,
RA Artiguenave F., Saurin W., Weissenbach J., Mewes H.W., Lemcke K.,
RA Mayer K.F.X., Quetier F., Salanoubat M.;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
DR ENBL; AL133315; CAB62351.1; -.
DR PIR; T46206; T46206.
DR InterPro; IPR007928; Antifreeze_CF.
KW Hypothetical protein.
SQ SEQUENCE 328 AA; 36233 MW; CDB4D2B1EA2530C6 CRC64;

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 8.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 654 GGLGVRGY 662
DB 152 GGLGVRGY 160

RESULT 10

```

ID	Q6L543	PRELIMINARY;	PRT;	361 AA.
AC	Q6L543;			
DT	05-JUL-2004	(TrEMBLrel. 27, Created)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last sequence update)		
DT	05-JUL-2004	(TrEMBLrel. 27, Last annotation update)		
DE	Hypothetical protein O01005_Bll.2.			
GN	Names=O01005_Bll.2;			
OS	Oryza sativa (japonica cultivar-group).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;			
OC	Elephantidaceae; Oryzaceae; Oryza.			
OX	NCBI_TaxID=39947;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Chow T.-Y., Hsing Y.-I.-C., Chen C.-S., Chen H.-H., Liu S.-M.,			
RA	Chao Y.-T., Chang S.-J., Chen H.-C., Chen S.-K., Chen T.-R.,			
RA	Chen Y.-L., Cheng C.-H., Chung C.-I., Han S.-Y., Hsiao S.-H.,			
RA	Hsiung J.-N., Hsu C.-H., Huang J.-J., Kau P.-I., Lee M.-C., Leu H.-L.,			
RA	Li Y.-F., Lin S.-J., Lin Y.-C., Wu S.-W., Yu C.-Y., Yu S.-W.,			
RA	Wu H.-P., Shaw J.-F.;			
RL	Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.			
DR	EMBL: AC108873; AAT44133.1; -			
DR	InterPro; IPR000184; Bac_surfag_D15.			
DR	Pfam; PF01103; Bac_surface_Ag; 1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 361 AA; 2737C18B5F63779E CRC64;			
Query Match	1.1%; Score 9; DB 2; Length 361;			
Best Local Similarity	100.0%; Pred. No. 8.8;			
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	654 GGLGSRVGRY 662			
DB				
	255 GGLGSRVGRY 263			
RESULT 11				
Q9LXP7				
ID	Q9LXP7	PRELIMINARY;	PRT;	435 AA.
AC	Q9LXP7;			
DT	01-OCT-2000	(TrEMBLrel. 15, Created)		
DT	01-OCT-2000	(TrEMBLrel. 15, Last sequence update)		
DT	01-MAR-2004	(TrEMBLrel. 26, Last annotation update)		
DE	Hypothetical protein F26G5_110.			
GN	Names=F26G5_110;			
OS	Arabidopsis thaliana (Mouse-ear cress).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;			
OC	eurosid II; Brassicales; Brassicaceae; Arabidopsids.			
OX	NCBI_TaxID=3702;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	D'Angelo M., Verzi A., Modesto D., Pigazzi M., Valle G., Mewes H.W.,			
RA	Rudd S., Lemcke K., Mayer K.F.X., Quetier F., Salanoubat M.;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RA	EU Arabidopsis sequencing project;			
RL	Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.			
DR	EMBL; AL353814; CAB88424.1; -			
DR	PIR; T49132; T49132.			
DR	InterPro; IPR000184; Bac_surfag_D15.			
DR	Pfam; PF01103; Bac_surface_Ag; 1.			
KW	Hypothetical protein.			
SQ	SEQUENCE 435 AA; 47528 MW; C148B36074E49427 CRC64;			
Query Match	1.1%; Score 9; DB 2; Length 435;			
Best Local Similarity	100.0%; Pred. No. 10;			
Matches	9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	654 GGLGSRVGRY 662			

```

RL  Nat. Biotechnol. 22:547-553(2004).
DR  EMBL; AE017303; AAS81120.1; -.
DR  GO; GO:0000175; F:3'-5'-exoribonuclease activity; IEA.
DR  GO; GO:0003723; F:RNA binding; IEA.
DR  GO; GO:0006396; F:RNA processing; IEA.
DR  InterPro; IPR001247; 3 ExonNase.
DR  InterPro; IPR004088; KH type 1.
DR  InterPro; IPR008994; Nucleic_acid_OB.
DR  InterPro; IPR003029; S1.
DR  Pfam; PF00013; KH_1; 1.
DR  Pfam; PF03726; PNPase; 1.
DR  Pfam; PF01138; RNase PH; 2.
DR  Pfam; PF01725; RNase PH_C; 2.
DR  Pfam; PF00575; S1; 1.
DR  SMART; SM00322; KH; 1.
DR  SMART; SM00316; S1; 1.
DR  PROSITE; PS50084; KH_TYPE_1; 1.
DR  PROSITE; PS50126; S1; 1.
KW  Complete proteome.
SQ  SEQUENCE 713 AA; 78192 MW; 2979859D9AC5EA82 CRC64;

Query Match      1.1%; Score 9; DB 2; Length 713;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  362 DEVVRELR 370
DB  310 DEVVRELR 318
|||||

RESULT 14
Q62JD2  PRELIMINARY; PRT; 769 AA.
AC  Q62JD2;
DT  25-OCT-2004 (TrEMBLrel. 28, Created)
DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT  23-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Outer membrane protein, OMP85 family.
GN  ORFNames=BMA1547;
OS  Burkholderia mallei ATCC 23344.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC  Burkholderiaceae; Burkholderia.
OC  NCBI_TaxID=243160;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=ATCC 23344;
RA  Nieman W.C., DeShazer D., Kim H.S., Tettelin H., Nelson K.R.,
RA  Feldblyum T., Ulrich R.L., Ronning C.M., Brinkac L.M., Daugherty S.C.,
RA  Davidson T.D., Deboy R.T., Dimitrov G., Dodson R.J., Durkin A.S.,
RA  Winn M.L., Haft D.H., Khouri H., Kolonay J.F., Madupu R.,
RA  Mohammed Y., Nelson W.C., Radune D., Romero C.M., Sarria S.,
RA  Selengut J., Shamblin C., Sullivan S.A., White O., Yu Y., Zafar N.,
RA  Zhou L., Frazer C.M.;
RT  "Structural flexibility in the Burkholderia mallei genome.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:14247-14251(2004).
DR  EMBL; CP000010; AAU47747.1; -.
SQ  SEQUENCE 769 AA; 84848 MW; AADD3DE1446B20E0 CRC64;

Query Match      1.1%; Score 9; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  360 TRDEVVRRE 368
DB  367 TRDEVVRRE 375
|||||

Search completed: July 6, 2005, 15:50:38
Job time : 214 secs

```

```

DT  25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT  25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE  Putative outer membrane protein.
GN  ORFNames=BPSL2151;
OS  Burkholderia pseudomallei K96243.
OC  Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC  Burkholderiaceae; Burkholderia.
OC  NCBI_TaxID=272560;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=X96243;
RX  PubMed=15377794;
RA  Holden M.T.G., Titball R.W., Peacock S.J., Cerdano-Tarraga A.M.,
RA  Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA  Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA  Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA  Chillingworth T., Cronin A., Crossset B., Davis P., DeShazer D.,
RA  Fellwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA  Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA  Rabinowitsch E., Rutherford K., Sanders M., Simmonds M.,
RA  Songvilai S., Stevens K., Tumapa S., Vesaratchavest M.,
RA  Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
RT  "Genomic plasticity of the causative agent of melioidosis,
RT  Burkholderia pseudomallei.";
RL  Proc. Natl. Acad. Sci. U.S.A. 101:14240-14245(2004).
DR  EMBL; BX571965; CAH36153.1; -.
SQ  SEQUENCE 769 AA; 84906 MW; 9E0E33B0197B11B1 CRC64;

Query Match      1.1%; Score 9; DB 2; Length 769;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  360 TRDEVVRRE 368
DB  367 TRDEVVRRE 375
|||||

Search completed: July 6, 2005, 15:50:38
Job time : 214 secs

```

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 222.937 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4
Perfect score: 4152
Sequence: 1 MKLKQIASALMLGIGISPLAF.....LKKKPEDEIQRFQGLGTF 797

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4152	100.0	797	2 O30912	O30912 neisseria m
2	4140	99.7	797	2 O9KLH0	O9KLH0 neisseria m
3	4136	99.6	797	2 O9JX31	O9JX31 neisseria m
4	3937.5	94.8	792	2 P95359	P95359 neisseria g
5	2052	49.4	771	2 O7NVY6	O7NVY6 chromobacte
6	1555.5	37.5	758	2 O82U03	O82U03 nitrosomona
7	1497.5	36.1	765	2 O8X2I3	O8X2I3 ralstonia s
8	1477	35.6	769	2 O63T20	O63T20 burkholderi
9	1476	35.5	769	2 O62JD2	O62JD2 burkholderi
10	1395.5	33.6	778	2 O7VYC2	O7VYC2 bordetella
11	1392.5	33.5	778	2 O7WJ86	O7WJ86 bordetella
12	1384.5	33.3	778	2 O7WA52	O7WA52 bordetella
13	1320	31.8	795	2 O88GNS	O88GNS pseudomonas
14	1295	31.2	786	2 O88MH2	O88MH2 pseudomonas
15	1279.5	30.8	797	2 O9HXI4	O9HXI4 pseudomonas
16	1279	30.8	787	2 O88HI4	O88HI4 pseudomonas
17	1259.5	30.3	788	2 O8PML3	O8PML3 xanthomonas
18	1254	30.2	784	2 O87E11	O87E11 xylella fas
19	1252.5	30.2	825	2 O6FCG7	O6FCG7 acinetobact
20	1249	30.1	818	2 O8PAW1	O8PAW1 xanthomonas
21	1241	29.9	784	2 O9PE12	O9PE12 xylella fas
22	1240	29.9	797	2 O7N8N9	O7N8N9 photorhabdu
23	1226	29.5	797	2 O9S341	O9S341 photorhabdu
24	1213.5	29.2	814	2 O6D8D5	O6D8D5 erwinia car
25	1212	29.2	803	2 O8Z9A3	O8Z9A3 salmonella
26	1206.5	29.1	826	2 O8EGG7	O8EGG7 shewanella
27	1201.5	28.9	804	2 O8ZRP0	O8ZRP0 salmonella
28	1198	28.9	805	2 O6LN32	O6LN32 photobacter
29	1197	28.8	795	2 O667J7	O667J7 versinia ps
30	1197	28.8	795	2 O8ZHS8	O8ZHS8 versinia pe
31	1192.5	28.7	804	2 O87ME5	O87ME5 vibrio para

32	1180.5	28.4	804	2 O7MIG8	O7MIG8 vibrio vuln
33	1180.5	28.4	804	2 O8DBF3	O8DBF3 vibrio vuln
34	1178.5	28.4	810	1 UP05 ECOLI	UP05 ECOLI
35	1168.5	28.1	810	2 O8KR94	O8KR94 escherichia
36	1168	28.1	803	2 O9KPW0	O9KPW0 vibrio chol
37	1161	28.0	785	2 O9R2E3	O9R2E3 escherichia
38	1160	27.9	789	2 O6SR79	O6SR79 mannheimia
39	1159	27.9	808	2 O6Q8T1	O6Q8T1 uncultured
40	1148	27.6	793	2 O93PM2	O93PM2 haemophilus
41	1136	27.4	797	1 D151_HAEIN	D151_HAEIN
42	1135	27.3	795	1 D152_HAEIN	D152_HAEIN
43	1122.5	27.0	792	2 O326Z5	O326Z5 haemophilus
44	1116	26.9	793	1 D153_HAEIN	D153_HAEIN
45	1113	26.8	803	2 O83DT2	O83DT2 coxiella bu

ALIGNMENTS

RESULT 1

ID	O30912	PRELIMINARY;	PRT;	797 AA.
AC	O30912;			
DT	01-JAN-1998 (Tremblrel. 05, Created)			
DT	01-JAN-1998 (Tremblrel. 05, Last sequence update)			
DT	01-MAR-2004 (Tremblrel. 26, Last annotation update)			
DE	Outer membrane protein Omp85.			
GN	Name=omp85;			
OS	Neisseria meningitidis.			
OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;			
OC	Neisseriaceae; Neisseria.			
OX	NCBI_TaxID=487;			
[1]				
RN	SEQUENCE FROM N.A.			
RC	STRAIN=HH;			
RX	MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;			
RA	Manning D.S., Reschke D.K., Judd R.C.;			
RT	"Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis			
RT	are similar to Haemophilus influenzae D-15-Ag and Pasteurella			
RT	multocida Oms87.";			
RL	Microb. Pathog. 25:11-21 (1998).			
DR	EMBL; AF021245; AAC17599.1; "			
DR	InterPro; IPR000184; Bac_surfAg D15.			
DR	InterPro; IPR010827; Surf_Ag_VNR.			
DR	Pfam; PF01103; Bac surface_Ag; 1.			
DR	Pfam; PF07244; Surf_Ag_VNR; 5.			
SQ	SEQUENCE 797 AA; 88539 MW; CF911B5F70B999CF CRC64;			

Query Match	100.0%	Score 4152;	DB 2;	Length 797;
Best Local Similarity	100.0%	Pred. No. 5.3e-234;	Mismatches 0;	Indels 0;
Matches 797;	Conservative 0;			Gaps 0;
OY	1	MKLKQIASALMLGIGISPLAFADFTI	QIRVEGIQRTSPSTVFNYPVKVGDTYNDTHGSA	60
Db	1	MKLKQIASALMLGIGISPLAFADFTI	QIRVEGIQRTSPSTVFNYPVKVGDTYNDTHGSA	60
OY	61	ITKSLYATGFFDDVRVETADGQLLLT	VIERTPTIGSLNITGAKMLQNDATKKNLESFGLAQ	120
Db	61	ITKSLYATGFFDDVRVETADGQLLLT	VIERTPTIGSLNITGAKMLQNDATKKNLESFGLAQ	120
OY	121	SOYFNOATLNQAVAGKEEYVGRGKLN	QITPKVTKLARNVDITIDTIDEGSAKITDIE	180
Db	121	SOYFNOATLNQAVAGKEEYVGRGKLN	QITPKVTKLARNVDITIDTIDEGSAKITDIE	180
OY	181	FEQNOYVSRDKLMRQMSLTGGIWTW	LTSSNQNEQFAQDMKVTDFFYONNGYFFPRIL	240
Db	181	FEQNOYVSRDKLMRQMSLTGGIWTW	LTSSNQNEQFAQDMKVTDFFYONNGYFFPRIL	240
OY	241	DTDIDQTNEDKTKQITIKITVHEGGR	FRWGKVSIEGDTNEVPKAELEKLLTMKPKGYERQQ	300
Db	241	DTDIDQTNEDKTKQITIKITVHEGGR	FRWGKVSIEGDTNEVPKAELEKLLTMKPKGYERQQ	300
OY	301	MTAVLGEIQNRMGSGAYISVQPLPNA	EFTKTVDFVLHIEPGRKIYNEIHITGNKKT	360

Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNK 360
Qy 361 RDEVVRRELQMESAPYDTSKLRSEKVELLGYFDNVQDPAVPLAGTPDKVDLNSLSTE 420
Db 361 RDEVVRRELQMESAPYDTSKLRSEKVELLGYFDNVQDPAVPLAGTPDKVDLNSLSTE 420
Qy 421 RSTGSLDLSAGWQDVTGLVNSAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSTPDYF 480
Db 421 RSTGSLDLSAGWQDVTGLVNSAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSTPDYF 480
Qy 481 DGVSGLGYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTV 540
Db 481 DGVSGLGYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTV 540
Qy 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAE 600
Db 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAE 600
Qy 601 LPGSKLOYYSATHNQWTFPFLSKTFTLLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPFLSKTFTLLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDVEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDVEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KYDDNSSSAGTGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPKMFYAYPLKK 780
Db 721 KYDDNSSSAGTGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPKMFYAYPLKK 780
Qy 781 KPEDEIQRFQFOLGTTTF 797
Db 781 KPEDEIQRFQFOLGTTTF 797

RESULT 2

Q9K1H0 ID Q9K1H0 PRELIMINARY; PRT; 797 AA.
AC Q9K1H0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN OrderedLocusNames=NM0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxId=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterone H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qian H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizzi M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
MC58";
RL Science 287:1809-1815(2000).
DR EMBL; AE002375; AAF40639.1; -.
DR TIGR; G81228; G81228.
DR PIR; NM0182; -.
DR InterPro; IPR00184; Bac surfAg D15.
DR ExePro; IPR010827; SurF_Ag_VNR.
DR Pfam; PF01103; Bac surface_Ag_1.
DR Pfam; PF07244; SurF_Ag_VNR; 5.
KW Complete proteome.

SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A43D22EE8 CRC64;
Query Match 99.7%; Score 4140; DB 2; Length 797;
Best Local Similarity 99.7%; Pred. No. 2.7e-233;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MKLKQIASLMMGLGISPLAPADFTIODIRVEGLQRTPESTVFNYLVPKVGDTYNDTHGSA 60
Db 1 MKLKQIASLMMGLGISPLALADFTIODIRVEGLQRTPESTVFNYLVPKVGDTYNDTHGSA 60
Qy 61 ITKSLYATGFDDVRVETADGQLLTVERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 ITKSLYATGFDDVRVETADGQLLTVERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITDIE 180
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITDIE 180
Qy 181 FEGNQVYSRKLQMRQMSLTEGGIWTWTRSNQFNEQKFAQDMKVKVDFYQNNGYDFRIL 240
Db 181 FEGNQVYSRKLQMRQMSLTEGGIWTWTRSNQFNEQKFAQDMKVKVDFYQNNGYDFRIL 240
Qy 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSLEGDTNEVPKAELEKLLTMKPKGVYERQ 300
Db 241 DTDIOTNEDKTKOTIKITVHEGGRFRWGVKVSLEGDTNEVPKAELEKLLTMKPKGVYERQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNK 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNK 360
Qy 361 RDEVVRRELQMESAPYDTSKLRSEKVELLGYFDNVQDPAVPLAGTPDKVDLNSLSTE 420
Db 361 RDEVVRRELQMESAPYDTSKLRSEKVELLGYFDNVQDPAVPLAGTPDKVDLNSLSTE 420
Qy 421 RSTGSLDLSAGWQDVTGLVNSAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSTPDYF 480
Db 421 RSTGSLDLSAGWQDVTGLVNSAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSTPDYF 480
Qy 481 DGVSGLGYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTV 540
Db 481 DGVSGLGYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTV 540
Qy 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAE 600
Db 541 YNKAPKHAYADFIKKYKGTGTDGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAE 600
Qy 601 LPGSKLOYYSATHNQWTFPFLSKTFTLLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPFLSKTFTLLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDVEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDVEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KYDDNSSSAGTGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPKMFYAYPLKK 780
Db 721 KYDDNSSSAGTGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPKMFYAYPLKK 780
Qy 781 KPEDEIQRFQFOLGTTTF 797
Db 781 KPEDEIQRFQFOLGTTTF 797
RESULT 3
Q9JX31 ID Q9JX31 PRELIMINARY; PRT; 797 AA.
AC Q9JX31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NWA0085;
OS Neisseria meningitidis (serogroup A).

OC	Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;	
OC	Neisseriaceae; Neisseria.	
OX	NCBI_TaxID=65699;	
RP	[1]	
RN	SEQUENCE FROM N.A.	
RC	STRAIN=Z2491 / Serogroup A / Serotype 4A;	
RX	MEDLINE=2022256; PubMed=10761919; DOI=10.1038/35006655;	
RA	Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,	
RA	Klee S.R., Morelli G., Baahm D., Brown D., Chillingworth T.,	
RA	Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,	
RA	Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,	
RA	Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,	
RA	Whitehead S., Spratt B.G., Barrall B.G.;	
RT	"Complete DNA sequence of a serogroup A strain of Neisseria	
RT	meningitidis Z2491";	
RL	Nature 404:502-506(2000).	
DR	EMBL; AL162752; CAB83401.1; -.	
DR	PIR; D82000.	
DR	InterPro; IPR00184; Bac surfAg D15.	
DR	InterPro; IPR010827; Surf_Ag_VNR.	
DR	Pfam; PF01103; Bac surface_Ag; 1.	
DR	Pfam; PF07244; Surf_Ag_VNR; 5.	
KW	Complete proteome.	
SQ	SEQUENCE 797 AA; 88404 MW; 65DE47E00C9E1D1F CRC64;	
Query Match 99.68; Score 4136; DB 2; Length 797;		
Best Local Similarity 99.68; Pred. No. 4.5e-233;		
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;		
QY	1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60
DB	1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60
QY	61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120
DB	61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120
QY	121 SOYFNOATLNOAVAGLKEEYVLRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIE	180
DB	121 SOYFNOATLNOAVAGLKEEYVLRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIE	180
QY	181 FEGNOVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL	240
DB	181 FEGNOVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL	240
QY	241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ	300
DB	241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ	300
QY	301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPRKIYNEIHTGNKT	360
DB	301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPRKIYNEIHTGNKT	360
QY	361 RDEVVRRELQMESAPYDTSKLORSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL	420
DB	361 RDEVVRRELQMESAPYDTSKLORSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL	420
QY	421 RSTGSLDLSAGVQDTGLVMSAGVSQDNLFCTGKSAALRASRKTLLNGSLSTFDPYFTA	480
DB	421 RSTGSLDLSAGVQDTGLVMSAGVSQDNLFCTGKSAALRASRKTLLNGSLSTFDPYFTA	480
QY	481 DGVSLGVDYVTKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
DB	481 DGVSLGVDYVTKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
QY	541 YNKAPHYADP IKKYGKTGDCGSKWLYKGTGWRNKTDSALMPTRCYLTVGNVABIA	600
DB	541 YNKAPHYADP IKKYGKTGDCGSKWLYKGTGWRNKTDSALMPTRCYLTVGNVABIA	600
QY	601 LPGSKLOYISATHNQTFWFFLSKTFITLMLGGEVGIAGGYRTKEIIPFFENFYGGGLGSVR	660
DB	601 LPGSKLOYISATHNQTFWFFLSKTFITLMLGGEVGIAGGYRTKEIIPFFENFYGGGLGSVR	660
Query Match 94.88; Score 3937.5; DB 2; Length 792;		
Best Local Similarity 95.18; Pred. No. 1.8e-221;		
Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;		
QY	1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60
DB	1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60
QY	61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120
DB	61 IIKSLYATGFFDVRVETADQGLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ	120
QY	121 SOYFNOATLNOAVAGLKEEYVLRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIE	180
DB	121 SOYFNOATLNOAVAGLKEEYVLRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIE	180
QY	181 FEGNOVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL	240
DB	181 FEGNOVYSRDKLMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVDFYQNGYFDFRIL	240
QY	241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ	300
DB	241 DTDIQTNEKTKQTIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQ	300
QY	301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPRKIYNEIHTGNKT	360
DB	301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPRKIYNEIHTGNKT	360
QY	361 RDEVVRRELQMESAPYDTSKLORSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL	420
DB	361 RDEVVRRELQMESAPYDTSKLORSKERVVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL	420

QY 421 RSTGSLDSAGWQDTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
 DB 421 RSTGSLDSAGWQDTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
 QY 481 DGVSGLGVYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPTVEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSGLGVYDVYKAPDPKPKASTSVKQYKTTTAGGVRMGIPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYKTDGTSFGKWLKGTGVRGNKTDGALWPTGRLYLGTVNAEIA 600
 DB 541 YNKAPKHYADFIKKYKTDGTSFGKLLYKGTGVRGNKTDGALWPTGRLYLGTVNAEIA 600
 QY 601 LPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
 DB 601 LPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
 QY 661 GYSGTGLPKVYDEYGEKISYGGNKKANVSAEALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYSGTGLPKVYDEYGEKISYGGNKKANVSAEALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 780
 DB 721 RTY-----TAENGNKSVY-SENAHKSFTNELRYSAGGAVTWLSPGPMKFRYAYPLKK 775
 QY 781 KPEDEIQRFOQLGTTTF 797
 DB 776 KPEDEIQRFOQLGTTTF 792

RESULT 5
 Q7NVY6
 ID Q7NVY6 PRELIMINARY; PRT; 771 AA.
 AC Q7NVY6
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Probable outer membrane protein.
 GN OrderedLocusNames=CV2204;
 OS Chromobacterium violaceum.
 OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
 OC Neisseriaceae; Chromobacterium.
 OX NCBI_TaxID=536;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 12472 / DSM 30191;
 RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
 RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
 RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
 RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.P.,
 RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
 RA Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
 RA Bordignon J., Brígido M.M., Brito C.A., Brocchi M., Burity H.A.,
 RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
 RA Carvalho C.M.B., Cascado J.C.M., Cavada B.S., Chueire L.M.O.,
 RA Crezynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
 RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
 RA Ferro M.I.T., Franco G.R., Freitas M.S.A., Furlan L.R.,
 RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
 RA Grattapaglia D., Grisar E.C., Hanna E.S., Jardim S.N., Laurino J.,
 RA Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.P.,
 RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
 RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
 RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
 RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
 RA Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
 RA Ramalho-Neto C.B., Reis A.M.M., Rigo L.U., Rondinelli E.,
 RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanez H.N.,
 RA Silva A.M.R., da Silva A.I.C., Silva D.W., Silva R., Simoes I.C.,
 RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
 RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
 RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
 RT "The complete genome sequence of Chromobacterium violaceum reveals

RT remarkable and exploitable bacterial adaptability.";
 RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665 (2003).
 DR EMBL; AE016917; AAQ59877.1; -;
 DR InterPro; IPR000184; Bac_surfAg D15.
 DR InterPro; IPR010827; Surf_Ag_VNR.
 DR Pfam; PF01103; Bac_surface_Ag; 1.
 DR Pfam; PF07244; Surf_Ag_VNR; 5.
 KW Complete proteome.
 SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;
 Query Match 49.4%; Score 2052; DB 2; Length 771;
 Best Local Similarity 50.5%; Pred. No. 2.3e-111;
 Matches 404; Conservative 140; Mismatches 224; Indels 32; Gaps 9;
 QY 1 MKLKLQIASALMMLGISPLAFA--DFTIQDIRVEGLQRTPEFTVFNLYLPVKVGYDNTDTHG 58
 DB 1 MKLKLQIASALMMLGISPLAFA--DFTIQDIRVEGLQRTPEFTVFNLYLPVKVGYDNTDTHG 58
 QY 59 SAIIKSLYATGFPDDVRVETADGQLLTIVIERPTIGSLNITGAKMLONDAIKQNLSEFGL 118
 DB 59 SAIIKSLYATGFPDDVRVETADGQLLTIVIERPTIGSLNITGAKMLONDAIKQNLSEFGL 118
 QY 61 KEAIKALFGTGFENDVRVESRGDTLIVTVAERPVIQTQNINGAKESKQDKKALKDNGF 120
 DB 61 KEAIKALFGTGFENDVRVESRGDTLIVTVAERPVIQTQNINGAKESKQDKKALKDNGF 120
 QY 119 AQSOYFNQATLQAVAGLKEEYLGRGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
 DB 119 AQSOYFNQATLQAVAGLKEEYLGRGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
 QY 121 AESLIPDQALLDGAQVELKRYYSRGKYSVEITPTVTKLERNRVAVTLDINEGVTAIRE 180
 DB 121 AESLIPDQALLDGAQVELKRYYSRGKYSVEITPTVTKLERNRVAVTLDINEGVTAIRE 180
 QY 179 IBPEGNQVYSDRKLNRQMSLTGEGIWTWLTNRNQFNEQKFAODMEKVTDFYQNNGYDFDR 238
 DB 179 IBPEGNQVYSDRKLNRQMSLTGEGIWTWLTNRNQFNEQKFAODMEKVTDFYQNNGYDFDR 238
 QY 181 IRIVGANAFQSKLLDDEFSLTITGGWLSWITKDDQYSKQKLTGDLKAKAFYQNOGYMEG 240
 DB 181 IRIVGANAFQSKLLDDEFSLTITGGWLSWITKDDQYSKQKLTGDLKAKAFYQNOGYMEG 240
 QY 239 ILDTDIQTNEDKTKQTIKITVHEGGRFRWGKYSIEGDTNEVPKAELEKLLTWKPGKWER 298
 DB 239 ILDTDIQTNEDKTKQTIKITVHEGGRFRWGKYSIEGDTNEVPKAELEKLLTWKPGKWER 298
 QY 241 IDSSQVSIQADKKDMYLVNVNHEGKKTYSVDVRLAGDL-KVPEAEMLKMLQVKRGDTFNN 299
 DB 241 IDSSQVSIQADKKDMYLVNVNHEGKKTYSVDVRLAGDL-KVPEAEMLKMLQVKRGDTFNN 299
 QY 299 QQMTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKLYVNEIHTGNN 358
 DB 299 QQMTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKLYVNEIHTGNN 358
 QY 300 EKVTESVKALSDRLGNEGYAFANVNLDPIDREKQTAFTFFVDPGRKTYVRVRVAGNS 359
 DB 300 EKVTESVKALSDRLGNEGYAFANVNLDPIDREKQTAFTFFVDPGRKTYVRVRVAGNS 359
 QY 359 KTRDEVVRRELQMESAPYDTSKLORSKERVLLGYFDVNVQDPAVPLAGTTPDKVDLNMSL 418
 DB 359 KTRDEVVRRELQMESAPYDTSKLORSKERVLLGYFDVNVQDPAVPLAGTTPDKVDLNMSL 418
 QY 360 KTRDEVIRRELQLEGAPYNAANVKERLELLGYFEDVNVETPAVADAPQVDNIGL 419
 DB 360 KTRDEVIRRELQLEGAPYNAANVKERLELLGYFEDVNVETPAVADAPQVDNIGL 419
 QY 419 TERSTGSLDSAGWQDTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYF 478
 DB 419 TERSTGSLDSAGWQDTGLVMSAGVSDNLFCTGKSAALRASRSKTTTLNGSLSFDPYF 478
 QY 420 KERSTGSIQSLGYVQGEGLVLANISQSNIRFSGKYSMLGMSGTGKVNKNYSLSFTDPYF 479
 DB 420 KERSTGSIQSLGYVQGEGLVLANISQSNIRFSGKYSMLGMSGTGKVNKNYSLSFTDPYF 479
 QY 479 TADGSLGVYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPTVEYDRVNFGLVAEHLTV 538
 DB 479 TADGSLGVYDVYKAPDPKPKASTSIKQYKTTTAGAGIRMSVPTVEYDRVNFGLVAEHLTV 538
 QY 480 TPDGSLGVYDLYNRVYNP--DATSISAYKTSITTGADMRFGVPIEYDRINFTIGAERTDI 537
 DB 480 TPDGSLGVYDLYNRVYNP--DATSISAYKTSITTGADMRFGVPIEYDRINFTIGAERTDI 537
 QY 539 NTYNKAPKHYADFIKKYKTDGTSFGKWLKGTGVRGNKTDGALWPTGRLYLGTVNAE 598
 DB 539 NTYNKAPKHYADFIKKYKTDGTSFGKWLKGTGVRGNKTDGALWPTGRLYLGTVNAE 598
 QY 538 TTYNSPQYIDFVKQYGNSTY-----VLGTVGWGRDTRDSALWTRGASIRVNAD 589
 DB 538 TTYNSPQYIDFVKQYGNSTY-----VLGTVGWGRDTRDSALWTRGASIRVNAD 589
 QY 599 IALPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGS 658
 DB 599 IALPGSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGS 658
 QY 590 FGLPGGLQYSLYTHQQTWFFPLSKDFTLMLNGELGYADGYGKTKQLPFFKQFYMGGLGS 649
 DB 590 FGLPGGLQYSLYTHQQTWFFPLSKDFTLMLNGELGYADGYGKTKQLPFFKQFYMGGLGS 649
 QY 659 VRGYESGTLPKPYDEYGEKISY-CGNKKNVSAEALLFPMPGAKDARTVRLSLFADAGSV 717
 DB 659 VRGYESGTLPKPYDEYGEKISY-CGNKKNVSAEALLFPMPGAKDARTVRLSLFADAGSV 717
 QY 650 VRGYDSSSTGIP--YDSVAN--SYLGNRRKAVANVELFFPFGMKDKNSLRTSLFFDAGLT 705
 DB 650 VRGYDSSSTGIP--YDSVAN--SYLGNRRKAVANVELFFPFGMKDKNSLRTSLFFDAGLT 705
 QY 718 WDQKTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYP 777
 DB 718 WDQKTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGPMKFRYAYP 777
 QY 706 W-----NTNLTAEKAQGI-----TSSPDGFRYSAGLALTWLSPMGPMKFRYAYP 751
 DB 706 W-----NTNLTAEKAQGI-----TSSPDGFRYSAGLALTWLSPMGPMKFRYAYP 751
 QY 778 LKXKPEDEIQRFOQLGTTTF 797
 DB 752 LKXKPEDEIQRFOQLGTTTF 771

RESULT 6
 Q82U03

ID Q82U03 PRELIMINARY; PRT; 758 AA.
AC Q82U03;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Bacterial surface antigen (D15).
GN OrderedLocusNames=NE1710;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19718 / IF0 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
HAUSER L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.,
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
obligate chemolithoautotroph Nitrosomonas europaea";
RL J. Bacteriol. 185:2759-2773 (2003).
DR ENBL; BX321862; CAD85621.1; -;
DR InterPro; IPR000184; Bac surfAg D15.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 758 AA; 85016 MW; 6B9630B7124B06C9 CRC64;

Query Match 37.5%; Score 1555.5; DB 2; Length 758;
Best Local Similarity 38.4%; Pred. No. 2.3e-82;
Matches 306; Conservative 167; Mismatches 285; Indels 39; Gaps 7;

QY 1 MKLQIASALMLGIGSLAPAFDTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLRFILFSLYSLGCMANDSLVWRDIRVEGIQRTAGTFVFPVKVGDVLDKSKASA 60

QY 61 IISKLVATGFFDVRVETADGQLLTIVERTPTGSLNITGAKMLQNDKAKNLESLGLAQ 120
DB 61 AIKALYATGFFSDVKLSEGLLIVQVPERPAIAQISNGAKEFDKDKLKEGKQAGLSE 120

QY 121 SQVFNQATLNQAVAGLKEEYGLRGKLNIOITPKVTKLARNRVDITIDGSKAKITDIE 180
DB 121 SRIFSRLLEKAEQELKQRIYSKGVAKITTTTTPLERNRIGNIDIEKGTAKRIKQIN 180

QY 181 FEGNQVYSDRLKMRQSLTEGGITWLTLSRQNEQKFAQDMKVDFYQNNGYDFDFRIL 240
DB 181 IVGNHVFPEDDLVDLFLSLKTPGFWFTKDDQYSKQKLSADLETLSYLLDRGLSEFNIE 240

QY 241 DTDIQNEDKTKOTIKITVHEGGRFRWKVSIQVPLPNAETKTVDFVLHIEPRKIYNEIHTGNKT 300
DB 241 STQVSTIPDMKDIYITVNVTEGPQYTVSDIKLAGEL-LVPEELRLKLIKLEPGGIFVREK 299

QY 301 MTAVLGEIQNEMSGAGVAYSEISVQPLPNAETKTVDFVLHIEPRKIYNEIHTGNKT 360
DB 300 LTSISIKLISDLRGNDGYAFANVASPELDKETRTAFTFFIDPGRYVVRINISGNERT 359

QY 361 RDEVRRELQMESAPYDTSKLOSKERVELLGVFDNVQFADVPLAGTPKVDLNNLSLTE 420
DB 360 RDEVIRREFQMEGGWHSTEQINRSQRVDRLOFFFTGVNIETFPVADVPQVDINNVVE 419

QY 421 RSTGSLDLSAGVQDVTGLNMSAGVSQDNLFGTGKSAALRASRSTKTLNGLSLSTDPYFTA 480
DB 420 KPTGAIMFGAGYSDREGIILNGSIAQNNILGTGFLSLQVNTGSKVNVKVISASFNPNPYTI 479

QY 481 DGVSLGVDYVTKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHTVNT 540
DB 480 NGVSLGLEAFKRDINTSLSL-SVGMFNTDTGTANIRFGIPVAENDIVSLGLGYEHTKIDL 538

QY 541 YNKAHPYADFIKYKGTGDTGDSFGKWLKGTGWRGNKNTSDSLMPTTRGKYLGVNAEIA 600
DB 539 RDDSPPQRKFVDQFGKISNN-----LPITLSWARDRRNSAIWTTSGTQRLFGEGF 590

QY 601 LPSGKLOYYSATHNOTWTFPLSKTFTMLGGEVGIAGGYGRTKETIPFFENFYGGGLGSVR 660
DB 591 LPFGDLNYYKVSVEQRWFVTFKMTMLNGEVGVGDYS-DKPLFFKXFFAGGNSVR 649

QY 661 GYESGTLGPKVYDEYGEKISYGCNKANYSAELLFPMPCAKAARTVRLSLFADAGSVDG 720
DB 650 GYNINTLGPDRSDDR---VLGSKRIVGNIEVLFPVPFWMKEDKSVRLSAFADGGTI--- 702

QY 721 KYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
DB 703 -----VNSFSLG-----FDDFRYSAGLAATWISPMGLKFSVAQPLNN 741

QY 781 KPDEIQRFQFOLGTF 797
DB 742 QSGDKLQRFQFQGT 758

RESULT 7
Q8XZ13 PRELIMINARY; PRT; 765 AA.
ID Q8XZ13;
AC Q8XZ13;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.
GN Name=RS05280; OrderedLocusNames=RScl412;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
RA Siguer P., Thebaud P., Boucher C.A.;
RA Weissenbach J., Whalen M., Wincker P., Levy M.,
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";
RL Nature 415:497-502 (2002).
DR ENBL; AL645064; CAD15114.1; -;
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf Ag_VNR; 5.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 36.1%; Score 1497.5; DB 2; Length 765;
Best Local Similarity 37.5%; Pred. No. 5.7e-79;
Matches 301; Conservative 161; Mismatches 294; Indels 47; Gaps 9;

QY 3 LKQIASALMLGIGSLP-----AFADTIQDIRVEGLQRTPESTVFNYLPVKVGDYND 54
DB 2 IQRHFPFLSMLAASLVTVCAQAHAVERPVIKDIRVEGVRVEPFGVFGVLPVKVGETFT 61

QY 55 DTHGSAIKSLVATGFFDVRVETADGQLLTIVERTPTGSLNITGAKMLQNDKAKNLE 114
DB 62 DDKGAESIRALYNTGFFKDVQIRAEGLVVRVEERPAISQLEFIGKEFDKTLRSRL 121

QY 115 SFLQAQSYFNQATLNQAVAGLKEEYGLRGKLNIOITPKVTKLARNRVDITIDGSKSA 174
DB 122 GGVAEARYYDKSLIDRAEQELKQYVSRGYAAADVQTTVPVDANRVSVTFVDEGPA 181

QY 175 KITDIEFEGNQVYSDRLKMRQSLTEGGITWLTLSRQNEQKFAQDMKVDFYQNNGY 234
DB 182 KIRQINIVGNKAFSEGLDRDEMQLSTPNWLSWTKYNDLYSKQKLTADLRLSRYLDRGY 241

QY 235 FDFRILDTDIQTNEDKTKOTIKITVHEGGRFRWKVSIQVPLPNAETKTVDFVLHIEPRKI 294
DB 242 LSEFAESTQVSTPDKDIYILNTHIEGQYKSDIKLTGELLS-KQAEKELIKLKQGD 300


```

RESULT 10
Q7VYC2 PRELIMINARY;      PRT;      778 AA.
AC Q7VYC2;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable surface antigen.
GN OrderedLocuNames=BPI1427;
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_Taxid=520;
[1]
RN RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RC MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngi1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Munga
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S.J., Jagerl
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Pri
RA Rabinowitz E., Rutter S., Saunders M., Saunders D., Seeger K
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Ste
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RA "Comparative analysis of the genome sequences of Bordetella per
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640415; CAB4171.1; -.
DR InterPro; IPR0010184; Bac surfAg D15.
DR InterPro; IPR005479; Cphd synth_L D2.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf Ag VNR; 5.
DR PROSITE; PS00867; CPSASE 2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86408 MW; 41E3A869DBF0BACC CRC64;

Query Match 33.6%; Score 1395.5; DB 2; Length 778;
Best Local Similarity 36.0%; Pred. No.5e-73;
Matches 287; Conservative 169; Mismatches 299; Indels 43;

QY 6 IASALMMLGISPLAFADFTTQIDIRVEGLQRTSTVNYLPVKVGDYTDYDTHG
DB 18 LAALALAPALAH-AFEPFVVRDVRVEGIQRTDAGTVFGYLPVKVKGKFTDEEA
QY 66 YATGFFDDVRVETADGQLLTVTIERPTIGSLNTITGAKMLONDATKKNLESFGL
DB 77 YGTGFFSDVOIQTDNNVVVVVVGVERPTIASISFNGMREFDSKATKTSKLAQVGF
QY 126 QATLNOAVAGLKEEYLGKGLNKLIQTIPKVTKLARNRVIDIDITIDEGSKAKITD
DB 137 QSMLERAEYELKEQYLAGKGYGEVETATVPLPRNRVGVSGFDVFEGEVAKIRE
QY 186 VYSDRKMLQMSLTGEGITWLTFRSQNFNEQKFAQDMKEKVTDFVQNNNGYFDFR
DB 197 AFSEGEQLDQFDLTTPGWLTYNTDQYKSYREKLEGIERLRSFYLDQGYLEFTV
QY 246 TNEDKTKQTIKIVHGGFRFWKGVIEGDTNEVPKAELEKLLTMKCKGWYER
DB 257 ISDPKDXDIYITIVTHEGEPYKVRKVLKAGMLMGL-DSEINNVLKEIKGPEVFSJA
QY 306 GEIQNRMGSGAYVYSISVQPLNPAETKTVDFVLHITPGRKIYVNEHTITGNNN
DB 316 KAITNYLDGLGVAFANVPNPQLDRKHAEDVTYVDPSPRRVVRVRIQIGNTV
QY 366 RRELQWESAPYDTSKLORSKERVLLGYPDNYQFQDAVPLAGTDPKVDLNNLSLT
DB 376 RREMROOEAWYDAGDIPKYSRDRVDRIQYENEVNNKTPDPVSPDQVDVNDV

```

```
QY 426 LDLSAGVQDTGLVMSAGVSDNLFGTGKSAALRASRSKTTLLNGSLSFDTDPYTAGVSL 485
D 436 INLVGVYGSSEKAILSAGISEDNVFSGTNLTQLNTSKTNRAVLWLSHTDPYFTKDGISR 495
QY 486 GYDVYKAFDPKRASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAP 545
D 496 TTSAYRVTEPDNDNG--DYRVKAMGLGNVGFPISEYDRIFLGGTFFERNQDLNNNSP 553
QY 546 KHYADFIKTKYKTDGTDGSGFGLYKGTGVGRNKTDSALWPTRGYLTGVNABIALPGSK 605
D 554 QAYRDFVDQVG-----NSTNALIF--NTGWSKDRDSALAPTKGATRLKGDFT--MD 603
QY 606 LOYYSATHNOTWFFPLSKTTTLLMGGEVGTAGYGRTEKIPFPENFYGGGLSVRGVYEG 665
D 604 LKYYLLTAQQYYLPLGRSYTLALNGMIDYGRSYGGL-DYFVTKNVYAGGIGTVRGVEGA 662
QY 666 TLGP--KVYDEYGEKISYGNKNKANVSAELLFPMGAKDARTVRLSLFADAGSVWDGKTY 723
D 663 SLGPRDLTGDI-----IGSRMRVANAQILYLPFGASKDRTLRWFTDAGQVAAG--- 714
QY 724 DNSSSATGGR---VONIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLK 779
D 715 --SGMCTAGKPGSEVEDPCG-----WRFSAIGLSQSPGLQLSYARPLN 760
QY 780 KKPDEIQRFOFOLGTTFF 797
D 761 SKSGDDTQAFQFQIGTGF 778

RESULT 11
Q7WJ86 PRELIMINARY; PRT; 778 AA.
ID Q7WJ86 AC Q7WJ86;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable surface antigen.
GN OrderedLocusNames=BB2613;
OS Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl1227;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.-M., Baker S., Basham D., Bason N., Cherevach I.,
RA Achtman M., Atkin R., Toller S., Toller S., Toller S., Toller S.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leather S., Moulé S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RN Nat. Genet. 35:32-40(2003).
DR EMBL; BX640444; CAB33106.1; -.
DR InterPro; IPR00184; Bac_surAg_D15.
DR InterPro; IPR005479; Cphp_synth_L_D2.
DR InterPro; IPR010827; Surf_Ag_VNR_.
DR Pfam; PF01103; Bac_surface_Ag_1.
DR Pfam; PF07244; Surf_Ag_VNR_Ag_1.
DR PROSITE; PS00867; CFSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86352 MW; BF0CA34BFF501CCF CRC64;
```

Query Match 33.58; Score 1392.5; DB 2; Length 778;
Best Local Similarity 36.08; Pred. No. 7.9e-73;
Matches 287; Conservative 169; Mismatches 299; Indels 43; Gaps 12;

```
QY 6 IASALMMLGISPLAFADFTIQDIRVEGLQRTBPTVFNILPVKVGDTYNDTHGSALIKSL 65
D 18 LAAALAPALAH-AFEFFVVRDIRVEGIQRTAGTVFGYLPVKVGKFTDEEATEAVRRL 76
QY 66 YATGFPDDRVETADGQLLTIVERTIGTSLNITGAKMLQNDAIKNLESFGLAQSOYFN 125
D 77 YGTGFPDDVQIQDNNVVVVVQVERPTIASISFNGKREFDSKAITKSLAQVGEGEGRIFD 136
QY 126 QATLNOQAVAGLKEEYLRGKLANIQTIPKVTKLARNRVDIDITIDEGSKAKITIDIEFEGN 185
D 137 QSMLEAEAYELKQYLAAGKYGEVETATVPLPRNVGVSFDFEVEGAKIREIRVVGSK 196
QY 186 VYSRDLKMQMSITTEGIIWTLTRSNQFNEQPAQMEKVTDPYQNGVFPDRILOTDIQ 245
D 197 AFSEGEQLDQFDITTPGMLTWYNTDKYSREKLEGIERLSFYLPDQGLYFVEPPQVT 256
QY 246 TNEKTKQTKITVHGGFRGKVSIEGDTNEVPKAELEKLLTMKPGKWKYERQOMTAVL 305
D 257 ISPRKDIITITVHEGEPYKVRVKLAGNLMGL-DSEINNLVEIKPGEVFSAAKANNSA 315
QY 306 GEIQNRMSGAGYAYSISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHITGNKTRDEVV 365
D 316 KAITDVLGDLGYAFANVNPQDLRAKHEADVTFFYDPSRVVVRRIQIGENTRTRDEVV 375
QY 366 RRELROMESAPYDTSKLQSKERVLLGYFDNVQFPAVPLAGTPDKVDLNMSLTERSTGS 425
D 376 RREMROQEAAYDAGDIKVSRRDRVRLGYFENEVNVKTDVPVPGSPDQVDVNVYKERTGI 435
QY 426 LDLSAGVQDTGLVMSAGVSDNLFGTGKSAALRASRSKTTLLNGSLSFDTDPYTAGVSL 485
D 436 INLVGVYGSSEKAILSAGISEDNVFSGTNLTQLNTSKTNRAVLWLSHTDPYFTKDGISR 495
QY 486 GYDVYKAFDPKRASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAP 545
D 496 TTSAYRVTEPDNDNG--DYRVKAMGLGNVGFPISEYDRIFLGGTFFERNQDLNNNSP 553
QY 546 KHYADFIKTKYKTDGTDGSGFGLYKGTGVGRNKTDSALWPTRGYLTGVNABIALPGSK 605
D 554 QAYRDFVDQVG--DSTNALI-----FNTGWSKDRDSALAPTKGATRLKGDFT--MD 603
QY 606 LOYYSATHNOTWFFPLSKTTTLLMGGEVGTAGYGRTEKIPFPENFYGGGLSVRGVYEG 665
D 604 LKYYLLTAQQYYLPLGRSYTLALNGMIDYGRSYGGL-DYFVTKNVYAGGIGTVRGVEGA 662
QY 666 TLGP--KVYDEYGEKISYGNKNKANVSAELLFPMGAKDARTVRLSLFADAGSVWDGKTY 723
D 663 SLGPRDLTGDI-----IGSRMRVANAQILYLPFGASKDRTLRWFTDAGQVAAG--- 714
QY 724 DNSSSATGGR---VONIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLK 779
D 715 --SGMCTAGKPGSEVEDPCG-----WRFSAIGLSQSPGLQLSYARPLN 760
QY 780 KKPDEIQRFOFOLGTTFF 797
D 761 SKSGDDTQAFQFQIGTGF 778

RESULT 12
Q7WA52 PRELIMINARY; PRT; 778 AA.
ID Q7WA52 AC Q7WA52;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable surface antigen.
GN OrderedLocusNames=BPPI533;
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
```


RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ngl1227;
RA Parkhill J.E., Sebahia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroft S., Jagels K.,
RA Leather S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica";
RL Nat. Genet. 35:32-40(2003).
DR EMBL: BX640427; CAE36837.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; CphP synth_L_D2.
DR InterPro; IPR010827; Surf_Ag_VNR_1.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR_5.
DR PROSITE; PS00867; CFSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86342 MW; 15C8F0F43B865298 CRC64;

Query Match 33.3%; Score 1384.5; DB 2; Length 778;
Best Local Similarity 35.8%; Pred. No. 2.3e-72;
Matches 286; Conservative 169; Mismatches 300; Indels 43; Gaps 12;

QY 6 IASALMMLGISPLAFADFTQDIRVEGLQRTSTFVNYLPVKVGTQDYNTHGSAIKSL 65
DB 18 LAALAPALAH-AFEPFVVRDVRVEGIQRTDAGTVFGLPVKVGKFTDEATEAVRL 76

QY 66 YATGFFDDVRVETADGOLLTVIERPTIGSLNTGAKMLQNDIAKKNLESFGLAQSYFN 125
DB 77 YGTGFFSDVQIQDNNVVVVQVQERTIASISFNGKREPDSKAITKSLAQVGFGEGRIPD 136

QY 126 QATLNQAVAGLKEEYLGRKLNLTQIPKVTKLARNRVDIDITDEGSAKITDIEFEGNQ 185
DB 137 QSLMRAEYELKEQYLAQKGYGEVATVTPLPNRVGVGSFDFVEGEVAKIREIRVVGSK 196

QY 186 VYSDRLKRMQSLTEGGIWTWLRSPNQBQFAQDMKQVTDYVQNNGYFDFRILDTDIQ 245
DB 197 AFSEGLLDQFDITTPGLWTWYNTDKYSREKLEGIERLSFYLOQVLEFTEVPQVT 256

QY 246 TNEDKTKQTITITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQTAVL 305
DB 257 ISPDKDIYITITVHEGEPYKREVKLAGNLMGL-DSEINNLVEIKSGEVFSAKANSNA 315

QY 306 GETQNRMGSGYAYSEISVQPLNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVV 365
DB 316 KAITDYLGLDGLYAFANVNPQDLRAKHEADVTFFYDPSRRVVRRIQIGGNTRTRDEV 375

QY 366 RRELQWESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGS 425
DB 376 RRMQRQEAANYDAGDIKVSRRDRLGYPVNVKTDVPVGSFQDVNVVDVKEKPTGI 435

QY 426 LDLSAGHVQDTGLVMGAGVSDQLFTGKSAALRASRSKTLTNGSLSFDPYPTADGVSL 485
DB 436 INLGVGVSSEKAILSAGISEDNVFSGTNTLTQLNTSKTNRAVLSDHTDPYTKDGISR 495

QY 486 GYDVYKAFDPKRASTSIKQYKTTTAGARIMSVPTVEDYRNVNFGVLVAEHLTVNTYKAP 545
DB 496 TTSAYRVTEPWNNDG--DYRVKAMGLGMNFGVPISYEDVRIPLGGTFERNQIDLNNSP 553

QY 546 KHVADFTKKYKGTGDTGSGFKGLYKGTGCGWGRNKTDLSALWTPRGVLTGVNAIALPGSK 605
DB 554 QATRDVDQIG--DSTNALI-----FNTGSKDTRDSALAPTKGAYTRLKGFST--MD 603

QY 606 LQYYSATHNQTFPPPLSKFTFLMLGGEGVGIAGGYGRTKETLPFFENFYGGGLGSRVGYESG 665
DB 604 LKYYLLTAQQYYLPLGRSYTLALNGMIDYGRSYGGL-DYFVLKKNYAGGIGTVRGYEGA 662

QY 666 TLGP--KVYDEVGEKISYGNKKANVSAELLPPMPGAKDARTVRLSLFADAGSVWDGKTY 723
DB 663 SLGPRDLTGTY-----IGSRRWANAQYLYLFPFGASKDRITLWVFTDAGQVAG-- 714

QY 724 DNSSSATGGR-----YQNIYAGNTHKSTFTNRLYSAGGAVTWLSPGLGPMKFRYAYPLK 779
DB 715 --SGMCTAGKPGSEVEDPCG-----WRFSAIGLGSQSPGLGQLSYARPLN 760

QY 780 KPEDEIQRFPQLGTTF 797
DB 761 SKSGDDTQAFQIGTGF 778

RESULT 13
Q886N5 PRELIMINARY; PRT; 795 AA.
AC Q886N5;
DT 01-JUN-2003 (TrEMBLrel. 24, Created)
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN OrderedLocusNames=PSPT01542;
OS Pseudomonas syringae (pv. tomato).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=323;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=DC3000;
RX MEDLINE=22834015; PubMed=12928499; DOI=10.1073/pnas.1731982100;
RA Buell C.R., Joardar V., Lindeberg M., Selengut J., Paulsen I.T.,
RA Gwinn M.L., Dodson R.J., DeBoy R.T., Durkin A.S., Kolonay J.F.,
RA Madupu R., Dougherty S.C., Brinkac L.M., Beanan M.J., Haft D.H.,
RA Nelson W.C., Davidson T.M., Zafar N., Zhou L., Liu J., Yuan Q.,
RA Khouri H.M., Fedorova N.B., Tran B., Russell D., Berry K.J.,
RA Kutterback T.R., Van Aken S.E., Feldblyum T.V., D'Ascenzo M.,
RA Deng W.-L., Ramos A.R., Alfano J.R., Cartinhour S., Chatterjee A.K.,
RA Delaney T.P., Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X.,
RA Bender C.L., White O., Fraser C.M., Collmer A.;
RT "The complete genome sequence of the Arabidopsis and tomato pathogen
RT Pseudomonas syringae pv. tomato DC3000";
RL Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).
DR EMBL; AS016861; AAO55062.1; --
DR TIGR; PSPT01542; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR_5.
KW Complete proteome.
SQ SEQUENCE 795 AA; 87504 MW; 7DCAA623FBA087B1 CRC64;

Query Match 31.8%; Score 1320; DB 2; Length 795;
Best Local Similarity 33.6%; Pred. No. 1.4e-68;
Matches 274; Conservative 167; Mismatches 335; Indels 40; Gaps 8;

QY 1 MKLKQIASALMMLGISPLAFADFTQDIRVEGLQRTSTFVNYLPVKVGTQDYNTHGSA 60
DB 1 MKRLLLTAVLSALMAEVAHESFTTDIRVNGLQVRVSGSVFGALPLNVGEQADGLVD 60

QY 61 ITKSLVATCFDDVRVETADGOLLTVIERPTIGSLNTGAKMLQNDIAKKNLESFGLAQ 120
DB 61 ATRSLFKTGFQDIIQGRDGNVLVINVERPSVASIEIEGNAISTEDLMKGLQKSGLA 120

QY 121 SOYFNOATLNQAVAGLKEEYLGRKLNLTQIPKVTKLARNRVDIDITDEGSAKITDIE 180
DB 121 GEIFQRTALEGVNRELQRYVAGRVAEVAEVPPQPNRVCLKININEGTVAHQIN 180

QY 181 FEGNQVYSRDKLRQMSLTGEGITWLTGNSQNFQKFAQDMKQVTDYVQNNGYFDFRIL 240
DB 181 VVGVNTVFSDEDLTDLFELKTSNWLSPFKNDKDYAREKLSGDLRLRSYYLDRCYINMDIA 240

QY 241 DTDIQTNEKTKQITIKITVHEGGRFWGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQ 300

Db 241 STQVSTPDKKNVYITVNNNEGEKYSVKVLSGDL-KVPEDQVKSLLLVPQGVFSRKV 299

Qy 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHITGNKKT 360

Db 300 MTTTSELITRLNEGVTFANVANGVTPPNEDHTVDITFVVDGKRAYNRYNRGNKTS 359

Qy 361 RDEVRELRQMSAPYDTSKLRQSKRVERBELLGYFNVQVDAVPLAGTPDKVDLNLSLTE 420

Db 360 EDEVLRREMRQMEGWASTYLIDQSKTRLDRLGFFKEVNVETPPVPGTDQDVNVAVEE 419

Qy 421 RSTGSLDSAGWQDTCGLVMSAGVSQDNLFCTGKSAALRASRSKTYTLNGSLSTFDVFFTA 480

Db 420 QASGSITASVGFQAQSLGLIGSSIQNNFLGTGNKVSIGLTRSEYOSRYNFSYVDPYTP 479

Qy 481 DGVSLGVDYVCKAFDPRKASTSKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Db 480 DGVSLGYSAYRTTNYDDLDVDVASVAVDSLGAGINLGYPISETSRLYTLGTVOQDEIKT 539

Qy 541 YNKAPHYADFIKKYKGTGDTGSGFKWLYKGTGVGMRNKTDLSALMPTFRGYLTVGNABIA 600

Db 540 GRVTVDEIFDVQEGD-----KYLNFKSGISGSESTLNKGVLATRGHSQSLVFEST 591

Qy 601 LPQSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYCRTKEIPFFENFYGGGLGSVR 660

Db 592 LPQSDLSFFKLDYRAQYFHPITDNYTLRLHTELGYGDGYGSTGLPFYENYAGGFNSVR 651

Qy 661 GYESGTLGPKVYDEYG-----EKISYGGNKKANVSAAELPPMPGAKDART 705

Db 652 GFKDSLGLPRSTPSRGVAVTGNQDTPDQDPLPFGGNALVOGGVEWVPLFIKDQRS 711

Qy 706 VRLSLFADAGSVNDGKTYDDNSSATGGRVQ--NIYGAGNTHKSTFTFNELRYSAGGAVTW 763

Db 712 LRTSVFMDVGNVFD-TNCDSTRTTASGKVCENIDLSG-----MASSVGIGVTW 760

Qy 764 LSLPGLPMKRYAYPLKPKPED--EIQRFPQLGTTTF 797

Db 761 ITALGLPSFALAMPI-KKPDEAETQVFQSLGQTF 795

RESULT 14

Q88MH2 PRELIMINARY; PRT; 786 AA.

AC Q88MH2;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Outer membrane protein, bacterial surface antigen family.

GN OrderedLocusNames=PF1599;

OC Pseudomonas putida (strain KT2440).

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;

OC Pseudomonadaceae; Pseudomonas.

OX NCBI_TaxID=160488;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=22423060; PubMed=12534463;

RA Nelson K.E., Weinel C., Paulsen I.T., Dodson R.J., Hilbert H.,

RA Martins dos Santos V.A.P., Fouts D.E., Gill S.R., Pop M., Holmes M.,

RA Brinkac L.M., Beanan M.J., DeBoy R.T., Daugherty S.C., Kolonay J.F.,

RA Madupu R., Nelson W.C., White O., Peterson J.D., Khouri H.M.,

RA Hance I., Chris Lee P., Holtzapple E.K., Scanlan D., Tran K.,

RA Moazzaz A., Uterback T.R., Rizzo M., Lee K., Kosack D., Moestl D.,

RA Wedler H., Lauber J., Stjepandic D., Hobeisel J., Straetz M., Heim S.,

RA Kiewitz C., Eisen J.A., Timmis K.N., Duesterhoeft A., Tuemmler B.,

RA Fraser C.M.;

RT "Complete genome sequence and comparative analysis of the

RT metabolically versatile Pseudomonas putida KT2440.";

RL Environ. Microbiol. 4:799-808 (2002).

DR ENBL; AE016779; AAN67220.1; -.

DR TIGR; PP1599; -.

DR InterPro; IPR000184; Bac_surfAg_D15.

DR InterPro; IPR010827; Surf_Ag_VNR.

DR Pfam; PF01103; Bac_surface_Ag; 1.

DR Pfam; PF07244; Surf_Ag_VNR; 5.

KW Complete proteome. 86513 MW; D88E288A938D9E98 CRC64;

SQ SEQUENCE 786 AA;

Query Match 31.2%; Score 1295; DB 2; Length 786;

Best Local Similarity 33.2%; Pred. No. 4e-67;

Matches 269; Conservative 163; Mismatches 334; Indels 44; Gaps 7;

Qy 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTSTFVNLVFKVGVDTYNDTHGSAIL 62

Db 6 LTAVMSALM--IAEVHAESFTISDIRVNGLRQVSAGSVFGLPLNVGDAQDADDRRLVDST 62

Qy 63 KSIYATGFPDDVRVETADGQLLLTVIERFTIGSLNITGAKMLQNDAIKNLESFGLAQSQ 122

Db 63 RSLFKTGFPFDIQLSRDGNVLINNVVERPSVSIEIEGNKAISTEDLMKGLQSGLAEGE 122

Qy 123 YFNOATLQAVAGLKEEYLGKGLNIQITPKVTKLARNVDDIDITIDEGSKAKITDIEPE 182

Db 123 IFORATLEGVRNELQYVAGRYSAEDVAEVVQPPNRNVALKIKINEGTVAAIQHINIV 182

Qy 183 GNQVYSDRKLMRQMSLTEGGIWTWLTNRSNQFNEQKFAQDMKVTFDYQNNGYPDFFRILDT 242

Db 183 GNNVPDETLGQLFELKTTNNWLSFFKNDKDYAREKLSGDLRLRSYYLDRGYINMDIAT 242

Qy 243 DIQTNEDETKQTIKITVHEGGRFWKGVISIEGDTNEVPKAELEKLLTMKPGKWKYERQOMT 302

Db 243 QVSITPDKKHVYITVINEGEKYTVRDVRLSGDL-KVPEDQVKSLLLVPQGVFSRKVMT 301

Qy 303 AVLGETQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHITGNKTRD 362

Db 302 TTSSELITRLNEGVTFANVANGVTPPNQDQDHTVDMFVVDGKRAYNRYNRGNKTKTD 361

Qy 363 EYVRELRQMSAPYDTSKLRQSKRVERBELLGYFNVQVDAVPLAGTPDKVDLNLSLTER 422

Db 362 EVLRREMRQMEGWASTYLIDQSKTRLERLGFKEVNVETPPVPGTDQDVNVYSVEEQ 421

Qy 423 TGSLLDSAGWQDTCGLVMSAGVSQDNLFCTGKSAALRASRSKTYTLNGSLSTFDVFFTA 482

Db 422 SGSITASVGFQAQSLGLIGSSIQSNFLGTGNKVSIGLTRSEYQTRYNFGVDPYFTADG 481

Qy 483 VSLGVDYVCKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542

Db 482 VSLGYNVAFRSTDYDDLVDVASVAVDSYGAGVSLGYPISETSRLYTLGSLVQDQDKITGK 541

Qy 543 KAPKHYADFIKKYKGTGDTGSGFKWLYKGTGVGMRNKTDLSALMPTFRGYLTVGNABIALP 602

Db 542 YTVDEIFDFLEBEG-----DNFLN--FKASIGWSESTLNKGVLATRGHSQSLTSTVP 593

Qy 603 GSKLQYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYCRTKEIPFFENFYGGGLGSVRGY 662

Db 594 GSDLSFFKLDYRGQLFKPITSDYTLRLHTELGYGDGYGSTGLPFYENYFAGGFNSVRGF 653

Qy 663 ESGTLGPKVYDEYGE-----KISYGGNKKANVSAAELFPMPGAKDARTVTR 707

Db 654 KQSSLGPRSTPSIGEAAGKPGTIADPDQDPLPFGGNVLVOGGAELLPFLPFVKDQRSUR 713

Qy 708 LSLFADAGSVNDGKTYDDNSSATGGRVQNIYGAGNTHKSTFTFNELRYSAGGAVTWLSPL 767

Db 714 TSFVMDVGNVFD-----TNCNKPDKCEKVGFSG-MASSVGLGVTWTAL 756

Qy 768 GPMKRYAYPLKPKPEDETORFQQLGTTTF 797

Db 757 GPLSFSFLAMPVKPKDDADTQVFQSLGQTF 786

RESULT 15

Q9HXI4 PRELIMINARY; PRT; 797 AA.

AC Q9HXI4;

DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Probable outer membrane protein.

GN OrderedLocusNames=PA3648;

OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PA01;
RX MEDLINE=20437337; PubMed=10984043; DOI=10.1038/35023079;
RA Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warriner P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltzy L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.N., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong K.-S., Wu Z., Paulsen I.T.,
RA Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
DR EMBL; AE004784; AAC07036.1; --
DR PIR; H83190; H83190.
DR InterPro; IPR00184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surface_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88286 MW; 717F9EF15BC89476 CRC64;

Query Match 30.8%; Score 1279.5; DB 2; Length 797;
Best Local Similarity 33.3%; Pred. No. 3.3e-66;
Matches 273; Conservative 157; Mismatches 338; Indels 51; Gaps 7;

QY 3 LKQIASALMMLGISPLAFADFTIQRVEGLQRTPEPSTVFNYLPVKVGYDYNTHGSAII 62.
DB 6 LPALLSALM--TAEVHAESFTVSDIRVGLQVRVAGSVFAALPLNVGETIDDOALVOAT 62

QY 63 KSLYATGFFDDVRVETADGOLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQ 122
DB 63 RSLFKTGFFQDIQGRDGNLVTVVVERPSISSTIEIGNKAKISKEDLLKGLKQSLAEGE 122

QY 123 YFQATLNQAVAGLKEYLGRGKLNIOITPKVYKLARNRVDIDITIDEGSAKITDIEFE 182
DB 123 IFQRATLEGVRNELQRYVAQGRYSABEAEVTPQPRNRVALKININEGTVAASHINVV 182

QY 183 GNOVYSDRKLQRMSLTGEGGIWTLTSNQFNQKFAQDMKVTDFYQNNGYDFRILDT 242
DB 183 GNTVFSEEDITDLFELTKTNWLSFFKNDDKYAREKJSGDLRLRSYYLDGRYINMDIAT 242

QY 243 DIQTNEDEKTKQITKITVHEGGRFRWGVSTEGDTNEVPKAELEKLLTMKPGKWYRQOMT 302
DB 243 QVSTTPDKKHVYITVINEGEKTIIRDVKLTGDL-KVPEEEVKKLLLVQKGQVFSRKVMT 301

QY 303 AVLGEIQNRVGSAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIYVNEIHITGNKTRD 362
DB 302 TTSDLTIRRLGNEGTYTPANVGVPEAHDDKTVSVTVFVDPGKRAYVNRINFRGNTKTD 361

QY 363 EVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFADVLACIAGTPDKVDLNMSLTERS 422
DB 362 EVLRREMRQMEGWASLYLIDQSKARLERLGYFKEVNVETPAVPGTDDQVDVNVSVVEEQP 421

QY 423 TGSLLDSAGWQDTGLVMSAGVQDNLFQTKSAALRAKRSKTLNGLSLSFTDPYFTADG 482
DB 422 SSGITASVGAQSAAGLLILGSSISONNPLGTVGNKVSIGLTRSEYQTRYNFGVDVYFVVDG 481

QY 483 VSLGYDVGKAFDPKRAKSTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
DB 482 VSLGYNAFYRKTDYDELDDVDVASYSVNSLGAAGMSIGYPISETSLTYGLSVQRDQIDTGR 541

QY 543 KAPKHYADFIKKYKTKDGTGSGFKGWLKGTGVGRNKTDSALWPTRGYLTGVNAEIALP 602
DB 542 YTVDEIYDFLDKEG-----DNFTN--FKASIGWSESTLNKGLVATRGHSQSLSLTLETL 593

QY 603 GSKLQYYSATHNQTFPLSKTFTLMLGGVGIAGGYGRKKEIPPEENFYGGGLGSRGY 662
DB 594 GSDLSFYKIDYRGQVAFPLTDNVTMRPHTELGYGDGYGSTERLPFPFVENVYAGGFNSVRGF 653

QY 663 ESCTLGP-----KVVDEYGEKISYGNKKANVSALLPMP 698
DB 654 KDTLGRSTPSVARNPDTGTPMKNQGPDSKGRYTDPDQDPEAFGGNILLITGGAEILLPPLP 713
QY 699 GAKDARTVRLSLFADAGSVWMDGKTYDDNSSATGGRVQNIYAGANTHKSFTTNELRYSAG 758
DB 714 FVKDQQLRTVLFWDVGS-----TFDTDCPTKTTTNCDGIK-----TDNLASSVG 758
QY 759 GAVTWLSPLGPMKFRVAYPLKKKPEDEIQRPQFOLGTTT 797
DB 759 VGLTWITALGPLSFLATPIKKPDNAETQVFQFSLGQTF 797

Search completed: July 6, 2005, 15:18:02
Job time : 228.937 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 ; Search time 61.3077 Seconds
(without alignments)
970.438 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQIASALMMGLGISPLAF.....LKKKPEDEIQRFOQLGTTTF 797

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4152	100.0	797	4	US-09-394-192-4
2	3937.5	94.8	792	4	US-09-394-192-2
3	1286	31.0	821	4	US-09-352-991A-21013
4	1266.5	30.5	865	4	US-09-328-352-7498
5	1259	30.3	827	4	US-09-543-681A-6425
6	1213.5	29.2	815	4	US-09-489-039A-12469
7	1187.5	28.6	825	4	US-09-489-039A-8469
8	1136	27.4	797	3	US-08-433-522A-2
9	1136	27.4	797	3	US-08-433-522A-4
10	1136	27.4	797	3	US-08-433-522A-6
11	1136	27.4	797	3	US-09-135-166-2
12	1136	27.4	797	3	US-09-135-166-4
13	1136	27.4	797	3	US-09-135-166-6
14	1136	27.4	797	3	US-08-942-046-2
15	1136	27.4	797	3	US-08-942-046-4
16	1136	27.4	797	3	US-08-942-046-6
17	1114	26.8	793	3	US-08-433-522A-10
18	1114	26.8	793	3	US-09-135-166-10
19	1114	26.8	793	3	US-08-942-046-10
20	1112	26.8	813	4	US-09-540-236-3472
21	1109.5	26.7	792	3	US-08-433-522A-8
22	1109.5	26.7	792	3	US-09-135-166-8
23	1109.5	26.7	792	3	US-08-942-046-8
24	1109	26.7	813	4	US-09-701-711-2
25	1109	26.7	813	4	US-09-701-711-4
26	703	16.9	896	4	US-09-589-065B-5
27	454.5	10.9	795	4	US-09-198-452A-314

28	454.5	10.9	795	4	US-09-438-185A-302	Sequence 302, App
29	304.5	7.3	605	4	US-09-252-991A-31355	Sequence 31355, A
30	233	6.1	889	4	US-09-914-168-4	Sequence 4, Appli
31	253	6.1	919	4	US-09-914-168-2	Sequence 2, Appli
32	251	6.0	609	4	US-09-857-669-2	Sequence 2, Appli
33	251	6.0	609	4	US-09-857-669-4	Sequence 4, Appli
34	250	6.0	947	4	US-09-540-236-1991	Sequence 1991, Ap
35	237	5.7	587	4	US-09-857-669-6	Sequence 6, Appli
36	232.5	5.6	913	4	US-09-328-352-7024	Sequence 7024, Ap
37	221	5.3	586	4	US-09-489-039A-8950	Sequence 8950, Ap
38	194.5	4.7	583	4	US-09-543-681A-5823	Sequence 5823, Ap
39	184.5	4.4	759	4	US-09-252-991A-17841	Sequence 17841, A
40	161.5	3.9	447	4	US-09-902-540-9863	Sequence 9863, Ap
41	160.5	3.9	1220	4	US-09-206-942-28	Sequence 28, Appl
42	160.5	3.9	1226	4	US-09-206-942-26	Sequence 26, Appl
43	156	3.8	915	4	US-09-206-942-35	Sequence 35, Appl
44	156	3.8	1222	4	US-09-206-942-37	Sequence 37, Appl
45	156	3.8	1228	4	US-09-206-942-34	Sequence 34, Appl

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 4152; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMGLGISPLAFADFTTQDIRVEGLQRTSTVFNYPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMMGLGISPLAFADFTTQDIRVEGLQRTSTVFNYPVKVGDYNDTHGSA 60
QY 61 IIKSIYATGFFDDVAVETADGQLLTIVIERPTIGSLNTGAKMLQNDATKKNLESFGLAQ 120
DB 61 IIKSIYATGFFDDVAVETADGQLLTIVIERPTIGSLNTGAKMLQNDATKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLRGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLNQAVAGLKEEYLRGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
QY 181 PEGNOVYSRDKLMRQMSLTGGIWTWTRSNQFNQKFAQDMKEVTDFFQNNGYDFRLL 240
DB 181 PEGNOVYSRDKLMRQMSLTGGIWTWTRSNQFNQKFAQDMKEVTDFFQNNGYDFRLL 240
QY 241 DTDIOTNEDKTQTKITITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKMYEROQ 300
DB 241 DTDIOTNEDKTQTKITITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKMYEROQ 300
QY 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

63 KSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQ 122
 90 RSLFKTGFFQDIQGRDGNVLVTVVERPSISIEGKNAISKEDLLKGLKQSLAGE 149
 123 YFNOATLNQAVAGKEBYLGRGKLNIOITPKVKLARNRVDIDITIDEGSKAKITDIEFE 182
 150 IFORATLIEGRNELQRYQVAGRYASABAEVIPPQPRNVALKININEGTVAASHINNV 209
 183 GNOVYSRDKLMRQMSLTGEGITWLTSTRNQFNQKFAQDMKVTDFYQNNGYDFRLLDT 242
 210 GNTVFSSEEDJTLFELTKTNWLSFFKNDKDYAREKUGSGLERLSYDLDGYINMDIAT 269
 243 DIOTNEDTKQTITITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPKGKMYERQOMT 302
 270 QVSTTPDKHVIYTVNINEGKTYIRDVLTGDL-KYPEEVEVKRLLLVQKGVFSRKVMT 328
 303 AVLGEIQNRMGSGAGYSEISVQPLPNAETKTVDFVLHIEPGKRIYVNEIHTGNKTRD 362
 329 TTSDLITRRLLGNEGYPANVGVPEAHDHDKTYSVTFWVDPGKRAYVNRINFRGNTKTD 388
 363 EVVRRELROMESAPYDTSKLQSKERVELLGYPDNQDFVPLAGTDPKVDLNMSLTERS 422
 389 EVLRERMQEGGWASTYLLDQSKARLERLGYFKEVNVETPAVPGTDDQVDVNVSVBEPQ 448
 423 TGSLLDSAGWQDTGLVMSAGVSDNLFGTGSAAALRASRKTTLNGSLSTFTDPTADG 482
 449 SCSITASVGAQAGLLILGSSISONNPLGTGNKVSIGLTRSEYQTRNFYGFVDPYTWVDG 508
 483 VSLGYDVGKAFPPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
 509 VSLGYNAPYKTDYDELDVDVASVSNLSGAGMSIGYPISETSRLTYGLSVQRDQIDTGR 568
 543 KAPKHYADFTKTKYKTDGCTGSKGMYLKYGTGWRGNKTSALWPRGYLTGVNAELALP 602
 569 YTVDEIYDFLDKEG-----DNFTN--FRASIGMSESTLNGVLAIRHGSQSLTLETLTP 620
 603 GSKLOYYSATHNOTWRRPLSKTFTMLGGRVGIAGGYGRTEKPEPFFNFGGGLGSRVG 662
 621 GSDLSPKIDYRGQVAFPLTDNMYRHTLGYGDBGYDGTSTERLPFFENYAGGFNSVRGF 680
 663 ESGTLGP-----KVY-----DEYG-----EKISYGGNKKANVSARELLFPMPGAK 701
 681 KDSITLGRSPSRAYKDGKIIIPGDERGRVTDPPDQPEAFEGGNLITGGAEALLFPLFPVK 740
 702 DARTVRLSLFADAGSVWDGTYDDNSSATGGRVQNIYAGNTHKSTFTTNELRYSGAGAV 761
 741 DQRLRLVLFWDVGS-----TFDTCPTKTTTNCDGIK-----TDNLASSVGVGL 785
 762 TWSPLGPMKFRVAYPLKKPDEIQRFOFQLGTTTF 797
 786 TWITALGPLSFLATPIKPPDPNAETQVQFSLGQTF 821

RESULT 4
 US-09-328-352-7498
 ; Sequence 7498, Application US/09328352
 ; Patent No. 6562958
 ; GENERAL INFORMATION:
 ; APPLICANT: Gary L. Breton et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
 ; FILE REFERENCE: GTC99-03PA
 ; CURRENT APPLICATION NUMBER: US/09/328,352
 ; CURRENT FILING DATE: 1999-06-04
 ; NUMBER OF SEQ ID NOS: 8252
 ; SEQ ID NO 7498
 ; LENGTH: 865
 ; TYPE: PRN
 ; ORGANISM: Acinetobacter baumannii
 ; US-09-328-352-7498
 Query Match 30.5%; Score 1266.5; DB 4; Length 865;
 Best Local Similarity 33.7%; Pred. No. 2.8e-98;

Matches 280; Conservative 153; Mismatches 329; Indels 69; Gaps 13;
 QY 22 DFTIQDIRVEGLQRTSPSTVFNVLVVKVGDYVNDTHGSAIKLSYATGFFDDVRVETADG 81
 DB 49 DFVRRIDHNVGLVRLTPANVYTWLPINSGRVNEPMAIEAIRTYATGLFDDDKASKEND 108
 QY 82 QALLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQYFNQATLNQAVAGKEEYL 141
 DB 109 TLVFNVIERPLISLKEFKGNKLIPKEALSGGLKMGIAEVEFKKSALQIETIETEQYT 168
 QY 142 GRKLNIOITPKVKLARNRVDIDITIDEGSKAKITDIEFEGNOVYSRDKLMRQMSLTG 201
 DB 169 QCGRYDADVTDTVARPNRVELKINFNECTPAKVFIDINVNTVPKDSBIKQAFVAKES 228
 QY 202 GIWTLTSTRNQFNQKFAQDMKVTDFYQNNGYDFRLLDTDIOTNEDTKTKITIKTVHE 261
 DB 229 GWASVVRTRNDYAREKQAALEALRAMYLKNGYINFNINNSQLNISEDKHHIEFVAVDE 288
 QY 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPKGKMYERQOMTAVLGEIQNRMGSGAGYSE 321
 DB 289 GSQFKSGQTKFLGDALYKPE-ELQALKIYKDGDTYSEKVNAYKQLLLRKYGNAGYFPAD 347
 QY 322 ISVQPLPNAETKTVDFVLHIEPGKRIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 381
 DB 348 VNIVPOINNETGVVDLNYVNPQGVTVRRINFNGSKTSDEVLRERMQEGALASNEK 407
 QY 382 LQSKERVELLGYPDNQDFVPLAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVMS 441
 DB 408 IDLSKVRLEERTGFFKTVDIKPAIPNSPDQVDLNVNVEEQHSGSTTLTLAGYSQSGITFQ 467
 QY 442 AGVSQDNLFTGKSAALRASRKTTLNGSLSTFTDPTADGVSGLGYDVGKAFDPKRAST 501
 DB 468 AGLSQNFMTGNRVALDLSRSETQDYNLSTVTDPTFTIDGVSRGVNY-----YRKTCL 522
 QY 502 ----SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFI----- 552
 DB 523 NDDYNNVNVYDTSFGSLSFGVPIDENQSLASVGVNDTKVTTPGVVTVRVDYLLANGG 582
 QY 553 KKYKGT-----DGTGSGFKW-----LYKGTGVRGNKTDSDA 584
 DB 583 KATGKSWCPGSKNKTDPNTQOPIPTCEGGEFDYNSAFEGEFTYNNLNLGNSYNTLNR 642
 QY 585 LMPTRGYLTVGNAEIALPGSKLQYYSATHNOTWFFPLSKT-FTLMLGGEVGIAGGYGRTK 643
 DB 643 IPTGSMHRVGLIEGLPGSDVDYQKVTYDQAFPIGTGTFVLRGVGKL-----GYG--N 696
 QY 644 EIPFFENFYGGGLGSRVYESGTLPK-----VYDEYGEKISYCGNKKANVSARELLF 695
 DB 697 DLFFYKFNFYAGGYGSRVGYDNLGPKYASVNLQETKQNDGSPPEEVGGNALVQFTELVL 756
 QY 696 PMPGAKD-ARTVRLSLFADAGSVWDGTYDDNSSATGGRVQNIYAGNTHKSTFTTNE-- 752
 DB 757 PMPFKGDWTRQVRPVLFAEGGQVFTKCNIDN--SVYGNKGMKINGQITIDVRKYCEDNY 814
 QY 753 -----LRYSGAGVNTWSPLGPMKFRVAYPLKKPDEIQRFOFQLGTTTF 797
 DB 815 GFDLGNLRYSVGVGTWITMIGPLSLSYAPPLNDKPGDETKETQFEGRTF 865

RESULT 5
 US-09-543-681A-6425
 ; Sequence 6425, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABIL
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344

```
; SEQ ID NO 6425
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6425

Query Match      30.3%; Score 1259; DB 4; Length 827;
Best Local Similarity 35.1%; Pred. No. 1.1e-97;
Matches 290; Conservative 146; Mismatches 335; Indels 56; Gaps 14;

QY 1 MLLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDVYNDTHGS 59
DB 27 MAMKLLIASLLSATAYSGDFVQDIOFEGQLRVAVGAALLNMPVRVGDVSDDDIS 86

QY 60 AIIKSLYATGFFDDRVVETADGOLLTVIERPTIGSLNITCAKMLQNDAIKKNLSPGLA 119
DB 87 RTIRSLFATGNFDDRVLRDGNVLIVQVKERPIASITFSGNKAIKEDMLKQNDASNIR 146

QY 120 QSYFNOATLNOAVAGLKEEYLGKUNIOITPKVTKLARNVDIDITIDEGKSAKITDI 179
DB 147 IGETLDRTMLANIEKGLDFYYSVGKYNATVKVWVTPLENRVLDLKLVPAGVSAITQOI 206

QY 180 EFGNQVYSRDKLMRQMSLTEGGIWTWLTFRSNQFNQKFAQDMKVTDFYQNNGYDFRI 239
DB 207 NIVGNKAFSTAEILNRFQLRDDVPWMNAADEKTKQKLAGDLETURSFYLDGRIARFDI 266

QY 240 LDTDIOTNEDTKTKITIVHEGGRFRWGVKVSIEGDTNEVPKAELEKLTMTKPKWYERQ 299
DB 267 ESTNVSLTPDKKGIYITINLKEGDKYTVESTEINGNTAGYTK-EIEDLIQIAPGSLYNGA 325

QY 300 QMTAVLGEIQNRMGSGAGYASEISVQPLPNAETKTVDVLHIIEPGRKIYVNEIHTGNKK 359
DB 326 QVTKTENEIKNLLGRYGYAYPRVMTNPEINDENKTKLVHNVVDAGNRYVQRIRFAGNDI 385

QY 360 TRDVVRRELROMESAPYDTSKLQSKRVERVELLYGPDNVQFQDAVPLAGTDPKVDLNSLT 419
DB 386 TKOSVLRERQMEGAWLGSDLVEQSGKRLNLRIYGFETVETETQRIPGSPQVDIVYRVK 445

QY 420 ERSTGSLDLGAGVQDVTGLVMSAGVSDNLPFGTKSAALRASRSTKLTLNGSLFTDPYFT 479
DB 446 ERVTGSLNFGVGTGTEGVSFQVGTQDNWLGTONAVAINASKNDYSTYAELSVTDPYFT 505

QY 480 ADGVSLGVDYVYKAF--DPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
DB 506 VNGVSLG---GRIFYNDFRANADLSGYTNKSYGLDGLTGLFPINEYNSARLGLGYTH-- 559

QY 538 VNTYNKAPKHYA--DFIKKYKTDGTD--CSPKGLWLYKGTGVHGRNKTDLSALWPTRGYLT 593
DB 560 -NGLSRMEPQVAMRWYLESNGENPGDFKRESFNADDYTVSLGWTFFNNLRGFPFPTSGARS 618

QY 594 GVNAETALPGSKLQYYSATHTQWTFPL--SKTFTLMLGGEVGIAGGYGRTKIIPFFENF 651
DB 619 NLGSRITIPGSDNKYYKVTWGHAYVPLDKEKSWVTLFKGRILGYDGLG-GKELPYENF 677

QY 652 YGGGLGSRVGYSGTGLGPKYDYEGEKI-----SYGNKKANVASAELLFP 696
DB 678 YAGSGTVGRFSRNNIGPKAI--YLKXIADGRTIIDPSLSSDAVGGNMAVASFELITP 735

QY 697 MPKAKD--ARTVRLSLFADAGSVWDGKTYDDNSSATG-----GRVONIYGAGNTHKSTFT 750
DB 736 TPFIDDKYSSSVRTSMFVDAGTVDMTNWNTSNSTNWTAGMPDFGKASNI----- 783

QY 751 NELRYSGAGVATWLSPLGPMKFRYAYPLKKKPEDEIQRFQGLGTF 797
DB 784 ---RVSTGVALQWLSPLGLPLVFSYAKPIKDYEGDKSEQGFNIGRTW 827
```

RESULT 6

```
US-09-489-039A-12469
; Sequence 12469; Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
```

```
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12469
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12469
```

```
Query Match      29.2%; Score 1213.5; DB 4; Length 815;
Best Local Similarity 34.2%; Pred. No. 8.1e-94;
Matches 284; Conservative 147; Mismatches 341; Indels 59; Gaps 14;

QY 6 IASALMMLGISPLAFAD-----FTIQDIRVEGLQRTPESTVFNYLPVKVGDVYNDTH 57
DB 5 ITMAMKLLIASLLFSATVYGAEGFVWVDIHPFGLQRVAVGAALLSMPVRPGDVTVD 64

QY 58 GSALIKSLYATGPPDDRVVETADGOLLTVIERPTIGSLNITCAKMLQNDAIKKNLSPG 117
DB 65 ISNTIRALFATGNFEDRVLRDGDITLLVQVKERPTIASITFSGNKSVKDDMLKQNL 124

QY 118 LAQSQVFNOATLNOAVAGLKEEYLGKUNIOITPKVTKLARNVDIDITIDEGKSAKIT 177
DB 125 VRVGESLDRTTADIIEKGLDFYYSVGKYSASVAVVTPLENRVLDLKLVPQGVSAKIQ 184

QY 178 DIEFEGNQVYSRDKLMRQMSLTEGGIWTWLTFRSNQFNQKFAQDMKVTDFYQNNGYDF 237
DB 185 QINIVGNHAFSTDELISHFQLRDEVPWMNVGVDRKYQKQKLAGDLETLSYSLYLD 244

QY 238 RILDTDIOTNEDTKTKITIVHEGGRFRWGVKVSIEGDTNEVPKAELEKLTMTKPKWY 297
DB 245 NIDSTQVSLTPDKKGIYITVNTIEGQYKFSGVQVVTGNL-AGHSABEIALTKVPE 303

QY 298 RQOMTAVLGEIQNRMGSGAGYASEISVQPLPNAETKTVDVLHIIEPGRKIYVNEIHTGN 357
DB 304 GAKVTQKENDIKLLGRYGYAYPRVQSQPEINDSKTVKLVHNVVDAGNRYVVRKIRFEGN 363

QY 358 NKTRDVRVRELROMESAPYDTSKLQSKRVERVELLYGPDNVQFQDAVPLAGTDPKVDL 417
DB 364 DTSKDAVLRERQMEGAWLGSDLVDQKDLNRLGFFETVDTDTQKVPQSPQVDVWYK 423

QY 418 LTERSTGSLDLGAGVQDVTGLVMSAGVSDNLPFGTKSAALRASRSTKLTLNGSLSTDPY 477
DB 424 VKERNTGSPNFGIGYGTGSGVSFQAGVQDDNMLGTGYAVGINTGKNDYQTYTETSL 483

QY 478 FTADGVSLGVDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
DB 484 FTVDGVSLGGRFYNDPFDANDADLS--DYTNKSYGTDITLGFVPEYNTLRAGVYVHNS 541

QY 538 VNTYNKAPK-----HYADFIKKYKTDGTDGSPKGLWLYKGTGVHGRNKTDLSALWPTRGYLT 593
DB 542 LS--NNQPQVAMRWYLSNGQYPDNTNDRNSFSANDFTFNYGWTYKNLDRGFPPTGSRV 599

QY 594 GVNAETALPGSKLQYYSATHTQWTFPLSKTFTLMLGGEV--GIAGGYGRTKIIPFFENF 651
DB 600 NLNGKVTIPGSDNEXYKATLDATVYPIDNDHQWVVLGRTRFGYGDGIG-GKEMPFFYENF 658

QY 652 YGGGLGSRVGYSGTGLGPK-VY-----DEYGEKI-----SYGNKKAN 688
DB 659 YAGSGTVGRFSQNTIGPKAVYFPASSRRHDDDDSYDNECKSTESAPCKSDDAVGGNMAV 718

QY 689 VSAELLFPMFGAKD--ARTVRLSLFADAGSVWDGKTYDDNSSATGGRVONIYGAGNTHK 746
DB 719 ASLELITPTTFISDKYANSVRTSVFWDMGTVMD--THWDSSAY-----AGYPDY 765

QY 747 STFTNELRYSGAGVATWLSPLGPMKFRYAYPLKKKPEDEIQRFQGLGTF 797
DB 766 SDPSN--IRMSAGIAVQWMSPLGLPLVFSYAPFKKYDGDGKAEQFQFNIGKTW 815
```

RESULT 7
US-09-489-039A-8469
; Sequence 8469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; PRIOR FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 8469
; LENGTH: 825
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-8469

Query Match 28.6%; Score 1187.5; DB 4; Length 825;
Best Local Similarity 33.3%; Pred. No. 1.3e-91;
Matches 276; Conservative 156; Mismatches 343; Indels 53; Gaps 15;

Qy 1 MLKQIASALMMLGISPLAFADFTIQIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 20 LKTHIISGLLIAPLTLYAATSQVDDIRPEGLQRTVIGAGLLSMPLHAGDVAITPDVSE 79

Qy 61 IISLYATGPDVVRVETADQGLLTIVERTIGSLNITGAKMLQNDAIKNLESFGLAQ 120
Db 80 AVRALYASGNFVQILRDGKTLVVQVKERTIASVSFGNKAVKDALXENITASGISA 139

Qy 121 SQYNQATLNOAVGLKEEYLGKRLNIQTPKVTKLARNVDITIDIEKSKAKITDIE 180
Db 140 GSALDRNLSIEIEKGLQDFYYSACKYSAQVAVVTPIPRNRVDLTVPFQGISAKIAQIN 199

Qy 181 FEGNQVSDRLKMFOMSLTEGGIITWITRNSQNFQKPAQMEKVDYQNNGYDFRIL 240
Db 200 IIGNQAFREETLLDQLRDNPVPMNVVADKKYQKLEADLETLSRFLDRGVARFAIE 259

Qy 241 DTDIOTNEDKTKQIKITVHEGGRFRGKYSIEGDTNEVPKAELEKLLTWKPGWYERQ 300
Db 260 STQVSMTPDKSLYITLALNEGERYRVDRTQVTGDLAQ-HGPETEALQPLAGAWYSGAQ 318

Qy 301 MTAVLGIQNRMSGAGYAYSEISVOP-LPNAETKVDVFLHIE--PGRKIYVNEIHTGN 357
Db 319 VTTVENEIKKHFGKYGAWPQVSTPEIDDAHRV---VLHIQVAGRRYSVRQIRFSGN 375

Qy 358 NKTRDEVVRRELQWESAPYDTSKLQSRKERVLLGYFDNVQFQDAVPLAGTPDKVDLNM 417
Db 376 DTSRDAVLRREMRQMEGAWLNNEKVDQGVRLDRDTGFFENVEQQIVPVSGTADQVDVYK 435

Qy 418 LTERSTGSLDSAGWODTGLMAGVSQDNLFOTGKSAALRARSKTTLNGSLSFDDPY 477
Db 436 VKERNITGSFNVGLGFGDSGYSYQLGVTQDNWLGTGNSVSPNGTRNSYQSYLELGATNP 495

Qy 478 FTADGVSIGVDVYKADPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRNFGVLVAH-- 535
Db 496 FTVDGISLGGKIFNYSYDADADAG--SYNQSYGLGSTLGFPISENKSNLNLGDYVHNR 553

Qy 536 -----LTNVTYNKAPKHYADFIKKYKTKDGTGDS-FKGWLYKGTVGWGRNKDTSALWP 587
Db 554 LTNMDPELTWRYLSSRGIEPSVTK-----DGDGSAKYSANDYPASLGWGYNDLDRGFFP 609

Qy 588 TRGYLTGVNABIALPGSKLOYYSATHNQTFPPLS--KTFTLMJGVBGVAGGYGRTKEI 645
Db 610 RAGNKSLSGKVTLPFGSDNSYKLSFDTAQYLPSENKRWWMERLRAVAGGLD-GKSV 668

Qy 646 PPFENFYGGGLSGVRGESYTGPKV--YDEYGEKISY-----GKNKXANVSA 691
Db 669 PFYDNFYAGGSSSVRGFSSNTIGPKAAYYRCNGSESSYACPLDASSDAVCGGNAMAVLNS 728

Qy 692 ELLFPMPGAKD--ARTVRLSLFADAGSVMDGKTYDDNSSSATGRVQNIYAGNTHKSTF 749
Db 729 EFIIPTFPVNDKYADSLRTSLFVDAGTVWSTSWHTAQTAAAG-----IPDYGD----- 777

Qy 750 TNELRYSAGCAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFQFQGLGTTF 797
Db 778 PSHIRLSAGIYAVQWMSPLGLVFSWAEFFPKKYDGDKAEOQFQFNIGKTW 825

RESULT 8
US-08-433-522A-2
; Sequence 2, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-2

Query Match 27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMMLGISPLAF-ADFTIQIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVAFVAKDIRVDVGQDLEQQIRASLPVRAGORVTDNDVANI 60

Qy 62 IKSLYATGPDVVRVETADQGLLTIVERTIGSLNITGAKMLQNDAIKNLESFGLAQ 121
Db 61 VRSLSVSGRFDVKAHQEGDVLVSVVAKSIIISDVKIKGNSVITPEALKQNDANGFKVG 120

Qy 122 QYNQATLNOAVAGLKEEYLGKRLNIQTPKVTKLARNVDITIDIEKSKAKITDIEP 181
Db 121 DVLIREKLENEFAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKLASLTF 180

Qy 182 EGNQVYSDRLKMFOMSLTEGGI--TWLTRSNQNFQKPAQMEKVDYQNNGYDFRIL 240
Db 181 KGNESVSSSTLQBMELQDPSWWKLM---GNKPEGAQFEKQDLSIRDYLYLNGYAKAQIT 237

RESULT 10
US-08-433-522A-6
; Sequence 6, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-433-522A-6

Query Match 27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;
QY 3 LKQIASALMMGLISPLAF-ADFTIQDIRVEGLQRTPESTVFNPLVKVGYDYNTHGSAI 61
DB 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVQVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSIXATGFDDVRVETADQQLLTWERTIGSLNITGAKMLQNDKAIKNLESFGLAQS 121
DB 61 VRSLSVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVITPEALQNLDANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNVDIITIDEKSKAKITDIEF 181
DB 121 DVLIREKLENEFAKSVKHYASVGRYATVEPIVNTLPNNRAELIQINEDDDKAKLASLTF 180
QY 182 EGNQVSDRKLMEQMSITEGGIW-TWLRNSQFNEQKFAQDMKVTDFYQNNQYDFRIL 240
DB 181 KGNESVSSSTLQEQMELQPSWKKLW---GNKFEQAQFQKDLQSIQIRDYLLNNGYAKAQIT 237
QY 241 DTDIQTNEDKTKQTIKTIYHEGFRWKGKVISIGDITNEVPKAELEKLT-MKEGKMYERQ 299
DB 238 KTDVQLNDEKTKNVNITDVNVEGLQDLRSARIIGNLGGM-SAELEPLLSALHLNDFRIS 296
QY 300 QMTAVLGEIQNRMGSGAGYAYSEISVQPLPAETKTVDVLHIEPGRKIYVNEITHGNK 359
DB 297 DIADVENAIKALGERGYGATVNSVPDFDDANKTLAITLVDAGRRLTVRQRFEGNTV 356

QY 360 TRDEVVRRELROMESAPYDTSKLQSKERVVELLYGFDNVQFQDAVPLAGTDPKVDLNMSLT 419
DB 357 SADTLRQEMRQOEGTWYNSQLVELGKIRLDRTGFFETVENRIDPINGSNDEVDVYTKVK 416
QY 420 ERSTGSLDLSAGWVQDTGLVMSAGVSDNLFGTGKSAALRASRSKTTTLGSLSFDTDPYFT 479
DB 417 ERNTGSINFGIGYGTESGISYQASVKQDNFLGTGAASVSTAGTKNDYGTSVNLGYTEPYFT 476
QY 480 ADGVSLGVDYVYKAFPRKASTSIKOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVN 539
DB 477 KCGVSLGNGVFFENYDYSKSDTS-SNYKRTTYGNSVTLGFPVNNENNSYYVGL-----GH 529
QY 540 TYNKAPEH-----YADFIKKYG--KTDGCGSGFKGWLKGYGVGGRNKTDSALMPT 588
DB 530 TYNKISNFALEYNRNLIQSMKPKNGIKTNDPFSF-----GWNYSNLRGYFT 580
QY 589 RGYLTGVNAEIALPGSKLQVYSATHNQTFPFLSKTFTLMLGGE--VGIAGGYGRTEIP 646
DB 581 KGVKASLGGRTVTPGSDNKYKLSADVQGFYPLDRDHLWVWSAKASAGYANGFG-NKRLP 639
QY 647 FFENFYGGGLSVRGYESGTLGPK-VYDEYG-----EKIS---YGNKNKANVSAELL 694
DB 640 FYOTYTAGGIGSLRGFPAYGSGIGNAIYASYGNGSGGTGTFKTKISSDVIGGNAIATASAELI 699
QY 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVONI-----YGAGNTHK 746
DB 700 VPTFPVSDKSQNTVTSFLVDAASVWNTKWSKDN-----GLESDDLKRLPDYK----- 749
QY 747 STFTNELRYSAGGAVTWLSPGLGPKFRYAYPLKPKPEDEIQRFOFOLGTTFF 797
DB 750 ---SSRIRASTGVGFQWQSPFGLPLVESYAKPIKKNYENDVEQFQFSIGSGF 797
RESULT 11
US-09-135-166-2
; Sequence 2, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-135-166-2

Query Match 27.4%; Score 1136; DB 3; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMLGISPAP-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAI 61
Db 1 MKKLLIASLLFGITTTVFAAPFVAKDIRVDVGQDLEQQIRASLPVRAGQRTDNDVANI 60

Qy 62 IKSLEYATGFDDVRVETADGQLLTIVIERPTTGLSLNITGAKMLONDAIKKNLESFGLAOS 121
Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNLNDANGFKVG 120

Qy 122 QYFNQATLNOAVAGLKEEYLRGKLNIIQITPKYTKLARNRVDIDITIDEGSKAKITDIEF 181
Db 121 DVLIREKLNFEAKSVKHYASVGRYNATVEPIVNTLPNNRAELIIQINEDDKAKLASLTF 180

Qy 182 EGNQVYSDRKLMRQMSLTGGIW-TWLTRSNQFNEQKFAQDMKVTDFYQNNGYDFDFRIL 240
Db 181 KGNESVSSSTLQOMELQPDSSWKWLW---GNKFEQAQFEKDLQSIIRDYLLNNGYAKAQIT 237

Qy 241 DTDIQTNEDEKTKQTIKITYHEGGRFRWGKVSIGDITNEVPKAELEKLLT-MKPGKMYERQ 299
Db 238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGGM-SAELEPLLSALHLNDTFRS 296

Qy 300 QMTAVLGEIQNRMGSAGYASEISVQPLPNAETKTVDVLHIEPGRKIYVNEITHIGNNK 359
Db 297 DIADVENAIKAKLGERGYGSATVNSVPDFDANKTLAITLVVDAGRLLTVRQLRFEGNTV 356

Qy 360 TRDEVVRRELQWESAPYDTSKLQSKRVELLGYFDNVQFVDAVPLAGTDPKVDLNNSLT 419
Db 360 TRDEVVRRELQWESAPYDTSKLQSKRVELLGYFDNVQFVDAVPLAGTDPKVDLNNSLT 419

Qy 3 LKQIASALMLGISPAP-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAI 61
Db 1 MKKLLIASLLFGITTTVFAAPFVAKDIRVDVGQDLEQQIRASLPVRAGQRTDNDVANI 60

Qy 62 IKSLEYATGFDDVRVETADGQLLTIVIERPTTGLSLNITGAKMLONDAIKKNLESFGLAOS 121
Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNLNDANGFKVG 120

Qy 122 QYFNQATLNOAVAGLKEEYLRGKLNIIQITPKYTKLARNRVDIDITIDEGSKAKITDIEF 181
Db 121 DVLIREKLNFEAKSVKHYASVGRYNATVEPIVNTLPNNRAELIIQINEDDKAKLASLTF 180

Qy 182 EGNQVYSDRKLMRQMSLTGGIW-TWLTRSNQFNEQKFAQDMKVTDFYQNNGYDFDFRIL 240
Db 181 KGNESVSSSTLQOMELQPDSSWKWLW---GNKFEQAQFEKDLQSIIRDYLLNNGYAKAQIT 237

Qy 241 DTDIQTNEDEKTKQTIKITYHEGGRFRWGKVSIGDITNEVPKAELEKLLT-MKPGKMYERQ 299
Db 238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGGM-SAELEPLLSALHLNDTFRS 296

Qy 300 QMTAVLGEIQNRMGSAGYASEISVQPLPNAETKTVDVLHIEPGRKIYVNEITHIGNNK 359
Db 297 DIADVENAIKAKLGERGYGSATVNSVPDFDANKTLAITLVVDAGRLLTVRQLRFEGNTV 356

Qy 360 TRDEVVRRELQWESAPYDTSKLQSKRVELLGYFDNVQFVDAVPLAGTDPKVDLNNSLT 419
Db 360 TRDEVVRRELQWESAPYDTSKLQSKRVELLGYFDNVQFVDAVPLAGTDPKVDLNNSLT 419

RESULT 12

US-09-135-166-4

; Sequence 4, Application US/09135166

; Patent No. 6083743

Db 357 SADSTLRQEMRQSGTWYNSOLVELGKIRLDRGTFFETVENRIDPINGSDEVDVYVKV 416
Qy 420 ERSTGSLDLGAGWQDTGLVMSAGVSDNLFPGTKSAALRASRKTTLNGLSFTDPYFT 479
Db 417 ERNTGSIINFGLGYGTESGISYQASVKQDNFLGTGAASVIAAGTKNDYGTSLNGLVTEPYFT 476
Qy 480 ADGVSIGDYVVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVN 539
Db 477 KDGVSIGCNVFFENYDMSKSDTS-SNYKRTYGSNVTGLGPPVNNNSYYVGL-----GH 529
Qy 540 TYNKAPKH-----YADFIKKYG---KTDGTDGSGFKGMLYKGTGWSGNKTDLSALWPT 588
Db 530 TYNKISNFALEYNRLYIOSMKFKNGIKTNDPFSF-----GWNYSNLNRGYFPT 580
Qy 589 RGYLTGVNAEIALPGSKLQYYSATHNOTWFFPLSKTFTLMLGGE--VGIAGGYGRKTEIP 646
Db 581 KGVKASLGRVTPISGDNKYKLSADVQGFYPLDRDLHVVSAKASAGYANGFG-NKRLP 639
Qy 647 PFENFYGGGLSGVRGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSAELL 694
Db 640 FYQYTAGGIGSLRGFAYGIGNAIYAEYGNNGSGTGTFFKISSDVTGGNAIATASAEI 699
Qy 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNI-----YAGNTHK 746
Db 700 VPTFPVSDKSONTVRTSLFVDAASVWNTKWSKDN-----GLESVLRKLPDYGK----- 749
Qy 747 STFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFQOLGTTT 797
Db 750 ---SSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDDVEQFQSIGSGSF 797

RESULT 13

US-09-135-166-6
; Sequence 6, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-135-166-6

Query Match 27.4%; Score 1136; DB 3; Length 797;

Best Local Similarity 31.8%; Pred. No. 2.9e-87;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy 3 LKQIASALMMLGISPLAF-ADFTIQIRVEGLQRTPEPSTVFNYLPVKVGYDNTDTHGSAI 61
Db 1 MKLLIASLLFGTTTVPAPFVAKDIRVDGVQGLEQIIRASLPVRAGORVTDNDVANI 60
Qy 62 IKSLYATGFDDVRVETADQGLLTIVIERPTIGSLNITGAKMLQNDAIKNLSFGLAQS 121
Db 61 VRSLPVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVITPEALKQNLQDANGFKVG 120
Qy 122 QYFNQATLQAQVAGLKEEYVLRGKLNIIQITPKVTKLARNRVIDIDITIDEGSKAKITDIEF 181
Db 121 DVLIRREKLNEPAKSVKEHYASVGRYNATVEPIVNTLPNNRAETLIIQINEDDKAKASLTF 180
Qy 182 EGNQVYSDRKLRQMSLTGEGIW-TWLTSSNOFNEQKEADMEKVTDFYONNGYDFRIL 240
Db 181 KGNESVSSSTLQEQMELQPDSSWKLW---GNKPEGAQFEDQLQSIDYIYLNNGYAKAQIT 237
Qy 241 DTDIQTNEDKTKQITIKITVHEGGRFRWGVSEGDITNEVPKAELEKLLT-MKPGKWYERQ 299
Db 238 KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGM-SAELEPLLSALHLNDFRRS 296
Qy 300 QMTAVLGEIQNRMSAGYAYSEISVQPLNAETKTVDFVHLIEPGRKIYVNEIHTGNKK 359
Db 297 DIADVENAIKALGERGYGSATVNSVPDFDANKTLAITLVWDAGRRLTVRLRFEGNTV 356
Qy 360 TRDEVVRRELROMESAPYDTSKLQSKERVELLYGFDNVQFQDAVPLAGTDPKVDLMSLT 419
Db 357 SADSTLRQEMRQSGTWYNSOLVELGKIRLDRGTFFETVENRIDPINGSDEVDVYVKV 416
Qy 420 ERSTGSLDLGAGWQDTGLVMSAGVSDNLFPGTKSAALRASRKTTLNGLSFTDPYFT 479
Db 417 ERNTGSIINFGLGYGTESGISYQASVKQDNFLGTGAASVIAAGTKNDYGTSLNGLVTEPYFT 476
Qy 480 ADGVSIGDYVVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVN 539
Db 477 KDGVSIGCNVFFENYDMSKSDTS-SNYKRTYGSNVTGLGPPVNNNSYYVGL-----GH 529
Qy 540 TYNKAPKH-----YADFIKKYG---KTDGTDGSGFKGMLYKGTGWSGNKTDLSALWPT 588
Db 530 TYNKISNFALEYNRLYIOSMKFKNGIKTNDPFSF-----GWNYSNLNRGYFPT 580
Qy 589 RGYLTGVNAEIALPGSKLQYYSATHNOTWFFPLSKTFTLMLGGE--VGIAGGYGRKTEIP 646
Db 581 KGVKASLGRVTPISGDNKYKLSADVQGFYPLDRDLHVVSAKASAGYANGFG-NKRLP 639
Qy 647 PFENFYGGGLSGVRGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSAELL 694
Db 640 FYQYTAGGIGSLRGFAYGIGNAIYAEYGNNGSGTGTFFKISSDVTGGNAIATASAEI 699
Qy 695 FPMF--GAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNI-----YAGNTHK 746
Db 700 VPTFPVSDKSONTVRTSLFVDAASVWNTKWSKDN-----GLESVLRKLPDYGK----- 749
Qy 747 STFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKKKPEDEIQRFQOLGTTT 797
Db 750 ---SSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDDDVEQFQSIGSGSF 797

RESULT 14

US-08-942-046-2
; Sequence 2, Application US/08942046
; Patent No. 6284954
; GENERAL INFORMATION:

		LENGTH: 797 amino acids	
		TYPE: amino acid	
		TOPOLOGY: linear	
		MOLECULE TYPE: protein	
		US-08-942-046-4	
Query Match		27.4%; Score 1136; DB 3; Length 797;	
Best Local Similarity		31.6%; Pred. No. 2.9e-87;	
Matches: 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;			
Qy	3	LKQIASALMMIGISPLAF-ADFTIQDIRVEGLQRTPESTVENYLPVKVGDYNDTHGSAI	61
Db	1	MKLLIASLLFGTTTTFVFAAPFAVDIRVQGVQGDLEQOIRASLPVRAGQRTDNDVANI	60
Qy	62	IKSIYATGFFDDVRVETADGQGLLTIVTPTIGSLNITGAKMLQNDAIKMLSEFGLAQ	121
Db	61	VRSLFSGRFDVQAHQEGDVLVVSVAKSIISDVKIKGNSVIPTKALKQNLDFANGFKVG	120
Qy	122	QYFNOATLNOAVAGLKEEYLGKGLNQTTPKVTKLARNRVDIDITIDEGSKAKITDIEF	181
Db	121	DVLRKLENEPAKSVKEHYASVGRYNATVEPIVTLNPNRAEILIQINEDDKAKLASLTF	180
Qy	182	EGNOVYSRDKLMRQMSLTEGGIM-TWLTNRNQFNEQKFAQMEKVTDFYQNNGYDFPRIL	240
Db	181	KGNEVSVSSTIQEQMELQPDSSWKLW---GNKFQAQPEKDLQSIQIRDYLLNNGYAKAQIT	237
Qy	241	DTDIQTNEDKTKQIKITVHEGGRFRGKVSIEGDTNEVPKAELEKULT-MKPGKWYERQ	299
Db	238	KTDVQLNDEKTKVNVITDVNEGLQYDLRSARIIGNLGM-SAELEPLLSALHLNDTPRRS	296
Qy	300	QMTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVLHIEPRKIYVNEIHTGNK	359
Db	297	DIADVENAIKAKLGERGYGSATVNSVDFODANKTLAITLVVDAGRRLTVRQLRFEQNTV	356
Qy	360	TRDEWVRRELQRMESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNMSLT	419
Db	357	SADSTLQEQWRQOEGTWNQSVOLVELGKIRLDRTOFFETVENRIDPINGSNDEVVVYKVK	416
Qy	420	ERSTGSLDLGAGVQDVTGLVMSAGVSQDNLFQTKSAALRASRSKTTINGSLSTDPYFT	479
Db	417	ERNTGSIQFQYGTSGISYQASVKQDNFLGTGAASVIACTKNDYGTSVNLGYTEPYFT	476
Qy	480	ADGVSIGDYVYKAFDPRKASTSIQYKTTTAGAGIRMSVPVTEYDRNFGLVAEHLTVN	539
Db	477	KDGVSLGQNVFFENYDMSKSDTS-SNYKRTTYGSNVTLGFPVNNNSYYVGL-----GH	529
Qy	540	TYNKAPKH-----YADFIKKYG---KTDGTDGTFKGMLYKGTGVMGRNKTDSALWPT	588
Db	530	TYNKISNFALEYNRNLTIQSKFKGNGIKINDFDFSP-----GWNYSNLNRGYFPT	580
Qy	589	RGYLTGVNAEIALPGSKLQYYSATHNQTFWFPPLSKTFTLMLGGE--VGIAGGYGRTKEIP	646
Db	581	KGKASLGGRTVITPGSNKYIKLSADYQGFYPLDRDLWVVSASAKASAGYANGFG-NKRLP	639
Qy	647	PFENFYGGGLGVSURCYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSALL	694
Db	640	FYQTYTAGGIGSLRGFAFGYSGPNAIYAEYGNSSGTGTFKKIISDVIQGNALATASAEI	699
Qy	695	FPMP--GAKDARTVRLSIFADAGSVWDGKTYDDNSSSATGGRVONI-----YGAGNTHK	746
Db	700	VPTPFVSDKQNTVRTSLFVDAASVWNTKWSKDN-----GLESVDLRLPDYDK-----	749
Qy	747	STFTNELRYSGAGAVTWLSPLGPMKFRYAVPLKKKPEDEIQRFOQLGTTTF	797
Db	750	---SSRIRASTGVGFQWQSPIGPLVFSYAKPIKKYENDVDEQFQFSIGGSF	797

Search completed: July 6, 2005, 15:20:39
Job time : 68.3077 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 235.676 Seconds
(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQIASALMMLGISLAF.....LKKKPEDEIQRFOQLGTTTF 797

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- 1: A_Geneseq16Dec04:*
- 2: Geneseqp1980s:*
- 3: Geneseqp1990s:*
- 4: Geneseqp2000s:*
- 5: Geneseqp2001s:*
- 6: Geneseqp2002s:*
- 7: Geneseqp2003as:*
- 8: Geneseqp2003bs:*
- 8: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	4152	100.0	797	3	AAY84947 Amino aci
2	4152	100.0	797	5	ABP79802 Neisseria
3	4140	99.7	797	4	AAU03957 Neisseria
4	4140	99.7	797	4	AAU03957 Neisseria
5	4140	99.7	797	4	AAU03957 Neisseria
6	4136	99.6	797	4	AAU03959 Neisseria
7	4136	99.6	797	4	AAU04451 Neisseria
8	4136	99.6	797	4	AAU04451 Neisseria
9	4136	99.6	797	4	AAU04451 Neisseria
10	3956.5	95.3	792	4	AAU03958 Neisseria
11	3956.5	95.3	792	4	AAU03958 Neisseria
12	3956.5	95.3	792	4	AAU03958 Neisseria
13	3956.5	95.3	792	4	AAU03958 Neisseria
14	3956.5	95.3	792	6	ABP79748 N. gonorr
15	3937.5	94.8	792	3	AAU03958 Neisseria
16	3937.5	94.8	792	5	ABP79748 N. gonorr
17	3937.5	94.8	792	5	ABP79748 N. gonorr
18	1286.5	31.0	821	7	ABO72267 Pseudomon
19	1266.5	30.5	865	6	ADA36211 Acinetoba
20	1259	30.3	827	7	ADP06140 Bacteri
21	1240	29.9	798	6	ABM67563 Phototrab
22	1213.5	29.2	815	7	ABO65952 Klebsiell
23	1187.5	28.6	825	7	ABO61952 Klebsiell
24	1136	27.4	797	2	AAU03958 Neisseria
25	1134	27.3	797	2	AAU03958 Neisseria

26	1131	27.2	797	2	AAU03958 Neisseria
27	1114	26.8	793	2	AAU03958 Neisseria
28	1112	26.8	813	8	ADL05786 M. catarr
29	1109.5	26.7	792	2	AAU03958 Neisseria
30	1109	26.7	813	3	AAU03958 Neisseria
31	1109	26.7	813	3	AAU03958 Neisseria
32	990.5	23.9	792	8	ADH12911 Francisel
33	870.5	21.0	639	4	ABG17654 Novel hum
34	703	16.9	896	4	AAU03958 Neisseria
35	703	16.9	896	6	ABU92009 Omp100 po
36	703	16.9	896	7	ADG33885 L. intrac
37	703	16.9	896	7	ADJ66790 Lawsonia
38	703	16.9	896	8	ADR72942 Lawsonia
39	533	12.8	916	4	ABU03958 Neisseria
40	532	12.8	847	2	AAU03958 Neisseria
41	526	12.7	925	2	AAU03958 Neisseria
42	526	12.7	925	2	AAU03958 Neisseria
43	454.5	10.9	795	2	AAU03958 Neisseria
44	453	10.9	706	5	ABU51298 Helicobac
45	452.5	10.9	790	5	ABB90599 Chlamydia

ALIGNMENTS

RESULT 1

AAU84947

ID AAY84947 standard; protein; 797 AA.

XX

AC AAY84947;

XX

DT 21-AUG-2000 (first entry)

XX

DB Amino acid sequence of outer membrane protein (omp) 85.

XX

KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease; meningococcal infection; protective immune response; vaccine.

XX

OS Neisseria meningitidis.

XX

PN WO200023595-A1.

XX

PD 27-APR-2000.

XX

PF 22-OCT-1998; 98WO-US022352.

XX

PR 22-OCT-1998; 98WO-US022352.

XX

PA (UYMO-) UNIV MONTANA.

XX

PI Judd RC, Manning SD;

XX

DR WPI; 2000-339694/29.

XX

DR N-PSDB; AAA15156.

XX

PT New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N. meningitidis useful for vaccine, therapeutic and diagnostic compositions for gonococcal or meningococcal infections.

XX

PS Claim 41; Page 89-92; 98pp; English.

XX

CC The present sequence represents an outer membrane protein (omp) 85 of Neisseria meningitidis. The omp polypeptides and polynucleotides are useful in compositions for use in the prevention, treatment and diagnosis of non-symptomatic gonococcal infection or meningococcal infection and symptomatic disease. They are also useful for the detection of hybridisation complexes. Antigens and antibodies specific omp proteins also provide diagnostic, therapeutic and prophylactic compositions for the treatment or prevention of the infections described above. The CC antibodies are useful for inducing a protective immune response in humans or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria species. The proteins, antibodies and polynucleotide sequences of the present invention may also be used in the screening and development of

CC chemical compounds such as drugs or vaccines

XX Sequence 797 AA;

Query Match 100.0%; Score 4152; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 9e-281;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNOAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNOAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRDKLRQMSLTGEGITWLTLSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGEGITWLTLSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Qy 241 DTDIQTNEDKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Db 241 DTDIQTNEDKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300
Qy 301 MTAVLGSIONRMSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGSIONRMSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQMESAPYDTSKLRQSKERVLLGYFDNVQFDPVPLAGTDPKVDLNMSLTE 420
Db 361 RDEVVRRELQMESAPYDTSKLRQSKERVLLGYFDNVQFDPVPLAGTDPKVDLNMSLTE 420
Qy 421 RSTGSLDLSAGWQDITGLVMSAGVSQDNLFQTKGSAALRASRKTTLNGLSFTDPYFTA 480
Db 421 RSTGSLDLSAGWQDITGLVMSAGVSQDNLFQTKGSAALRASRKTTLNGLSFTDPYFTA 480
Qy 481 DGVSLGYDVYVKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSLGYDVYVKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHAYDFIKYKGTGDSFGKWLKGTGWRNKTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHAYDFIKYKGTGDSFGKWLKGTGWRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKIIPFFENFYGGGLGSVR 660
Db 601 LPSKLOYYSATHNQTFWFFPLSKTFTLMLGGEVGIAGGYGRTKIIPFFENFYGGGLGSVR 660
Qy 661 GYESGTILGPKVYDYGKISYGGNKKANVSNELLFPMPGAKARTVRLSLFADAGSVWDG 720
Db 661 GYESGTILGPKVYDYGKISYGGNKKANVSNELLFPMPGAKARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIORFQGLGTTTF 797
Db 781 KPEDEIORFQGLGTTTF 797

RESULT 2

ID ABB79802

XX ABB79802 standard; protein; 797 AA.

AC ABB79802;

XX 15-NOV-2002 (first entry)

DT 15-NOV-2002 (first entry)

XX 15-NOV-2002 (first entry)

DE Neisseria meningitidis outer membrane protein Omp85.
XX Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
KW antibacterial.
KW Neisseria meningitidis.
OS Neisseria meningitidis.

XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= Signal_peptide
FT Protein 22..797
FT /label= Mature_protein

XX US2002086028-A1.

XX 04-JUL-2002.

XX 26-NOV-2001; 2001US-00994192.

XX 22-OCT-1998; 98US-00177039.

XX (JUDD/) JUDD R C.

XX (MANN/) MANNING D S.

XX Judd RC, Manning DS;

XX WPI; 2002-642234/69.

XX Novel immunogenic composition for vaccinating against meningococcal or gonococcal infection, comprises Omp85 protein of Neisseria meningitidis or Neisseria gonorrhoeae, or nucleic acid encoding the protein.

XX Claim 13; Fig 5; 30pp; English.

XX The present sequence is that of the Neisseria meningitidis strain HH outer membrane protein 85 (Omp85), as predicted from a gene that was obtained from a genomic DNA by PCR amplification using primers based on the gonococcal omp85 gene. The meningococcal Omp85 protein is 95% identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed immunogenic compositions comprise N. meningitidis Omp85, its fragments, fusion proteins including the Omp85, or nucleic acids encoding them, which induce a protective immune response in a subject. The immunogenic compositions may also include an antigen from a heterologous or homologous pathogen, or a nucleic acid encoding it. They are used in a claimed method of vaccinating a human or animal against non-symptomatic meningococcal infection or symptomatic disease. A kit for diagnosing infection with N. meningitidis comprising labelled Omp85 is also claimed. The Omp85 polypeptides and polynucleotides are also useful in drug screening and development

XX Sequence 797 AA;

Query Match 100.0%; Score 4152; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 9e-281;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNOAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SOYFNOATLNOAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRDKLRQMSLTGEGITWLTLSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Db 181 FEGNQVYSRDKLRQMSLTGEGITWLTLSNQFNEQKFAQDMEKVTDYQNNGYFDFRIL 240
Qy 241 DTDIQTNEDKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQ 300

Db 241 DTDIQTNEDEKTKQTIKIVHEGGRFWGKVSIEGDTNEVPKAELEKLTMPKPKWYERQQ 300
 Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 Qy 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNNLSLITE 420
 Db 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNNLSLITE 420
 Qy 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
 Db 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
 Qy 481 DGVSIGLVYDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Db 481 DGVSIGLVYDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Qy 541 YNKAPKHVADFIKKYKTKTDGTSFGKWLKGTGWRGNKTDLSALWPTRGVLTGVNAEIA 600
 Db 541 YNKAPKHVADFIKKYKTKTDGTSFGKWLKGTGWRGNKTDLSALWPTRGVLTGVNAEIA 600
 Qy 601 LPSGKLOYYSATHNQTFWFFPLSKTFTLLMGGEVGIAGGYGRTEIPEFFENFYGGGLGSVR 660
 Db 601 LPSGKLOYYSATHNQTFWFFPLSKTFTLLMGGEVGIAGGYGRTEIPEFFENFYGGGLGSVR 660
 Qy 661 GYESGTLGPKVYDYGEKISYGGNKKANVSABLLFPMPGAKDARTVRLSLFADAGSVWDG 720
 Db 661 GYESGTLGPKVYDYGEKISYGGNKKANVSABLLFPMPGAKDARTVRLSLFADAGSVWDG 720
 Qy 721 KTYDDNSSATGGVQNYGAGNTHKSTFTNELRYSAGGAVTWLSPGPKMKFRYAYPLKK 780
 Db 721 KTYDDNSSATGGVQNYGAGNTHKSTFTNELRYSAGGAVTWLSPGPKMKFRYAYPLKK 780
 Qy 781 KPEDEIQRFQGLGTTFF 797
 Db 781 KPEDEIQRFQGLGTTFF 797
 RESULT 3
 AAU03957
 ID AAU03957 standard; protein; 797 AA.
 AC AAU03957;
 AC
 AC
 XX 23-OCT-2001 (first entry)
 DT
 XX
 DE Neisseria meningitidis serogroup B antigenic protein.
 XX
 XX Serogroup B antigen; pharynx; meningitis; septicemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX
 XX Neisseria meningitidis.
 OS
 OS
 FH Key Location/Qualifiers
 FT Peptide 1..221
 FT /note= "Signal peptide"
 FT Protein 22..797
 FT /note= "Mature N. meningitidis serogroup B antigen"
 FT Binding-site 715..722
 FT /note= "ATP/GTP-binding site motif A (P-loop)"
 XX
 XX W0200138350-A2.
 FN
 XX
 XX 31-MAY-2001.
 XX
 XX 28-NOV-2000; 2000WO-IB001851.
 PF
 XX 29-NOV-1999; 99GB-00028197.
 PR
 XX 09-MAR-2000; 2000GB-00005698.
 PR
 XX (CHIR-) CHIRON SPA.
 PA

PA (STAT-) STATENS INST FOLKEHELSE.
 XX Giuliani MM, Pizsa M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR N-PSDE; AAS07277.
 XX
 PT Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX
 XX Claim 1; Fig 1; 92pp; English.
 XX
 CC The sequence represents a Neisseria meningitidis serogroup B 85 kDa
 CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic protein is useful in the manufacture of a medicament for
 CC treating or preventing infection due to Neisseria bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of Neisseria bacteria or antibodies raised against
 CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast
 XX
 SQ Sequence 797 AA;
 Query Match 99.7%; Score 4140; DB 4; Length 797;
 Best Local Similarity 99.7%; Pred. No. 6.2e-280;
 Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 Qy 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
 Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
 Qy 121 SQYFNQATNLQAVAGLKEEYGRGKLNIIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180
 Db 121 SQYFNQATNLQAVAGLKEEYGRGKLNIIQITPKVTKLARNRVDIITIDEGSKAKITDIE 180
 Qy 181 FEGNQVYSRDKLRQMSLTEGGIWTWLTNRNQNEQKFAQDMKVTDFYQNGYFDFRIL 240
 Db 181 FEGNQVYSRDKLRQMSLTEGGIWTWLTNRNQNEQKFAQDMKVTDFYQNGYFDFRIL 240
 Qy 241 DTDIQTNEDEKTKQTIKIVHEGGRFWGKVSIEGDTNEVPKAELEKLTMPKPKWYERQQ 300
 Db 241 DTDIQTNEDEKTKQTIKIVHEGGRFWGKVSIEGDTNEVPKAELEKLTMPKPKWYERQQ 300
 Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 Qy 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNNLSLITE 420
 Db 361 RDEVVRRELQWESAPYDTSKLQSKERVELLGYFDNVQFQDAVPLAGTDPKVDLNNLSLITE 420
 Qy 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
 Db 421 RSTGSLDLGAGVQDQTLGVMAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
 Qy 481 DGVSIGLVYDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Db 481 DGVSIGLVYDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Qy 541 YNKAPKHVADFIKKYKTKTDGTSFGKWLKGTGWRGNKTDLSALWPTRGVLTGVNAEIA 600
 Db 541 YNKAPKHVADFIKKYKTKTDGTSFGKWLKGTGWRGNKTDLSALWPTRGVLTGVNAEIA 600
 Qy 601 LPSGKLOYYSATHNQTFWFFPLSKTFTLLMGGEVGIAGGYGRTEIPEFFENFYGGGLGSVR 660

Db 601 LPGSKLOYYSATHNQWTFPFLSKTFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPILGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPILGPMKFRYAYPLKK 780
Qy 781 KPEDEIORFQFOLGTTTF 797
Db 781 KPEDEIORFQFOLGTTTF 797
RESULT 4
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX AAB23784;
XX 12-JAN-2001 (first entry)
DT Neisseria meningitidis serogroup B amino acid sequence.
DE CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX Neisseria meningitidis.
OS WO200050075-A2.
XX 31-AUG-2000.
XX 09-FEB-2000; 2000WO-IB000176.
XX 26-FEB-1999; 99US-0121792P.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX WPI; 2001-015529/02.
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX Claim 22; Page 32; 39pp; English.
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA23385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
XX Sequence 797 AA;
Query Match 99.7%; Score 4140; DB 4; Length 797;
Best Local Similarity 99.7%; Pred. No. 6.2e-280;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKUKQIASALMMLGISPLAFADPTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKUKQIASALMMLGISPLALADPTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLVIERPTIGSLNITGAKMLQNDALIKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLVIERPTIGSLNITGAKMLQNDALIKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTYKLARNRVDITIDEGSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTYKLARNRVDITIDEGSAKITDIE 180
Qy 181 FEGNQVYSRKLQMRQMSLTEGGIWTWLRNQNQNEQKPAQDMKVTDFYQNNGYFDFRIL 240
Db 181 FEGNQVYSRKLQMRQMSLTEGGIWTWLRNQNQNEQKPAQDMKVTDFYQNNGYFDFRIL 240
Qy 241 DTDIOTNEDKTQTIKITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300
Db 241 DTDIOTNEDKTQTIKITVHEGGRFRWGVKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300
Qy 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQWESAPYDTSKLQRSKERVLLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQWESAPYDTSKLQRSKERVLLGYFDNVQFDVAVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLNAGWVQDTGLVMSAGVSQDNLFPGTKSAALRASRKTTLNGSLSTDPYFETA 480
Db 421 RSTGSLDLNAGWVQDTGLVMSAGVSQDNLFPGTKSAALRASRKTTLNGSLSTDPYFETA 480
Qy 481 DGVSLSGVDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSLSGVDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHYADFIKKYKTKDGTGSPKGMWLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKTKDGTGSPKGMWLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPGSKLOYYSATHNQWTFPFLSKTFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPFLSKTFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPILGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPILGPMKFRYAYPLKK 780
Qy 781 KPEDEIORFQFOLGTTTF 797
Db 781 KPEDEIORFQFOLGTTTF 797
RESULT 5
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX AAB84744;
AC 17-SEP-2001 (first entry)
DT Amino acid sequence of a Neisseria serogroup B protein.
XX Serogroup B protein; outer membrane protein; Neisserial infection;
XX vaccine.
XX Neisseria meningitidis.
XX Key Location/Qualifiers
FH

FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX WO200152885-A1.
XX 26-JUL-2001.
XX 17-JAN-2001; 2001WO-IB000166.
XX 17-JAN-2000; 2000GB-00001067.
XX 09-MAR-2000; 2000GB-00005699.
XX (CHIR-) CHIRON SPA.
XX Pizza M, Rappuoli R, Giuliani M;
XX WPI; 2001-451895/48.
XX N-PSDB; AAH42128.
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisseria bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX Disclosure; Page 59-61; 83pp; English.
XX The present sequence represents a Neisseria serogroup B protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO99/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
CC bacteria or of antibodies raised against Neisseria bacteria; and/or a
CC reagent which can raise antibodies against Neisseria bacteria. It may
CC also be used as a vaccine
XX Sequence 797 AA;
Query Match 99.7%; Score 4140; DB 4; Length 797;
Best Local Similarity 99.7%; Pred. No. 6.2e-280;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMLGLISPLAFADFTIQDIRVEGLQRTSPSTVENYLPVKVGTNDTHGSA 60
DB 1 MKLQIASALMLGLISPLAFADFTIQDIRVEGLQRTSPSTVENYLPVKVGTNDTHGSA 60
QY 61 IISLYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
DB 61 IISLYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLSEFGLAQ 120
QY 121 SQYFNQATLQNAVAGLKEEHLGRGLNIQTPKVKTLARNRVDITIDEGKSAKITDIE 180
DB 121 SQYFNQATLQNAVAGLKEEHLGRGLNIQTPKVKTLARNRVDITIDEGKSAKITDIE 180
QY 181 PEGNQVSDRKLMEQMSLTGEGITWLTTRSNQFNEQFAQDMKVDFYQNNGVDFPRIL 240
DB 181 PEGNQVSDRKLMEQMSLTGEGITWLTTRSNQFNEQFAQDMKVDFYQNNGVDFPRIL 240
QY 241 DTDIQTNEEDTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKVERQ 300
DB 241 DTDIQTNEEDTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKVERQ 300
QY 301 MTAVLGEIQNRMSGAGYAYSEISVQPLNPAETKTVDVFLHIEPGRKTYVNEIHTGNKT 360
DB 301 MTAVLGEIQNRMSGAGYAYSEISVQPLNPAETKTVDVFLHIEPGRKTYVNEIHTGNKT 360
QY 361 RDEVVRELQMESAPYDTSKLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNLMSLTE 420

DB 361 RDEVVRELQMESAPYDTSKLQSKERVLLGYFDNVQFADVPLAGTDPKVDLNLMSLTE 420
QY 421 RSTGSLDLISAGWYQDTGLVMSAGVSDQNLFGTGSAAALRASRSKTTILNGSLSTFDTPYFTA 480
DB 421 RSTGSLDLISAGWYQDTGLVMSAGVSDQNLFGTGSAAALRASRSKTTILNGSLSTFDTPYFTA 480
QY 481 DGVSGLGYDVYGVKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDVYGVKAFDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFKGWLKGTGVMGRNKTDSALMPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKGTGDTGDSFKGWLKGTGVMGRNKTDSALMPTRGYLTGVNAEIA 600
QY 601 LPSGKLOYYSATNQTWFFPLSKTFTILMLGGEVGIAGGYORTKEIIPFPENFYGGGLGSVR 660
DB 601 LPSGKLOYYSATNQTWFFPLSKTFTILMLGGEVGIAGGYORTKEIIPFPENFYGGGLGSVR 660
QY 661 GYESGTLGPVKYDEYGEKISYGGNKKANVSARELLFPMGAKDARTVRLSLPADAGSVWDG 720
DB 661 GYESGTLGPVKYDEYGEKISYGGNKKANVSARELLFPMGAKDARTVRLSLPADAGSVWDG 720
QY 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQGLGTTTF 797
DB 781 KPEDEIQRFQFQGLGTTTF 797
RESULT 6
AAU03959
ID AAU03959 standard; protein; 797 AA.
XX AAU03959;
AC AAU03959;
XX 23-OCT-2001 (first entry)
XX Neisseria gonorrhoeae antigenic protein.
KW Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.
OS Neisseria gonorrhoeae.
FH Key Location/Qualifiers
FT Peptide 1..21 "Signal peptide"
FT Protein 22..797
FT /note= "Mature N. gonorrhoeae antigen"
XX WO200138350-A2.
XX 31-MAY-2001.
XX 28-NOV-2000; 2000WO-IB001851.
XX 29-NOV-1999; 99GB-00028197.
XX 09-MAR-2000; 2000GB-00005698.
XX (CHIR-) CHIRON SPA.
XX (STAT-) STATENS INST FOLKEHELSE.
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
XX N-PSDB; AAS07279.
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisseria bacterial infection.

XX PS Claim 1; Page 37-39; 92pp; English.

CC The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.

CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the

CC pharynx, causing meningitis and, occasionally, septicaemia in the absence

CC of meningitis. This antigenic protein is useful in the manufacture of a

CC medicament for treating or preventing infection due to Neisseria

CC bacteria, such as meningitis and septicaemia. It is also useful as a

CC diagnostic reagent for detecting the presence of Neisseria bacteria or

CC antibodies raised against Neisseria, and as a reagent for raising the

CC antibodies. The Neisserial nucleotide sequences can be expressed in a

CC variety of different expression systems, for example, mammalian cells,

CC baculoviruses, plants, bacteria and yeast

XX SQ Sequence 797 AA;

Query Match 99.6%; Score 4136; DB 4; Length 797;

Best Local Similarity 99.6%; Pred. No. 1.2e-279;

Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKOIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Db 1 MKLKOIASALMLGIGISPLADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Qy 121 SOYFNOATINQAVAGLKEEYVGRKLNITQPKVKTLARNRVDITIDEGKSAKITDIE 180

Db 121 SOYFNOATINQAVAGLKEEYVGRKLNITQPKVKTLARNRVDITIDEGKSAKITDIE 180

Qy 181 FEGNOVYSDRKLQMSLTGGITWLTNRNFOEQFAQDMKVDFYQNGVDFPRIL 240

Db 181 FEGNOVYSDRKLQMSLTGGITWLTNRNFOEQFAQDMKVDFYQNGVDFPRIL 240

Qy 241 DTDIQTNEKTKQITIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Db 241 DTDIQTNEKTKQITIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Qy 301 MTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKT 360

Db 301 MTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVFLHIEPGRKIYNEIHTGNKT 360

Qy 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGVDFNDVQFADVLACTPDKVDLNMSLTE 420

Db 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGVDFNDVQFADVLACTPDKVDLNMSLTE 420

Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSFDPVFTA 480

Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFQTKSAALRASRSKTTLLNGSLSFDPVFTA 480

Qy 481 DGVSLGVDYVTKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Db 481 DGVSLGVDYVTKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Qy 541 YNKAPKHVADFIKKYKGTGDCGFKWLYKGTWGRNKTDSALMPTRCYLTGVNAEIA 600

Db 541 YNKAPKHVADFIKKYKGTGDCGFKWLYKGTWGRNKTDSALMPTRCYLTGVNAEIA 600

Qy 601 LPQSKLYYSATHNQTFPFLSKTFTLLMGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660

Db 601 LPQSKLYYSATHNQTFPFLSKTFTLLMGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDYGKISYGGNKKANVAEALLFPMFGAKDARTVRLSLFADAGSVWDG 720

Db 661 GYESGTLGPKVYDYGKISYGGNKKANVAEALLFPMFGAKDARTVRLSLFADAGSVWDG 720

Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKERYAYPLKK 780

Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKERYAYPLKK 780

Qy 781 KPDEIQRFQFQLGTTTF 797

Db 781 KPDEIQRFQFQLGTTTF 797

RESULT 7

ID AAU04451

XX AAU04451 standard; protein; 797 AA.

AC AAU04451;

XX 23-OCT-2001 (first entry)

DE Neisseria meningitidis serogroup A antigenic protein #2.

XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;

XX bacterial infection; baculovirus; yeast.

OS Neisseria meningitidis.

FH Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "Signal peptide"

FT /note= "Mature N. meningitidis serogroup A antigen"

XX WO200138350-A2.

PN 31-MAY-2001.

PD 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

PR 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

PA (STAT-) STATENS INST FOLKEHELS.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

PI WPI; 2001-381289/40.

DR Novel 85 kDa antigen from Neisseria meningitidis and Neisseria

PT gonorrhoeae, useful in the manufacture of a medicament for treating and

PT preventing Neisserial bacteria infection.

XX Claim 1; Page 39-40; 92pp; English.

PS The sequence represents a Neisseria meningitidis serogroup A 85 kDa

CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing

CC meningitis and, occasionally, septicaemia in the absence of meningitis.

CC This antigenic protein is useful in the manufacture of a medicament for

CC treating or preventing infection due to Neisseria bacteria, such as

CC meningitis and septicaemia. It is also useful as a diagnostic reagent for

CC detecting the presence of Neisseria bacteria or antibodies raised against

CC Neisseria, and as a reagent for raising the antibodies. The Neisserial

CC nucleotide sequences can be expressed in a variety of different

CC expression systems, for example, mammalian cells, baculoviruses, plants,

CC bacteria and yeast. Note: There are two versions of this sequence

CC displayed in the specification (see AAU03958)

XX SQ Sequence 797 AA;

Query Match 99.6%; Score 4136; DB 4; Length 797;

Best Local Similarity 99.6%; Pred. No. 1.2e-279;

Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKOIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Db 1 MKLKOIASALMLGIGISPLADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120

Db 61 IISLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQ 120
 QY 121 SOYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGSKAKITDIE 180
 Db 121 SOYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGSKAKITDIE 180
 QY 181 FEGNQVYSRDLKMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDYQNGYFDFRIL 240
 Db 181 FEGNQVYSRDLKMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDYQNGYFDFRIL 240
 QY 241 DTDIQTNEKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTKMPKGYERQ 300
 Db 241 DTDIQTNEKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTKMPKGYERQ 300
 QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
 Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
 QY 361 RDEVVRRELQMESAPYDTSKLQSKERVELLGYFDNVQFPAVPLAGTPDKVDLNMSLTE 420
 Db 361 RDEVVRRELQMESAPYDTSKLQSKERVELLGYFDNVQFPAVPLAGTPDKVDLNMSLTE 420
 QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTA 480
 Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTA 480
 QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYKTDGTDGSGFKGLYKGTGWRNKTDLSALWPTRGVLTGVNAEIA 600
 Db 541 YNKAPKHYADFIKKYKTDGTDGSGFKGLYKGTGWRNKTDLSALWPTRGVLTGVNAEIA 600
 QY 601 LPGSKLQYISATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIIPFFENFYGGGLSVR 660
 Db 601 LPGSKLQYISATHNQTFWFFPLSKTFTLMLGGEVGIAGYGRKTEIIPFFENFYGGGLSVR 660
 QY 661 GYESGTILGPKVYDYBYSKISYGGNKKANVASALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 Db 661 GYESGTILGPKVYDYBYSKISYGGNKKANVASALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGATVWLSPLGPMKERYAYPLKK 780
 Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGATVWLSPLGPMKERYAYPLKK 780
 QY 781 KPEDEIQRFQGLGTF 797
 Db 781 KPEDEIQRFQGLGTF 797

RESULT 8

AAB23788
 ID AAB23788 standard; protein; 797 AA.
 AC AAB23788;
 DT 12-JAN-2001 (first entry)
 DE Neisseria meningitidis serogroup A amino acid sequence.
 KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
 KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
 KW immune response.
 OS Neisseria meningitidis.
 PN WO200050075-A2.
 XX 31-AUG-2000.
 PF 09-FEB-2000; 2000WO-IB000176.

XX 26-FEB-1999; 99US-0121792P.
 PA (CHIR-) CHIRON SPA.
 PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 DR WPI; 2001-015529/02.
 XX Immunogenic composition useful for stimulating an immune response in a
 PT mammal against Neisseria infection, comprises Neisseria antigen and an
 PT adjuvant composition comprising an oligonucleotide with a CG motif.
 XX Claim 22; Page 33; 39pp; English.
 XX The present invention describes an immunogenic composition (I) comprising
 CC a Neisseria antigen and an adjuvant composition comprising an
 CC oligonucleotide comprising at least 1 CG motif. Also described is an
 CC adjuvant composition (II) comprising an oligonucleotide which comprises
 CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
 CC oligonucleotide preferably comprises at least one phosphorothioate bond.
 CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
 CC the present invention. (I) is useful for stimulating an immune response
 CC in a mammal, preferably a human, against Neisseria infection, preferably
 CC Neisseria meningitidis infection and in the manufacture of a medicament
 CC for inducing a protective immune response in a mammal. The present
 CC sequence represents the claimed Neisseria meningitidis serogroup A amino
 CC acid sequence disclosed in GB-9928197.4, which is given in the present
 CC invention
 XX SQ Sequence 797 AA;
 Query Match 99.8%; Score 4136; DB 4; Length 797;
 Best Local Similarity 99.6%; Pred. No. 1.2e-279;
 Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 MKLKOTASALMWLGISPLAPADFTIODIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
 Db 1 MKLKQIASALMWLGISPLADFTIODIRVEGQRTPESTVFNYPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQ 120
 Db 61 IIKSLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDALKNLESFGLAQ 120
 QY 121 SOYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGSKAKITDIE 180
 Db 121 SOYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGSKAKITDIE 180
 QY 181 FEGNQVYSRDLKMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDYQNGYFDFRIL 240
 Db 181 FEGNQVYSRDLKMRQMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDYQNGYFDFRIL 240
 QY 241 DTDIQTNEKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTKMPKGYERQ 300
 Db 241 DTDIQTNEKTKQTIKITVHEGGRFRGKVSIEGDTNEVPKAELEKLLTKMPKGYERQ 300
 QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
 Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKT 360
 QY 361 RDEVVRRELQMESAPYDTSKLQSKERVELLGYFDNVQFPAVPLAGTPDKVDLNMSLTE 420
 Db 361 RDEVVRRELQMESAPYDTSKLQSKERVELLGYFDNVQFPAVPLAGTPDKVDLNMSLTE 420
 QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTA 480
 Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTA 480
 QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYKTDGTDGSGFKGLYKGTGWRNKTDLSALWPTRGVLTGVNAEIA 600

||||| 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
||||| 601 LPSGKLOYSAATHNOTWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
||||| 601 LPSGKLOYSAATHNOTWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
661 GYESGTLGPKVYDYBGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
661 GYESGTLGPKVYDYBGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
781 KPEDEIQRFQFQLGTTTF 797
781 KPEDEIQRFQFQLGTTTF 797
RESULT 9
AAB84746
ID AAB84746 standard; protein; 797 AA.
XX AAB84746;
XX AAB84746;
DT 17-SEP-2001 (first entry)
XX Amino acid sequence of a Neisseria serogroup A protein.
DE Serogroup A protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "signal peptide"
FT Protein 22..797
FT Protein /note= "mature protein"
XX WO200152885-A1.
XX
XX 26-JUL-2001.
XX 17-JAN-2001; 2001WO-IB000166.
XX 17-JAN-2000; 2000GB-00001067.
XX 09-MAR-2000; 2000GB-00005699.
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M, Rappuoli R, Giuliani M;
XX
XX WPI; 2001-451895/48.
XX N-PSDB; AAH42130.
XX
XX Composition for treating or preventing infection to, detecting, or for
XX raising antibodies against Neisserial bacteria, comprises an N.
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component.
XX
XX Disclosure; Page 71-74; 83pp; English.
XX
XX The present sequence represents a Neisseria serogroup A protein. The
XX protein is used to produce the compositions of the invention. The
XX specification describes a composition, comprising a Neisseria
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component. The immunogenic component is protein disclosed in WO99/57280,
XX WO99/36544, WO99/24578, WO99/56791, WO97/28273, WO96/29412, WO95/03413,
XX WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
XX TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
XX medicament for treating or preventing infection due to Neisserial

CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX
XX Sequence 797 AA;
Query Match 99.6%; Score 4136; DB 4; Length 797;
Best Local Similarity 99.6%; Pred. No. 1.2e-279;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 1 MKLKQIASALMLGIGSLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKLKQIASALMLGIGSLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYLGRGKLNIIQITPKVTKLARNRVDIDITIDEGKSAKITDIE 180
Qy 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQNEQKPAQDMKVTDFQNNNGYFDFRIL 240
Db 181 FEGNQVYSRDKLMRQMSLTEGGIWTWLTNRNQNEQKPAQDMKVTDFQNNNGYFDFRIL 240
Qy 241 DTDIQNEDKTKTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKWYERQQ 300
Db 241 DTDIQNEDKTKTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKWYERQQ 300
Qy 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEBGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEBGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQWESAPYDTSKLQSKERVVELLYGFQNVQFQFVPLAGTDPKVDLNNSLTE 420
Db 361 RDEVVRRELQWESAPYDTSKLQSKERVVELLYGFQNVQFQFVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFQTKSAAALRASRKTTLNGLSFTDPYFTA 480
Db 421 RSTGSLDLGAGWQDVTGLVMSAGVSQDNLFQTKSAAALRASRKTTLNGLSFTDPYFTA 480
Qy 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPHYADFIKKYKTDGDFGSKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIA 600
Qy 601 LPSGKLOYSAATHNOTWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
Db 601 LPSGKLOYSAATHNOTWFFPLSKTFTLMLGGEVGIAGYGRKTEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYBGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDYBGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQFQLGTTTF 797
Db 781 KPEDEIQRFQFQLGTTTF 797
RESULT 10
AAU03958
ID AAU03958 standard; protein; 792 AA.
XX
XX AAU03958;

XX 23-OCT-2001 (first entry)
 XX Neisseria meningitidis serogroup A antigenic protein #1.
 DE Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX Neisseria meningitidis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21 /note= "Signal peptide"
 FT Protein 22..792 /note= "Mature N. meningitidis serogroup A antigen"
 FT
 XX WO200138350-A2.
 FN
 XX 31-MAY-2001.
 PD
 XX 28-NOV-2000; 2000WO-IB001851.
 PF
 XX 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 PR
 XX (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 PA
 XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
 PI
 XX WPI; 2001-381289/40.
 DR N-PSDB; AAS07278.
 DR
 XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX
 XX Claim 1; Page 66-68; 92pp; English.
 PS
 XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa
 CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic protein is useful in the manufacture of a medicament for
 CC treating or preventing infection due to Neisseria bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of Neisseria bacteria or antibodies raised against
 CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast. Note: There are two versions of this sequence
 CC displayed in the specification (see AAU04451)
 XX
 XX Sequence 792 AA;
 SQ
 Query Match 95.38; Score 3956.5; DB 4; Length 792;
 Best Local Similarity 95.48; Pred. No. 3.9e-267;
 Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQIRVEGLQRTPESTVFVYLPVKVGDTYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQIRVEGLQRTPESTVFVYLPVKVGDTYNDTHGSA 60
 QY 61 IISLSYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
 DB 61 IISLSYATGFFDVRVETADQQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLAQ 120
 QY 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVKLARNRVDITIDEGSAKITDIE 180
 DB 121 SOYFNQATLNQAVAGLKEEYLGKGLNIQITPKVKLARNRVDITIDEGSAKITDIE 180
 QY 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRNQNEOKFAODMEKVTDFYQNNGVDFPRIL 240
 DB 181 FEGNQVYSDRKLQMSLTGGIWTWLTNRSDRDFQKFAODMEKVTDFYQNNGVDFPRIL 240

QY 241 DTDIQTNEKTKOTIKITVHEGGRFRWGVKYSIRGDTNEVPKAELEKLLTMKPGKMYERQQ 300
 DB 241 DTDIQTNEKTKOTIKITVHEGGRFRWGVKYSIRGDTNEVPKAELEKLLTMKPGKMYERQQ 300
 QY 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 QY 361 RDEVRRERLQMESAPYDTSKLORSKERVVELLGYFDNVQPDVPLAGTDPKVDLNNSLTE 420
 DB 361 RDEVRRERLQMESAPYDTSKLORSKERVVELLGYFDNVQPDVPLAGTDPKVDLNNSLTE 420
 QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGCKSAALRASRSKTTLNGSLSTFDPVFTA 480
 DB 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFGTGCKSAALRASRSKTTLNGSLSTFDPVFTA 480
 QY 481 DGVSIGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVSIGYDVYVGKAFDPRKASTSVKQYKTTTAGGVRMGIPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPHYADFIKKYOKTDTGSGFKGWLKYGTVGGRNKTDTSALWPTRGYLTGCVNAEIA 600
 DB 541 YNKAPRYADFIKKYOKTDTGSGFKGWLKYGTVGGRNKTDTSALWPTRGYLTGCVNAEIA 600
 QY 601 LPGSKLOYYSATHNQTWFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
 DB 601 LPGSKLOYYSATHNQTWFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
 QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANYSALLPMPGAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANYSALLPMPGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVAVTWLSPLGPMKFRYAYPLKK 780
 DB 721 RTY- ---TAAENGNNKSVY- SENAHKSTFTNELRYSGAGVAVTWLSPLGPMKFRYAYPLKK 775
 QY 781 KPEDEIQRFQFQGLGTTTF 797
 DB 776 KPEDEIQRFQFQGLGTTTF 792
 RESULT 11
 AAB23786
 ID AAB23786 standard; protein; 792 AA.
 XX
 XX AAB23786;
 AC
 XX 11-SEP-2003 (revised)
 DT 12-JAN-2001 (first entry)
 XX
 XX Neisseria gonorrhoeae amino acid sequence.
 XX
 XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
 KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
 KW immune response.
 XX
 XX Neisseria gonorrhoeae.
 OS
 XX WO200050075-A2.
 PN
 XX 31-AUG-2000.
 PD
 XX 09-FEB-2000; 2000WO-IB000176.
 PF
 XX 26-FEB-1999; 99US-0121792P.
 PR (CHIR-) CHIRON SPA.
 PA
 XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 PI WPI; 2001-015529/02.
 XX

XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against *Neisseria* infection, comprises *Neisseria* antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
PS Claim 22; Page 32; 39pp; English.
XX

CC The present invention describes an immunogenic composition (I) comprising
CC a *Neisseria* antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against *Neisseria* infection, preferably
CC *Neisseria meningitidis* infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed *Neisseria gonorrhoeae* amino acid sequence
CC disclosed in GB-9928197.4, which is given in the present invention.
CC (Updated on 11-SEP-2003 to standardise OS field)
XX Sequence 792 AA;
SQ

Query Match 95.3%; Score 3956.5; DB 4; Length 792;
Best Local Similarity 95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

Qy 1 MKLKOIASALMMLGISPLAFADFTIQDIRVEGQRTPESTFVFNLPVKVGDYNDTHGSA 60
Db 1 MKLKOIASALMMLGISPLAFADFTIQDIRVEGQRTPESTFVFNLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTIVERTPTIGSLNITGAKMLQNDIAIKNLESFGLAQ 120
Qy 121 SQYFNQATLQNAVAGLKEEYVGRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLQNAVAGLKEEYVGRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Qy 181 PEGNOVYSDRKLMQMSLTGGIITWLTTRSNQFNEQKFAQDMKVDFYQNGVDFPRIL 240
Db 181 PEGNOVYSDRKLMQMSLTGGIITWLTTRSDRDFQRKFAQDMKVDFYQNGVDFPRIL 240
Qy 241 DTDITQTNEDKTKQITKIVTVEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
Db 241 DTDITQTNEDKTKQITKIVTVEGGRFRGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQ 300
Qy 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDEVVRRELQMESAPYDTSKLQSKERVLLGYFDNVQDPAVLACTPDKVDLNLSTE 420
Db 361 RDEVVRRELQMESAPYDTSKLQSKERVLLGYFDNVQDPAVLACTPDKVDLNLSTE 420
Qy 421 RSTGSLDLASAGVQDVTGLNVMSAGVSDNLPFTGKSAALRASRKTTLNGSLSTFDPYFTA 480
Db 421 RSTGSLDLASAGVQDVTGLNVMSAGVSDNLPFTGKSAALRASRKTTLNGSLSTFDPYFTA 480
Qy 481 DGVSGLYDVTGKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLYDVTGKAPDPKASTSVKQYKTTTAGGGVRMGIPVTEYDRVNFGLAAEHLTVNT 540
Qy 541 YNKAPKHVAFIKKYGKTDGDSFKGLYKVTGCKNTDSALWTRCVLTGVNAEIA 600
Db 541 YNKAPKHVAFIRKYGKTDGDSFKGLYKVTGCKNTDSASWTRCVLTGVNAEIA 600
Qy 601 LPQSKLOYYSATHNQTFWFFPLSKTFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPQSKLOYYSATHNQTFWFFPLSKTFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDYEYGEKISYGGNKKANVSAELLFPMPGAADARTVRLSLFADAGSVWDG 720

Db 661 GYESGTLGPKVYDYEYGEKISYGGNKKANVSAELLFPMPGAADARTVRLSLFADAGSVWDG 720
Qy 721 KYTDDNSAGTGRVQNIYAGAGTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 RTY----TAENGNNKSVY-SENAHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 775
Qy 781 KPDEIQRFQFQGLGTTTF 797
Db 776 KPDEIQRFQFQGLGTTTF 792

RESULT 12
AAB84745
ID AAB84745 standard; protein; 792 AA.
XX AAB84745;
XX AC
XX 11-SEP-2003 (revised)
DT 17-SEP-2001 (first entry)
XX XX
DE Amino acid sequence of a *Neisseria gonorrhoeae* protein.
XX
XX Serogroup B protein; outer membrane protein; *Neisseria* infection;
KW vaccine.
XX
XX *Neisseria gonorrhoeae*.
XX
XX Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Protein 22..792 /note= "mature protein"
FT
XX
XX WC200152885-A1.
XX
XX 26-JUL-2001.
XX
XX 17-JAN-2001; 2001WO-1B000166.
XX
XX 17-JAN-2000; 2000GB-00001067.
XX 09-MAR-2000; 2000GB-00005699.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Pizza M, Rappuoli R, Giuliani M;
XX
XX WPI; 2001-451895/48.
XX N-PSDB; AAH42129.
XX
XX Composition for treating or preventing infection to, detecting, or for
XX raising antibodies against *Neisseria* bacteria, comprises an N.
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component.
XX
XX Disclosure; Page 65-67; 83pp; English.
XX
XX The present sequence represents a *Neisseria gonorrhoeae* protein. The
XX protein is used to produce the compositions of the invention. The
XX specification describes a composition, comprising a *Neisseria*
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component. The immunogenic component is protein disclosed in WO99/57280,
XX WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
XX WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
XX TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
XX medicament for treating or preventing infection due to *Neisseria*
XX bacteria; a diagnostic reagent for detecting the presence of *Neisseria*
XX bacteria; or of antibodies raised against *Neisseria* bacteria; and/or a
XX reagent which can raise antibodies against *Neisseria* bacteria. It may
XX also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS
XX field)
XX Sequence 792 AA;

Query Match 95.3%; Score 3956.5; DB 4; Length 792;
Best Local Similarity 95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGPDVVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGPDVVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLRGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SOYFNOATLNQAVAGLKEEYLRGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180

QY 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRSNQFNQKPAQDMKVTDFYQNNGYDFPRIL 240
DB 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRSDRFDQKFAQDMKVTDFYQNNGYDFPRIL 240

QY 241 DTDIOTNEDKTKQTIKIVHEGGRFRNGKVSIEGDTNEVPKAELEKLLTWKPKWYERQ 300
DB 241 DTDIOTNEDKTKQTIKIVHEGGRFRNGKVSIEGDTNEVPKAELEKLLTWKPKWYERQ 300

QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

QY 361 RDEYVRELRQMESAPYDTSKLQSKERVELLGYFDNVQFADVPDAVLACTPKVDLNSLTE 420
DB 361 RDEYVRELRQMESAPYDTSKLQSKERVELLGYFDNVQFADVPDAVLACTPKVDLNSLTE 420

QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSTFDYFETA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSTFDYFETA 480

QY 481 DGVSLSGVDYVKGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLSGVDYVKGKAFDPRKASTSVQYKTTTAGGGVRMGIPTVEYDRVNFGLAAEHLTVNT 540

QY 541 YNKAPKHYADPIKYGKTDGSGFKGWLKGTGMRNKTDSALMPTRGYLETVNAEIA 600
DB 541 YNKAPKHYADPIKYGKTDGSGFKGWLKGTGMRNKTDSASWPTRGYLETVNAEIA 600

QY 601 LPGSKLYYSATHNQTFWPLSKTFTLMLGGEVGIAGYGRKTEIIPFFENFYGGGLGSVR 660
DB 601 LPGSKLYYSATHNQTFWPLSKTFTLMLGGEVGIAGYGRKTEIIPFFENFYGGGLGSVR 660

QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720

QY 721 KTYDDNSSSATGGRVQNIYGAGNTHKSTFNEILRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
DB 721 RTY----TAENGNNKSVY-SENAAKSTFNEILRYSAGGAVTWLSPLGPMKFRYAYPLKK 775

QY 781 KPEDEIQRFQGLGTTTF 797
DB 776 KPEDEIQRFQGLGTTTF 792

RESULT 13

ABP80499
ID ABP80499 standard; protein; 792 AA.

XX AC ABP80499;

XX DT 07-MAR-2003 (first entry)

XX DE N. gonorrhoeae amino acid sequence SEQ ID 7528.

XX KW Antibacterial; infection; vaccine; gene therapy.

XX OS Neisseria gonorrhoeae.
XX PN WO200279243-A2.
XX 10-OCT-2002.
XX PD 12-FEB-2002; 2002WO-IB002069.
XX PF 12-FEB-2001; 2001GB-00003424.
XX PR (CHIR-) CHIRON SPA.
XX PA Fontana MR, Pizza M, Maignani V, Monaci E;
XX PI WPI; 2003-058415/05.
XX DR N-PSDB; ABZ41469.
XX PT New protein from Neisseria gonorrhoeae, useful for the manufacture of a
XX PS medicament for treating or preventing N. gonorrhoeae infection.
XX PS Disclosure; Page 736; 815pp; English.
XX CC The present invention relates to proteins from Neisseria gonorrhoeae.
XX CC Also disclosed are the nucleic acid molecules encoding the proteins and
XX CC antibodies that specifically bind to the proteins. The composition
XX CC comprising the protein, nucleic acid or antibody is useful for the
XX CC manufacture of a medicament for treating or preventing N. gonorrhoeae
XX CC infection, this may be in the form of a vaccine or gene therapy.
XX CC Sequences given in records ABP76736-ABP81046 represent nucleic acid
XX CC molecules of the invention
XX SQ Sequence 792 AA;

Query Match 95.3%; Score 3956.5; DB 6; Length 792;
Best Local Similarity 95.4%; Pred. No. 3.9e-267;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGPDVVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGPDVVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

QY 121 SOYFNOATLNQAVAGLKEEYLRGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
DB 121 SOYFNOATLNQAVAGLKEEYLRGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180

QY 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRSNQFNQKPAQDMKVTDFYQNNGYDFPRIL 240
DB 181 FEGNQVYSRDKLMQMSLTGGIWTWLTNRSDRFDQKFAQDMKVTDFYQNNGYDFPRIL 240

QY 241 DTDIOTNEDKTKQTIKIVHEGGRFRNGKVSIEGDTNEVPKAELEKLLTWKPKWYERQ 300
DB 241 DTDIOTNEDKTKQTIKIVHEGGRFRNGKVSIEGDTNEVPKAELEKLLTWKPKWYERQ 300

QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

QY 361 RDEYVRELRQMESAPYDTSKLQSKERVELLGYFDNVQFADVPDAVLACTPKVDLNSLTE 420
DB 361 RDEYVRELRQMESAPYDTSKLQSKERVELLGYFDNVQFADVPDAVLACTPKVDLNSLTE 420

QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSTFDYFETA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSTFDYFETA 480

QY 481 DGVSLSGVDYVKGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLSGVDYVKGKAFDPRKASTSVQYKTTTAGGGVRMGIPTVEYDRVNFGLAAEHLTVNT 540

Qy	541	YNKPKHYADFIKKYGKTDGDSFGKGLYKGTVGWGRNKTDGALMPTRGYLTVGNVNAEIA	600
Db	541	YNKPKRYADFIKKYGKTDGADGSGFKGLLYKGTVGWGRNKTDGASWPTRGYLTVGNVNAEIA	600
Qy	601	LPGSKLOYYSATHNOTWFFPPLSKFTFTMLGGEVGIAGGYGRTEIIPFFENFYGGGLGSVR	660
Db	601	LPGSKLOYYSATHNOTWFFPPLSKFTFTMLGGEVGIAGGYGRTEIIPFFENFYGGGLGSVR	660
Qy	661	GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAADARTVRLSLFADAGSVWDG	720
Db	661	GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAADARTVRLSLFADAGSVWDG	720
Qy	721	KTYDSSSSATGRYONTYAGANTHKSTFTNLEYSAGGAVTWLSPGPMKFRYAYPLKK	780
Db	721	RTV---TAAENGNNKSVY-SENAHKSTFTNLEYSAGGAVTWLSPGPMKFSYAYPLKK	775
Qy	781	KPEDEIQRFQFOLGTTTF 797	
Db	776	KPEDEIQRFQFOLGTTTF 792	
RESULT 14			
ABP79748			
ID	ABP79748 standard; protein; 792 AA.		
XX	AC		
XX	ABP79748;		
XX	DT 07-MAR-2003 (first entry)		
XX	N. gonorrhoeae amino acid sequence SEQ ID 6026.		
DE	Antibacterial; infection; vaccine; gene therapy.		
XX	Neisseria gonorrhoeae.		
OS	WO200279243-A2.		
XX	10-OCT-2002.		
XX	12-FEB-2002; 2002WO-IB002069.		
XX	12-FEB-2001; 2001GB-00003424.		
PR	(CHIR-) CHIRON SPA.		
XX	Fontana MR, Pizza M, Masignani V, Monaci E;		
PI	WPI; 2003-058415/05.		
XX	N-PSDB; AB240718.		
DR	New protein from Neisseria gonorrhoeae, useful for the manufacture of a		
PT	medicament for treating or preventing N. gonorrhoeae infection.		
XX	Disclosure; Page 628; 815pp; English.		
PS	The present invention relates to proteins from Neisseria gonorrhoeae.		
XX	Also disclosed are the nucleic acid molecules encoding the proteins and		
CC	antibodies that specifically bind to the proteins. The composition		
CC	comprising the protein, nucleic acid or antibody is useful for the		
CC	manufacture of a medicament for treating or preventing N. gonorrhoeae		
CC	infection, this may be in the form of a vaccine or gene therapy.		
CC	Sequences given in records ABP76736-ABP81046 represent nucleic acid		
CC	molecules of the invention		
XX	Sequence 792 AA;		
SQ	Query Match 95.3%; Score 3956.5; DB 6; Length 792;		
	Best Local Similarity 95.4%; Pred No. 3.9e-267;		
	Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2		
Qy	1	MKLKQIASLMMGLISPLAFADFTIQDIRVEGLQRTPEFTVFNLYPVKVGDTVNDTHGSA	60

/note= "signal peptide"

PT WO200023595-A1.
PN 27-APR-2000.
PD 22-OCT-1998; 98WO-US022352.
PF 22-OCT-1998; 98WO-US022352.
PR 22-OCT-1998; 98WO-US022352.
PX (UYMO-) UNIV MONTANA.
PY Judd RC, Manning SD;
PZ WPI; 2000-339694/29.
DR N-PSDB; AAA15155.
XX New isolated outer membrane protein 85 of *Neisseria gonorrhoeae* and *N.*
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions
XX for gonococcal or meningococcal infections.
XX Claim 1; Fig 2; 98pp; English.
XX
XX The present sequence represents an outer membrane protein (omp) 85 of
XX *Neisseria gonorrhoeae*. The omp polypeptides and polynucleotides are
XX useful in compositions for use in the prevention, treatment and diagnosis
XX of non-symptomatic gonococcal infection or meningococcal infection and
XX of symptomatic disease. They are also useful for the detection of
XX hybridisation complexes. Antigens and antibodies specific omp proteins
XX also provide diagnostic, therapeutic and prophylactic compositions for
XX the treatment or prevention of the infections described above. The
XX antibodies are useful for inducing a protective immune response in humans
XX or animals with *N. gonorrhoeae*, *N. meningitidis*, or other *Neisseria*
XX species. The proteins, antibodies and polynucleotide sequences of the
XX present invention may also be used in the screening and development of
XX chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
XX Sequence 792 AA;
Query Match 94.8%; Score 3937.5; DB 3; Length 792;
Best Local Similarity 95.1%; Pred. No. 8.3e-266;
Matches 758; Conservative 16; Mismatches 18; Indels 5; Gaps 2;
QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
DB 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60
QY 61 IISLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
DB 61 IISLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNOAVAGLKEEYLGRKLNIOITPKYTKLARNRVDITIDTDEGSAKITDIE 180
DB 121 SQYFNQATLNOAVAGLKEEYLGRKLNIOITPKYTKLARNRVDITIDTDEGSAKITDIE 180
QY 181 FEGNQVYSRDLKMRQMSLTGEGITWLTLSRNFQNEQFAQDMKVTDYQNGGYDFDFRIL 240
DB 181 FEGNQVYSRDLKMRQMSLTGEGITWLTLSRNFQNEQFAQDMKVTDYQNGGYDFDFRIL 240
QY 241 DTDIQTNEEDTKTQIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQ 300
DB 241 DTDIQTNEEDTKTQIKITVHEGGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKMYERQQ 300
QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVLAHIEGRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVLAHIEGRKIYVNEIHTGNKKT 360
QY 361 RDEVVRELQMESAPYDTSKLQRSEKRVLLGYFDNVQFQDVPAGTDPKVDLNMSLTE 420
DB 361 RDEVVRELQMESAPYDTSKLQRSEKRVLLGYFDNVQFQDVPAGTDPKVDLNMSLTE 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480

DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTLLNGSLSFDPYFTA 480
QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTATAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDIYKAFDPRKASTSVKQYKTTTATAGGVRMGI PVTEYDRVNFGLAAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTKTGTGSPFKWLYKGVGGRNKTDLSALMPTRGYLTGVNAEIA 600
DB 541 YNKAPKRYADFIKQYKTKTGTGADGSPFKGLLYKGVGGRNKTDLSALMPTRGYLTGVNAEIA 600
QY 601 LPSGKLOYYSATHNQTFWFFPLSKTFTLMLGCEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
DB 601 LPSGKLOYYSATHNQTFWFFPLSKTFTLMLGCEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSSATGGRVONIYGAGNTHKSTFTNELRYLSAGGAVTWLSPGLGPMKFRYAYPLKK 780
DB 721 RTY----TAAENGNNKSVY--SENAHKSTFTNELRYLSAGGAVTWLSPGLGPMKFRYAYPLKK 775
QY 781 KPEDEIQRFQFQGLGTTTF 797
DB 776 KPEDEIQRFQFQGLGTTTF 792

Search completed: July 6, 2005, 15:13:13
Job time : 239.676 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:19:22 ; Search time 49 Seconds
(without alignments)
1214.190 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MLKQIASALMLGISLAP.....LKKPDEIQRFQQLGTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 0

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
- 2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
- 3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
- 4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
- 5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*
- 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	4	US-09-994-192-4
2	157	19.7	792	4	US-09-994-192-2
3	8	1.0	94	4	US-09-489-039A-8163
4	8	1.0	97	4	US-09-205-258-1092
5	8	1.0	230	4	US-09-270-767-45805
6	8	1.0	274	4	US-09-902-540-15552
7	8	1.0	648	4	US-09-252-991A-24628
8	8	1.0	1589	4	US-09-543-681A-4998
9	7	0.9	23	4	US-09-674-973A-147
10	7	0.9	58	3	US-08-971-089-10
11	7	0.9	60	4	US-09-513-999C-7231
12	7	0.9	86	4	US-09-328-352-6252
13	7	0.9	86	4	US-09-489-039A-10485
14	7	0.9	88	4	US-09-461-325-325
15	7	0.9	88	4	US-10-012-542-325
16	7	0.9	88	4	US-10-115-123-325
17	7	0.9	97	4	US-09-252-991A-18360
18	7	0.9	106	4	US-09-270-767-62368
19	7	0.9	110	4	US-09-513-999C-6601
20	7	0.9	129	4	US-09-543-681A-5037
21	7	0.9	147	2	US-08-942-819-13
22	7	0.9	147	4	US-09-522-955A-21
23	7	0.9	157	4	US-09-543-681A-7658
24	7	0.9	157	4	US-09-270-767-39460
25	7	0.9	157	4	US-09-270-767-54677
26	7	0.9	159	4	US-09-270-767-38687
27	7	0.9	159	4	US-09-270-767-53904

28	7	0.9	165	4	US-09-270-767-46749	Sequence 45749, A
29	7	0.9	176	4	US-09-902-540-16369	Sequence 15369, A
30	7	0.9	178	4	US-09-716-129-55	Sequence 55, Appl
31	7	0.9	179	4	US-09-252-991A-24524	Sequence 24524, A
32	7	0.9	193	4	US-09-252-991A-17828	Sequence 17828, A
33	7	0.9	213	4	US-09-252-991A-17280	Sequence 17280, A
34	7	0.9	228	4	US-09-270-767-31864	Sequence 31864, A
35	7	0.9	234	4	US-09-270-767-47081	Sequence 47081, A
36	7	0.9	228	4	US-09-270-767-61520	Sequence 61520, A
37	7	0.9	228	4	US-09-248-796A-18574	Sequence 18574, A
38	7	0.9	244	4	US-09-489-039A-14079	Sequence 14079, A
39	7	0.9	253	4	US-09-540-236-2592	Sequence 2592, Ap
40	7	0.9	254	4	US-09-586-106D-127	Sequence 127, App
41	7	0.9	257	4	US-09-252-991A-31224	Sequence 31224, A
42	7	0.9	260	4	US-09-902-540-15829	Sequence 15829, A
43	7	0.9	263	4	US-09-252-991A-26300	Sequence 26300, A
44	7	0.9	267	4	US-09-634-238-360	Sequence 360, App
45	7	0.9	268	4	US-09-252-991A-23138	Sequence 23138, A
46	7	0.9	268	4	US-09-252-991A-23139	Sequence 23139, A
47	7	0.9	268	4	US-09-252-991A-31998	Sequence 31998, A
48	7	0.9	270	4	US-09-252-991A-23186	Sequence 23186, A
49	7	0.9	282	4	US-09-107-532A-5538	Sequence 5538, Ap
50	7	0.9	288	4	US-09-538-092-764	Sequence 764, App
51	7	0.9	291	4	US-09-252-991A-28354	Sequence 28354, A
52	7	0.9	294	4	US-09-107-532A-4247	Sequence 4247, Ap
53	7	0.9	300	4	US-09-489-039A-9673	Sequence 9673, Ap
54	7	0.9	310	4	US-09-902-540-15612	Sequence 15612, A
55	7	0.9	316	4	US-09-248-796A-19882	Sequence 19882, A
56	7	0.9	327	4	US-09-252-991A-30618	Sequence 30618, A
57	7	0.9	351	4	US-09-489-039A-9415	Sequence 9415, Ap
58	7	0.9	355	4	US-08-178-257-4	Sequence 4, Appli
59	7	0.9	355	4	US-09-328-352-5414	Sequence 5414, Ap
60	7	0.9	357	4	US-09-252-991A-33139	Sequence 33139, A
61	7	0.9	357	4	US-09-902-540-13021	Sequence 13021, A
62	7	0.9	363	4	US-09-902-540-16014	Sequence 16014, A
63	7	0.9	366	3	US-09-040-681A-6	Sequence 6, Appli
64	7	0.9	366	3	US-09-497-897-6	Sequence 6, Appli
65	7	0.9	366	4	US-09-270-767-45981	Sequence 45981, A
66	7	0.9	389	4	US-09-248-796A-23182	Sequence 23182, A
67	7	0.9	393	4	US-09-252-991A-16771	Sequence 16771, A
68	7	0.9	399	4	US-09-252-991A-18432	Sequence 18432, A
69	7	0.9	413	4	US-09-902-540-13562	Sequence 13562, A
70	7	0.9	425	3	US-09-310-363C-8	Sequence 8, Appli
71	7	0.9	425	4	US-10-117-015-8	Sequence 8, Appli
72	7	0.9	434	4	US-09-252-991A-27235	Sequence 27235, A
73	7	0.9	441	4	US-09-134-000C-4521	Sequence 4521, Ap
74	7	0.9	444	4	US-09-721-870-42	Sequence 42, Appl
75	7	0.9	458	4	US-09-435-956A-1	Sequence 1, Appli
76	7	0.9	459	4	US-09-252-991A-25839	Sequence 25839, A
77	7	0.9	464	4	US-09-711-164-441	Sequence 441, App
78	7	0.9	464	4	US-09-492-709A-281	Sequence 281, App
79	7	0.9	465	4	US-09-252-991A-29387	Sequence 29387, A
80	7	0.9	472	3	US-09-516-914-3	Sequence 3, Appli
81	7	0.9	473	4	US-09-328-352-5279	Sequence 5279, Ap
82	7	0.9	480	3	US-09-252-149B-26	Sequence 26, Appl
83	7	0.9	437	4	US-09-583-110-5088	Sequence 5088, Ap
84	7	0.9	504	4	US-09-107-433-3732	Sequence 3732, Ap
85	7	0.9	514	4	US-09-949-016-11380	Sequence 11380, A
86	7	0.9	517	4	US-09-723-368-4	Sequence 4, Appli
87	7	0.9	518	4	US-09-919-172-20	Sequence 20, Appl
88	7	0.9	529	3	US-09-504-358-22	Sequence 22, Appl
89	7	0.9	529	4	US-09-354-314-22	Sequence 22, Appl
90	7	0.9	529	4	US-10-230-562-22	Sequence 22, Appl
91	7	0.9	536	4	US-09-370-767-46294	Sequence 46294, A
92	7	0.9	544	1	US-08-387-156-10	Sequence 10, Appl
93	7	0.9	544	2	US-08-694-865-10	Sequence 10, Appl
94	7	0.9	544	2	US-08-878-748-10	Sequence 10, Appl
95	7	0.9	544	3	US-09-124-491-10	Sequence 10, Appl
96	7	0.9	544	4	US-09-383-912-10	Sequence 10, Appl
97	7	0.9	559	4	US-09-252-991A-24692	Sequence 24692, A
98	7	0.9	568	4	US-09-949-016-10896	Sequence 10896, A
99	7	0.9	576	4	US-09-252-991A-23246	Sequence 23246, A
100	7	0.9	587	4	US-09-538-092-1130	Sequence 1130, Ap

101	7	0.9	604	4	US-09-345-473B-17	Sequence 17, Appl	174	7	0.9	1447	3	US-08-954-668-19	Sequence 19, Appl
102	7	0.9	609	4	US-09-311-021-196	Sequence 196, App	175	7	0.9	1447	3	US-09-268-140-5	Sequence 5, Appli
103	7	0.9	614	4	US-09-328-352-4504	Sequence 4504, Ap	176	7	0.9	1447	4	US-08-918-658-19	Sequence 19, Appl
104	7	0.9	620	1	US-08-484-105-4	Sequence 4, Appli	177	7	0.9	1447	4	US-09-724-631-19	Sequence 19, Appl
105	7	0.9	620	1	US-08-484-106-4	Sequence 4, Appli	178	7	0.9	1447	4	US-08-954-701A-19	Sequence 19, Appl
106	7	0.9	621	4	US-09-232-991A-19125	Sequence 19125, A	179	7	0.9	1447	5	PCT-US95-13233-19	Sequence 19, Appl
107	7	0.9	671	3	US-08-858-207A-301	Sequence 301, App	180	7	0.9	1454	4	US-09-673-896-2	Sequence 2, Appli
108	7	0.9	671	4	US-09-583-110-3642	Sequence 3642, Ap	181	7	0.9	1454	4	US-09-673-896-4	Sequence 4, Appli
109	7	0.9	676	4	US-09-107-433-4098	Sequence 4098, Ap	182	7	0.9	1633	4	US-09-502-540-12892	Sequence 12892, A
110	7	0.9	699	2	US-08-694-865-16	Sequence 16, Appl	183	7	0.9	1636	4	US-09-355-160D-2	Sequence 2, Appli
111	7	0.9	699	3	US-09-124-491-16	Sequence 16, Appl	184	7	0.9	1686	4	US-10-092-219-2	Sequence 2, Appli
112	7	0.9	699	4	US-09-383-912-16	Sequence 16, Appl	185	7	0.9	2431	1	US-07-920-281C-2	Sequence 2, Appli
113	7	0.9	699	4	US-09-232-991A-17073	Sequence 17073, A	186	7	0.9	2431	3	US-08-466-277-2	Sequence 2, Appli
114	7	0.9	783	4	US-09-248-796A-15502	Sequence 15502, A	187	7	0.9	2431	3	US-09-688-842-2	Sequence 2, Appli
115	7	0.9	821	4	US-09-232-991A-21013	Sequence 21013, A	188	7	0.9	3122	4	US-10-237-551-201	Sequence 201, App
116	7	0.9	827	4	US-09-543-681A-6425	Sequence 6425, Ap	189	7	0.9	3122	4	US-10-237-551-250	Sequence 250, App
117	7	0.9	901	4	US-09-270-767-45367	Sequence 45367, A	190	6	0.8	7	1	US-08-384-680-2	Sequence 2, Appli
118	7	0.9	908	4	US-08-714-741-44	Sequence 44, Appl	191	6	0.8	7	1	US-08-384-680-12	Sequence 12, Appl
119	7	0.9	924	3	US-08-619-812-8	Sequence 8, Appli	192	6	0.8	9	2	US-08-986-234-84	Sequence 84, Appl
120	7	0.9	926	1	US-07-908-253-2	Sequence 2, Appli	193	6	0.8	10	1	US-08-397-101-7	Sequence 7, Appli
121	7	0.9	926	1	US-08-455-970A-2	Sequence 2, Appli	194	6	0.8	10	4	US-08-135-319A-4	Sequence 4, Appli
122	7	0.9	926	1	US-08-387-156-6	Sequence 6, Appli	195	6	0.8	10	4	US-08-135-319A-5	Sequence 5, Appli
123	7	0.9	926	2	US-08-694-865-6	Sequence 6, Appli	196	6	0.8	10	4	US-08-135-319A-6	Sequence 6, Appli
124	7	0.9	926	2	US-08-878-748-6	Sequence 6, Appli	197	6	0.8	10	4	US-08-135-319A-19	Sequence 19, Appl
125	7	0.9	926	2	US-08-535-837-2	Sequence 2, Appli	198	6	0.8	10	5	PCT-US93-08436-7	Sequence 7, Appli
126	7	0.9	926	3	US-09-124-491-6	Sequence 6, Appli	199	6	0.8	13	1	US-08-803-899-13	Sequence 13, Appl
127	7	0.9	926	4	US-09-383-912-6	Sequence 6, Appli	200	6	0.8	18	1	US-08-279-058B-20	Sequence 20, Appl
128	7	0.9	926	4	US-08-976-566-2	Sequence 2, Appli	201	6	0.8	18	4	US-08-828-323-20	Sequence 20, Appl
129	7	0.9	926	6	5476657-3	Patent No. 5476657	202	6	0.8	19	1	US-08-634-060-42	Sequence 42, Appl
130	7	0.9	926	6	5476657-3	Patent No. 5476657	203	6	0.8	19	3	US-08-676-186-1	Sequence 1, Appli
131	7	0.9	934	1	US-08-215-805A-80	Sequence 80, Appl	204	6	0.8	19	4	US-09-932-923-1	Sequence 22, Appl
132	7	0.9	936	1	US-08-455-370A-12	Sequence 12, Appl	205	6	0.8	20	1	US-08-279-906A-22	Sequence 22, Appl
133	7	0.9	936	4	US-08-976-566-12	Sequence 12, Appl	206	6	0.8	24	4	US-09-843-221A-129	Sequence 129, App
134	7	0.9	943	1	US-08-455-970A-10	Sequence 10, Appl	207	6	0.8	24	4	US-09-843-221A-130	Sequence 130, App
135	7	0.9	943	1	US-08-976-566-10	Sequence 10, Appl	208	6	0.8	25	4	US-09-911-927-35	Sequence 35, Appl
136	7	0.9	951	1	US-08-455-370A-14	Sequence 14, Appl	209	6	0.8	25	4	US-09-911-882-35	Sequence 35, Appl
137	7	0.9	951	4	US-08-976-566-14	Sequence 14, Appl	210	6	0.8	25	4	US-09-911-888-35	Sequence 35, Appl
138	7	0.9	963	4	US-09-914-259-20	Sequence 20, Appl	211	6	0.8	26	3	US-08-965-762-35	Sequence 35, Appl
139	7	0.9	963	4	US-09-914-259-22	Sequence 22, Appl	212	6	0.8	27	3	US-08-433-522A-35	Sequence 35, Appl
140	7	0.9	963	4	US-09-538-092-1060	Sequence 1060, Ap	213	6	0.8	27	3	US-09-135-166-35	Sequence 35, Appl
141	7	0.9	974	4	US-09-248-796A-16191	Sequence 16191, A	214	6	0.8	27	3	US-08-942-046-35	Sequence 35, Appl
142	7	0.9	977	1	US-08-387-156-8	Sequence 8, Appli	215	6	0.8	28	2	US-08-724-774B-4	Sequence 4, Appli
143	7	0.9	977	2	US-08-694-865-8	Sequence 8, Appli	216	6	0.8	28	3	US-09-089-595-4	Sequence 4, Appli
144	7	0.9	977	2	US-08-878-748-8	Sequence 8, Appli	217	6	0.8	28	3	US-09-382-855-4	Sequence 4, Appli
145	7	0.9	977	4	US-09-124-491-8	Sequence 8, Appli	218	6	0.8	28	3	US-09-183-714B-4	Sequence 4, Appli
146	7	0.9	977	4	US-09-383-912-8	Sequence 8, Appli	219	6	0.8	28	3	US-09-642-281-4	Sequence 4, Appli
147	7	0.9	978	4	US-09-949-016-10196	Sequence 10196, A	220	6	0.8	28	4	US-09-589-717-4	Sequence 4, Appli
148	7	0.9	1022	4	US-09-949-016-10242	Sequence 10242, A	221	6	0.8	28	4	US-09-843-221A-93	Sequence 93, Appl
149	7	0.9	1069	1	US-07-777-715-9	Sequence 9, Appli	222	6	0.8	28	4	US-09-843-221A-94	Sequence 94, Appl
150	7	0.9	1069	1	US-08-170-126-4	Sequence 4, Appli	223	6	0.8	28	4	US-09-471-276-1203	Sequence 1203, Ap
151	7	0.9	1069	3	US-08-954-418-4	Sequence 4, Appli	224	6	0.8	30	4	US-09-843-221A-124	Sequence 124, App
152	7	0.9	1098	1	US-07-777-715-7	Sequence 7, Appli	225	6	0.8	30	4	US-09-843-221A-125	Sequence 125, App
153	7	0.9	1098	1	US-08-170-126-2	Sequence 2, Appli	226	6	0.8	30	4	US-09-843-221A-158	Sequence 158, App
154	7	0.9	1098	3	US-08-954-418-2	Sequence 2, Appli	227	6	0.8	31	4	US-09-228-990-50	Sequence 50, Appl
155	7	0.9	1121	4	US-08-915-048A-2	Sequence 2, Appli	228	6	0.8	33	1	US-08-209-747-19	Sequence 19, Appl
156	7	0.9	1129	4	US-09-252-991A-28552	Sequence 28552, A	229	6	0.8	33	1	US-08-458-298-19	Sequence 19, Appl
157	7	0.9	1296	6	5476657-1	Patent No. 5476657	230	6	0.8	34	1	US-07-915-247A-23	Sequence 23, Appl
158	7	0.9	1334	6	5476657-1	Patent No. 5476657	231	6	0.8	34	1	US-08-443-863-23	Sequence 23, Appl
159	7	0.9	1334	6	5476657-1	Patent No. 5476657	232	6	0.8	34	1	US-08-448-070-23	Sequence 23, Appl
160	7	0.9	1403	1	US-07-908-253-3	Sequence 3, Appli	233	6	0.8	34	1	US-08-449-500-23	Sequence 23, Appl
161	7	0.9	1403	2	US-08-694-865-17	Sequence 17, Appl	234	6	0.8	34	1	US-08-449-317A-23	Sequence 23, Appl
162	7	0.9	1403	2	US-08-535-837-3	Sequence 3, Appli	235	6	0.8	34	2	US-08-477-022-23	Sequence 23, Appl
163	7	0.9	1403	3	US-09-124-491-17	Sequence 17, Appl	236	6	0.8	34	2	US-08-449-447-23	Sequence 23, Appl
164	7	0.9	1403	4	US-09-383-912-17	Sequence 17, Appl	237	6	0.8	34	2	US-08-184-328-23	Sequence 23, Appl
165	7	0.9	1434	2	US-08-540-406-10	Sequence 10, Appl	238	6	0.8	34	2	US-08-521-097-23	Sequence 23, Appl
166	7	0.9	1434	3	US-08-556-055-10	Sequence 10, Appl	239	6	0.8	34	4	US-09-843-221A-88	Sequence 88, Appl
167	7	0.9	1434	3	US-08-694-868-10	Sequence 10, Appl	240	6	0.8	34	4	US-09-843-221A-89	Sequence 89, Appl
168	7	0.9	1434	4	US-08-918-658-10	Sequence 10, Appl	241	6	0.8	34	4	US-09-843-221A-122	Sequence 122, App
169	7	0.9	1434	4	US-09-724-631-10	Sequence 10, Appl	242	6	0.8	36	4	US-09-902-540-14017	Sequence 14017, A
170	7	0.9	1434	5	US-08-954-701A-10	Sequence 10, Appl	243	6	0.8	37	3	US-08-751-344B-18	Sequence 18, Appl
171	7	0.9	1434	5	PCT-US95-13233-10	Sequence 10, Appl	244	6	0.8	39	1	US-08-209-747-23	Sequence 23, Appl
172	7	0.9	1447	2	US-08-540-406-19	Sequence 19, Appl	245	6	0.8	39	1	US-08-458-298-23	Sequence 23, Appl
173	7	0.9	1447	3	US-08-656-055-19	Sequence 19, Appl	246	6	0.8	39	4	US-09-270-767-31845	Sequence 31845, A

247	6	0.8	39	4	US-09-270-767-47062	Sequence 47062, A	320	80	4	US-09-640-211A-905	Sequence 905, App
248	6	0.8	40	3	US-07-741-453A-4	Sequence 4, Appli	321	82	3	US-09-134-001C-2351	Sequence 2351, Ap
249	6	0.8	42	5	PCT-US96-10043-13	Sequence 13, Appl	322	84	4	US-09-621-976-5976	Sequence 5976, A
250	6	0.8	47	1	US-08-209-747-24	Sequence 24, Appl	323	84	4	US-09-270-767-32345	Sequence 32345, A
251	6	0.8	47	1	US-08-209-747-26	Sequence 26, Appl	324	84	4	US-09-270-767-46371	Sequence 46371, A
252	6	0.8	47	1	US-08-458-298-24	Sequence 24, Appl	325	84	4	US-09-270-767-47562	Sequence 47562, A
253	6	0.8	47	1	US-08-458-298-26	Sequence 26, Appl	326	84	4	US-09-311-021-100	Sequence 100, App
254	6	0.8	48	1	US-08-209-747-21	Sequence 21, Appl	327	84	4	US-09-513-999C-5815	Sequence 5815, Ap
255	6	0.8	48	1	US-08-458-298-21	Sequence 21, Appl	328	86	1	US-08-680-726A-82	Sequence 82, Appl
256	6	0.8	49	1	US-08-209-747-22	Sequence 22, Appl	329	86	3	US-09-092-409-82	Sequence 82, Appl
257	6	0.8	49	1	US-08-458-298-20	Sequence 20, Appl	330	86	4	US-09-270-767-34956	Sequence 34956, A
258	6	0.8	50	1	US-08-458-298-22	Sequence 22, Appl	331	86	4	US-09-270-767-50173	Sequence 50173, A
259	6	0.8	50	1	US-08-209-747-27	Sequence 27, Appl	332	87	4	US-09-543-681A-7373	Sequence 7373, Ap
260	6	0.8	51	1	US-08-458-298-27	Sequence 27, Appl	333	87	4	US-09-270-767-32832	Sequence 32832, A
261	6	0.8	51	1	US-08-209-747-30	Sequence 30, Appl	334	87	4	US-09-270-767-48049	Sequence 48049, A
262	6	0.8	51	1	US-08-458-298-20	Sequence 20, Appl	335	88	4	US-09-489-039A-10714	Sequence 10714, A
263	6	0.8	51	1	US-08-458-298-30	Sequence 30, Appl	336	88	4	US-09-687-637B-29	Sequence 29, Appl
264	6	0.8	52	3	US-09-277-078-46	Sequence 46, Appl	337	89	4	US-09-687-637B-30	Sequence 30, Appl
265	6	0.8	55	1	US-08-209-747-25	Sequence 25, Appl	338	90	1	US-08-209-747-16	Sequence 16, Appl
266	6	0.8	55	1	US-08-458-298-25	Sequence 25, Appl	339	90	1	US-08-458-298-16	Sequence 16, Appl
267	6	0.8	56	3	US-08-936-165A-332	Sequence 332, App	340	90	4	US-09-621-976-4742	Sequence 4742, Ap
268	6	0.8	56	4	US-09-621-976-5925	Sequence 5925, Ap	341	96	4	US-09-107-532A-6122	Sequence 6122, Ap
269	6	0.8	56	4	US-09-270-767-57982	Sequence 57982, A	342	98	4	US-09-147-875A-1	Sequence 1, Appli
270	6	0.8	57	4	US-09-006-428A-5	Sequence 5, Appli	343	98	2	US-08-710-749-9	Sequence 9, Appli
271	6	0.8	57	4	US-09-615-387C-5	Sequence 5, Appli	344	99	2	US-08-710-749-10	Sequence 10, Appl
272	6	0.8	58	4	US-09-270-767-57771	Sequence 57771, A	345	99	2	US-08-710-749-11	Sequence 11, Appl
273	6	0.8	59	4	US-09-621-976-6937	Sequence 6937, Ap	346	99	4	US-09-732-210-1583	Sequence 1583, Ap
274	6	0.8	59	4	US-09-270-767-61138	Sequence 61138, A	347	99	4	US-09-147-875A-11	Sequence 11, Appl
275	6	0.8	60	3	US-08-928-213B-70	Sequence 70, Appl	348	99	4	US-09-147-875A-14	Sequence 14, Appl
276	6	0.8	60	4	US-09-248-796A-25960	Sequence 25960, A	349	99	4	US-09-147-875A-15	Sequence 15, Appl
277	6	0.8	61	4	US-09-248-796A-24801	Sequence 24801, A	350	99	4	US-09-147-875A-16	Sequence 16, Appl
278	6	0.8	61	4	US-09-248-796A-26402	Sequence 26402, A	351	100	2	US-08-308-494A-19	Sequence 19, Appl
279	6	0.8	63	4	US-09-673-395A-403	Sequence 403, App	352	100	4	US-09-147-875A-4	Sequence 4, Appli
280	6	0.8	64	2	US-09-621-976-521-20	Sequence 20, Appl	353	100	4	US-09-147-875A-8	Sequence 8, Appli
281	6	0.8	64	3	US-08-961-810-130	Sequence 130, App	354	100	4	US-09-147-875A-10	Sequence 10, Appl
282	6	0.8	64	3	US-08-352-902D-130	Sequence 130, App	355	100	4	US-09-147-875A-12	Sequence 12, Appl
283	6	0.8	64	4	US-09-265-503B-130	Sequence 130, App	356	101	2	US-08-710-749-3	Sequence 3, Appli
284	6	0.8	64	4	US-09-270-767-61944	Sequence 61944, A	357	101	2	US-08-710-749-7	Sequence 7, Appli
285	6	0.8	65	4	US-09-248-796A-25471	Sequence 25471, A	358	101	4	US-09-147-875A-9	Sequence 9, Appli
286	6	0.8	65	4	US-09-640-211A-604	Sequence 604, App	359	102	1	US-08-169-701-1	Sequence 1, Appli
287	6	0.8	66	4	US-09-621-976-4488	Sequence 4488, App	360	102	2	US-08-710-749-8	Sequence 8, Appli
288	6	0.8	66	4	US-09-270-767-60792	Sequence 60792, A	361	102	2	US-08-710-749-21	Sequence 21, Appl
289	6	0.8	67	4	US-09-248-796A-23279	Sequence 23279, A	362	102	2	US-08-760-903-1	Sequence 1, Appli
290	6	0.8	68	4	US-09-252-991A-30574	Sequence 30574, A	363	102	2	US-08-482-191-1	Sequence 1, Appli
291	6	0.8	68	4	US-09-489-039A-11466	Sequence 11466, A	364	102	4	US-09-270-767-57873	Sequence 18, Appl
292	6	0.8	68	4	US-09-902-540-11724	Sequence 11724, A	365	102	4	US-09-270-767-57873	Sequence 18, Appl
293	6	0.8	69	4	US-09-902-540-11724	Sequence 1004, Ap	366	102	4	US-09-902-540-14676	Sequence 14676, A
294	6	0.8	70	2	US-08-691-814B-34	Sequence 34, Appl	367	102	5	PCT-US96-10227-1	Sequence 1, Appli
295	6	0.8	70	4	US-09-732-210-883	Sequence 883, App	368	103	1	US-08-467-393-4	Sequence 4, Appli
296	6	0.8	70	4	US-09-621-976-5508	Sequence 5508, Ap	369	103	1	US-08-209-747-4	Sequence 4, Appli
297	6	0.8	70	6	5453566-2	Patent No. 5453566	370	103	1	US-08-458-298-4	Sequence 4, Appli
298	6	0.8	70	6	5453566-2	Patent No. 5453566	371	104	2	US-08-710-749-19	Sequence 19, Appl
299	6	0.8	71	4	US-09-732-210-93	Sequence 93, Appl	372	104	2	US-08-710-749-20	Sequence 20, Appl
300	6	0.8	71	4	US-09-270-767-56690	Sequence 56690, A	373	104	3	US-08-479-089A-5	Sequence 5, Appli
301	6	0.8	71	4	US-09-949-016-8499	Sequence 8499, Ap	374	104	3	US-08-479-089A-6	Sequence 6, Appli
302	6	0.8	73	4	US-09-489-039A-12244	Sequence 12244, A	375	104	3	US-07-669-545B-5	Sequence 5, Appli
303	6	0.8	73	4	US-09-902-540-10352	Sequence 10252, A	376	104	4	US-07-669-545B-6	Sequence 6, Appli
304	6	0.8	74	4	US-09-543-681A-8341	Sequence 8341, Ap	377	104	4	US-09-147-875A-20	Sequence 20, Appl
305	6	0.8	74	4	US-09-248-796A-25832	Sequence 25832, A	378	104	4	US-09-147-875A-21	Sequence 21, Appl
306	6	0.8	74	4	US-09-513-999C-5011	Sequence 5011, Ap	379	105	2	US-08-889-013C-6	Sequence 6, Appli
307	6	0.8	75	4	US-09-252-991A-21927	Sequence 21927, A	380	105	2	US-09-205-258-1082	Sequence 1082, Ap
308	6	0.8	75	4	US-09-198-452A-1228	Sequence 1228, Ap	381	105	4	US-09-583-110-5144	Sequence 5144, Ap
309	6	0.8	75	4	US-09-270-767-33600	Sequence 33600, A	382	105	4	US-09-640-211A-924	Sequence 924, Ap
310	6	0.8	75	4	US-09-270-767-48817	Sequence 48817, A	383	105	4	US-09-640-211A-2239	Sequence 2239, Ap
311	6	0.8	76	4	US-09-621-976-6191	Sequence 6191, Ap	384	106	1	US-07-732-242C-2	Sequence 2, Appli
312	6	0.8	78	4	US-09-732-210-1591	Sequence 1591, Ap	385	106	2	US-08-290-592B-34	Sequence 34, Appl
313	6	0.8	79	4	US-09-270-767-39286	Sequence 39286, A	386	106	2	US-08-290-592B-35	Sequence 35, Appl
314	6	0.8	79	4	US-09-270-767-54503	Sequence 54503, A	387	106	2	US-08-956-047-33	Sequence 33, Appl
315	6	0.8	80	1	US-08-209-747-12	Sequence 12, Appl	388	106	3	US-08-397-411-8	Sequence 8, Appli
316	6	0.8	80	1	US-08-458-298-12	Sequence 12, Appl	389	106	3	US-08-397-411-9	Sequence 9, Appli
317	6	0.8	80	2	US-08-710-749-18	Sequence 18, Appl	390	106	4	US-09-771-415-1	Sequence 1, Appli
318	6	0.8	80	4	US-09-336-536-35	Sequence 35, Appl	391	106	4	US-09-771-415-17	Sequence 17, Appl
319	6	0.8	80	4	US-09-147-875A-19	Sequence 19, Appl	392	106	4	US-09-232-290-24	Sequence 24, Appl

393	6	0.8	106	4	US-09-996-288-8	Sequence 8, Appli	466	6	0.8	123	4	US-09-270-767-43402	Sequence 43402, A
394	6	0.8	106	4	US-09-996-288-11	Sequence 11, Appl	467	6	0.8	123	4	US-09-438-185A-585	Sequence 585, App
395	6	0.8	106	4	US-09-996-288-54	Sequence 54, Appl	468	6	0.8	124	4	US-09-509-738C-15	Sequence 15, Appl
396	6	0.8	106	5	PCT-US95-10053-31	Sequence 31, Appl	469	6	0.8	126	2	US-08-656-586-6	Sequence 6, Appli
397	6	0.8	106	5	PCT-US95-10053-32	Sequence 32, Appl	470	6	0.8	126	2	US-09-663-600A-102	Sequence 102, App
398	6	0.8	106	5	PCT-US96-09448-34	Sequence 34, Appl	471	6	0.8	126	4	US-09-270-767-41467	Sequence 41467, A
399	6	0.8	106	5	PCT-US96-09448-35	Sequence 35, Appl	472	6	0.8	126	4	US-09-270-767-58058	Sequence 58058, A
400	6	0.8	107	1	US-08-942-245-3	Sequence 3, Appli	473	6	0.8	128	2	US-08-656-586-2	Sequence 2, Appli
401	6	0.8	107	2	US-08-303-569B-25	Sequence 26, Appl	474	6	0.8	128	2	US-08-956-047-31	Sequence 31, Appl
402	6	0.8	107	2	US-08-303-569B-26	Sequence 26, Appl	475	6	0.8	128	3	US-08-444-644-25	Sequence 25, Appl
403	6	0.8	107	2	US-08-303-569B-27	Sequence 27, Appl	476	6	0.8	128	3	US-08-232-246A-25	Sequence 25, Appl
404	6	0.8	107	2	US-08-303-569B-28	Sequence 28, Appl	477	6	0.8	128	3	US-09-134-001C-4164	Sequence 4164, Ap
405	6	0.8	107	2	US-08-303-569B-29	Sequence 29, Appl	478	6	0.8	128	4	US-09-270-767-57599	Sequence 57599, A
406	6	0.8	107	2	US-08-070-116A-8	Sequence 6, Appli	479	6	0.8	129	4	US-09-134-000C-5429	Sequence 5429, Ap
407	6	0.8	107	2	US-08-070-116A-8	Sequence 8, Appli	480	6	0.8	129	4	US-09-513-999C-5540	Sequence 5540, Ap
408	6	0.8	107	2	US-08-070-116A-9	Sequence 9, Appli	481	6	0.8	129	4	US-09-513-999C-8080	Sequence 8080, Ap
409	6	0.8	107	2	US-08-070-116A-18	Sequence 18, Appl	482	6	0.8	129	4	US-09-902-540-12956	Sequence 12956, A
410	6	0.8	107	2	US-08-116-247-8	Sequence 8, Appli	483	6	0.8	131	4	US-09-270-767-38194	Sequence 38194, A
411	6	0.8	107	2	US-08-116-247-26	Sequence 26, Appl	484	6	0.8	131	4	US-09-270-767-53411	Sequence 53411, A
412	6	0.8	107	2	US-08-116-247-27	Sequence 27, Appl	485	6	0.8	133	4	US-09-621-976-6550	Sequence 6550, Ap
413	6	0.8	107	2	US-08-116-247-28	Sequence 28, Appl	486	6	0.8	134	4	US-08-529-055-65	Sequence 65, Appl
414	6	0.8	107	2	US-08-116-247-29	Sequence 29, Appl	487	6	0.8	134	4	US-09-248-796A-27186	Sequence 27186, A
415	6	0.8	107	4	US-09-370-838-113	Sequence 113, App	488	6	0.8	135	4	US-09-252-991A-22092	Sequence 22092, A
416	6	0.8	107	4	US-08-557-050-6	Sequence 6, Appli	489	6	0.8	135	4	US-09-107-433-5156	Sequence 5156, Ap
417	6	0.8	107	4	US-08-557-050-8	Sequence 8, Appli	490	6	0.8	136	4	US-09-270-767-39814	Sequence 39814, A
418	6	0.8	107	4	US-08-557-050-9	Sequence 9, Appli	491	6	0.8	136	4	US-09-270-767-55031	Sequence 55031, A
419	6	0.8	107	4	US-09-795-515-25	Sequence 25, Appl	492	6	0.8	137	4	US-09-489-039A-7466	Sequence 7466, Ap
420	6	0.8	107	4	US-09-795-515-26	Sequence 26, Appl	493	6	0.8	137	4	US-09-270-767-59938	Sequence 59938, A
421	6	0.8	107	4	US-09-795-515-27	Sequence 27, Appl	494	6	0.8	138	4	US-09-472-087-79	Sequence 79, Appl
422	6	0.8	107	4	US-09-795-515-28	Sequence 28, Appl	495	6	0.8	138	4	US-09-270-767-57429	Sequence 57429, A
423	6	0.8	107	4	US-09-795-515-29	Sequence 29, Appl	496	6	0.8	139	4	US-09-252-991A-22593	Sequence 22593, A
424	6	0.8	107	4	US-09-348-224-8	Sequence 8, Appli	497	6	0.8	139	4	US-09-902-540-10025	Sequence 10025, A
425	6	0.8	107	4	US-09-348-224-26	Sequence 26, Appl	498	6	0.8	140	4	US-09-248-796A-27587	Sequence 27587, A
426	6	0.8	107	4	US-09-348-224-27	Sequence 27, Appl	499	6	0.8	141	4	US-09-286-981B-2	Sequence 2, Appli
427	6	0.8	107	4	US-09-348-224-28	Sequence 28, Appl	500	6	0.8	141	4	US-09-270-767-43497	Sequence 43497, A
428	6	0.8	107	4	US-09-348-224-29	Sequence 29, Appl	501	6	0.8	142	4	US-09-252-991A-27627	Sequence 27627, A
429	6	0.8	107	4	US-09-854-133-113	Sequence 113, App	502	6	0.8	143	3	US-09-039-859-7	Sequence 7, Appli
430	6	0.8	108	2	PCT-US91-01360-3	Sequence 3, Appli	503	6	0.8	143	4	US-09-252-991A-22066	Sequence 22066, A
431	6	0.8	108	2	US-09-710-749-24	Sequence 24, Appl	504	6	0.8	144	1	US-09-252-991A-29827	Sequence 29827, A
432	6	0.8	108	4	US-09-147-875A-25	Sequence 25, Appl	505	6	0.8	144	2	US-08-133-979A-21	Sequence 21, Appl
433	6	0.8	108	4	US-09-726-219A-241	Sequence 241, App	506	6	0.8	144	2	US-08-436-890-21	Sequence 21, Appl
434	6	0.8	108	4	US-09-726-219A-242	Sequence 242, App	507	6	0.8	144	2	US-08-451-213-21	Sequence 21, Appl
435	6	0.8	108	4	US-09-726-219A-243	Sequence 243, App	508	6	0.8	145	4	US-09-602-787A-330	Sequence 330, App
436	6	0.8	108	4	US-09-726-219A-251	Sequence 251, App	509	6	0.8	145	4	US-09-640-211A-698	Sequence 698, App
437	6	0.8	108	4	US-09-726-219A-252	Sequence 252, App	510	6	0.8	146	4	US-09-902-540-13747	Sequence 13747, A
438	6	0.8	108	4	US-09-726-219A-253	Sequence 253, App	511	6	0.8	146	4	US-09-252-991A-24703	Sequence 24703, A
439	6	0.8	110	3	US-08-836-561-33	Sequence 33, Appl	512	6	0.8	146	4	US-09-902-540-13495	Sequence 13495, A
440	6	0.8	110	4	US-09-434-122-33	Sequence 33, Appl	513	6	0.8	147	4	US-09-602-787A-332	Sequence 332, App
441	6	0.8	110	4	US-09-107-532A-6721	Sequence 6721, Ap	514	6	0.8	148	4	US-09-328-352-8000	Sequence 8000, App
442	6	0.8	110	4	US-09-489-039A-10081	Sequence 10081, A	515	6	0.8	150	3	US-08-857-076-17	Sequence 17, Appl
443	6	0.8	110	4	US-09-902-540-11433	Sequence 11433, A	516	6	0.8	150	4	US-09-663-600A-196	Sequence 196, App
444	6	0.8	112	4	US-09-543-681A-4827	Sequence 4827, Ap	517	6	0.8	150	4	US-09-902-540-12171	Sequence 12171, A
445	6	0.8	112	4	US-09-710-279-2114	Sequence 2114, Ap	518	6	0.8	151	4	US-09-252-991A-16814	Sequence 16814, A
446	6	0.8	113	2	US-08-256-568B-85	Sequence 85, Appl	519	6	0.8	151	4	US-09-328-352-5731	Sequence 5751, Ap
447	6	0.8	113	3	US-09-038-369B-85	Sequence 85, Appl	520	6	0.8	151	4	US-09-540-236-2801	Sequence 2801, Ap
448	6	0.8	113	3	US-08-836-075A-82	Sequence 82, Appl	521	6	0.8	151	4	US-09-248-796A-16825	Sequence 16825, A
449	6	0.8	113	3	US-08-836-075A-98	Sequence 98, Appl	522	6	0.8	152	4	US-09-270-767-48811	Sequence 48811, A
450	6	0.8	113	4	US-09-378-900A-85	Sequence 85, Appl	523	6	0.8	153	4	US-09-732-210-1748	Sequence 1748, Ap
451	6	0.8	113	4	US-09-899-044-85	Sequence 85, Appl	524	6	0.8	153	4	US-09-270-767-32681	Sequence 32681, A
452	6	0.8	113	4	US-09-489-039A-8111	Sequence 8131, Ap	525	6	0.8	153	4	US-09-270-767-47898	Sequence 47898, A
453	6	0.8	113	4	US-09-878-281A-218	Sequence 218, App	526	6	0.8	153	4	US-09-902-540-12086	Sequence 12086, A
454	6	0.8	114	4	US-09-710-279-2252	Sequence 2252, Ap	527	6	0.8	155	1	US-08-209-747-15	Sequence 15, Appl
455	6	0.8	114	4	US-09-513-999C-5777	Sequence 5777, Ap	528	6	0.8	155	1	US-08-458-298-15	Sequence 15, Appl
456	6	0.8	117	1	US-08-274-661B-38	Sequence 38, Appl	529	6	0.8	155	4	US-09-489-039A-7928	Sequence 7928, Ap
457	6	0.8	117	4	US-09-513-999C-6175	Sequence 6175, Ap	530	6	0.8	156	4	US-09-134-000C-6299	Sequence 6299, Ap
458	6	0.8	119	4	US-09-732-210-678	Sequence 678, App	531	6	0.8	157	4	US-09-328-352-4155	Sequence 4165, Ap
459	6	0.8	119	4	US-09-270-767-47348	Sequence 47348, A	532	6	0.8	157	4	US-09-902-540-14881	Sequence 14881, A
460	6	0.8	120	4	US-09-308-345A-21	Sequence 21, Appl	533	6	0.8	158	4	US-09-252-991A-29352	Sequence 29352, A
461	6	0.8	122	4	US-09-198-452A-510	Sequence 510, App	534	6	0.8	158	4	US-09-134-000C-4025	Sequence 4025, App
462	6	0.8	122	4	US-09-270-767-33422	Sequence 33422, A	535	6	0.8	158	4	US-09-265-585C-130	Sequence 130, App
463	6	0.8	122	4	US-09-270-767-48639	Sequence 48639, A	536	6	0.8	159	4	US-09-252-991A-22914	Sequence 22914, A
464	6	0.8	122	4	US-09-902-540-13323	Sequence 13323, A	537	6	0.8	159	4	US-09-602-787A-102	Sequence 102, App
465	6	0.8	123	4	US-09-198-452A-625	Sequence 625, App	538	6	0.8	159	4	US-09-270-767-37981	Sequence 37981, A

539	6	0.8	159	4	US-09-270-767-46525	Sequence 46525, A	612	191	4	US-08-671-548C-2	Sequence 2, Appli
540	6	0.8	159	4	US-09-270-767-53198	Sequence 53198, A	613	191	4	US-09-252-991A-24515	Sequence 24515, A
541	6	0.8	160	3	US-09-117-257-38	Sequence 38, Appl	614	191	4	US-09-328-352-6761	Sequence 6761, Ap
542	6	0.8	160	3	US-09-489-352-38	Sequence 38, Appl	615	191	4	US-09-640-211A-1080	Sequence 1080, Ap
543	6	0.8	160	3	US-08-858-207A-322	Sequence 322, App	616	192	4	US-09-149-476-419	Sequence 419, App
544	6	0.8	160	4	US-09-252-991A-16641	Sequence 16641, A	617	192	4	US-09-543-681A-7846	Sequence 7846, Ap
545	6	0.8	160	4	US-09-621-976-6030	Sequence 6030, Ap	618	193	4	US-08-671-548C-16	Sequence 16, Appl
546	6	0.8	160	4	US-09-270-767-39354	Sequence 39354, A	619	194	4	US-09-248-796A-27860	Sequence 27860, A
547	6	0.8	160	4	US-09-270-767-45565	Sequence 45565, A	620	195	2	US-08-403-852B-24	Sequence 24, Appl
548	6	0.8	160	4	US-09-270-767-54571	Sequence 54571, A	621	195	3	US-08-510-646B-25	Sequence 25, Appl
549	6	0.8	161	4	US-09-902-540-10892	Sequence 10892, A	622	195	3	US-09-231-818-24	Sequence 24, Appl
550	6	0.8	161	4	US-09-902-540-16115	Sequence 16115, A	623	195	4	US-09-635-359B-24	Sequence 24, Appl
551	6	0.8	162	3	US-09-446-504-27	Sequence 27, Appl	624	195	4	US-09-583-110-4558	Sequence 4558, Ap
552	6	0.8	162	3	US-09-712-366-27	Sequence 27, Appl	625	196	4	US-09-711-164-379	Sequence 379, App
553	6	0.8	162	4	US-09-439-148-5	Sequence 5, Appll	626	196	4	US-09-543-681A-7659	Sequence 7659, Ap
554	6	0.8	162	4	US-09-270-767-43246	Sequence 43246, A	627	197	1	US-08-567-509-1	Sequence 1, Appll
555	6	0.8	164	4	US-09-270-767-33348	Sequence 33348, A	628	197	2	US-08-779-870-1	Sequence 1, Appll
556	6	0.8	164	4	US-09-270-767-48565	Sequence 48565, A	629	197	4	US-08-529-055-44	Sequence 44, Appl
557	6	0.8	165	4	US-09-513-999C-7900	Sequence 7900, Ap	630	198	4	US-08-529-055-36	Sequence 36, Appl
558	6	0.8	166	4	US-09-252-991A-19472	Sequence 19472, A	631	198	4	US-08-529-055-61	Sequence 61, Appl
559	6	0.8	166	4	US-09-889-463A-12	Sequence 12, Appl	632	198	4	US-09-270-767-36571	Sequence 36571, A
560	6	0.8	167	3	US-09-062-440-8	Sequence 8, Appll	633	198	4	US-09-270-767-44202	Sequence 44202, A
561	6	0.8	167	3	US-09-062-440-9	Sequence 9, Appll	634	198	4	US-09-270-767-51788	Sequence 51788, A
562	6	0.8	167	3	US-09-062-440-11	Sequence 11, Appl	635	198	4	US-09-538-092-1045	Sequence 1045, Ap
563	6	0.8	167	3	US-09-712-495-8	Sequence 8, Appll	636	198	4	US-09-949-016-11711	Sequence 11711, A
564	6	0.8	167	3	US-09-712-495-9	Sequence 9, Appll	637	200	4	US-09-270-767-32508	Sequence 32508, A
565	6	0.8	167	3	US-09-712-495-11	Sequence 11, Appl	638	200	4	US-09-270-767-47725	Sequence 47725, A
566	6	0.8	167	4	US-09-252-991A-31970	Sequence 31970, A	639	201	4	US-09-270-767-32368	Sequence 32368, A
567	6	0.8	167	4	US-09-902-540-14730	Sequence 14730, A	640	201	4	US-09-270-767-47585	Sequence 47585, A
568	6	0.8	168	3	US-08-679-006-30	Sequence 30, Appl	641	202	4	US-09-949-016-7318	Sequence 7318, Ap
569	6	0.8	168	4	US-09-107-532A-3745	Sequence 3745, Ap	642	203	3	US-09-134-001C-3696	Sequence 3696, Ap
570	6	0.8	168	4	US-09-134-000C-4552	Sequence 4552, Ap	643	203	4	US-09-248-796A-20648	Sequence 20648, A
571	6	0.8	168	4	US-09-388-405-30	Sequence 30, Appl	644	204	4	US-09-328-352-6644	Sequence 6644, Ap
572	6	0.8	169	4	US-09-252-991A-31389	Sequence 31389, A	645	204	4	US-08-529-055-51	Sequence 51, Appl
573	6	0.8	169	4	US-09-270-767-36359	Sequence 36359, A	646	204	4	US-08-529-055-58	Sequence 58, Appl
574	6	0.8	169	4	US-09-270-767-39082	Sequence 39082, A	647	204	4	US-09-710-279-2394	Sequence 2394, Ap
575	6	0.8	169	4	US-09-270-767-51576	Sequence 51576, A	648	205	4	US-09-710-279-3020	Sequence 3020, Ap
576	6	0.8	169	4	US-09-270-767-54299	Sequence 54299, A	649	206	3	US-09-134-001C-4621	Sequence 4621, Ap
577	6	0.8	169	4	US-09-248-796A-26743	Sequence 26743, A	650	206	4	US-08-529-055-54	Sequence 54, Appl
578	6	0.8	170	4	US-09-732-210-558	Sequence 558, App	651	207	3	US-09-046-894-33	Sequence 33, Appl
579	6	0.8	170	4	US-08-529-055-60	Sequence 60, Appl-	652	207	3	US-09-134-001C-4132	Sequence 4132, Ap
580	6	0.8	171	4	US-09-248-796A-27723	Sequence 27723, A	653	208	4	US-09-583-110-2988	Sequence 2988, Ap
581	6	0.8	172	4	US-09-583-110-3305	Sequence 3305, Ap	654	209	4	US-09-107-433-3989	Sequence 3989, Ap
582	6	0.8	173	4	US-09-270-767-32051	Sequence 32051, A	655	210	4	US-09-543-681A-7093	Sequence 7093, Ap
583	6	0.8	173	4	US-09-270-767-47268	Sequence 47268, A	656	211	4	US-09-902-540-10681	Sequence 10681, A
584	6	0.8	174	4	US-09-149-476-413	Sequence 413, App	657	212	4	US-09-543-681A-6069	Sequence 6069, Ap
585	6	0.8	174	4	US-09-270-767-40521	Sequence 40521, A	658	212	4	US-09-248-796A-15317	Sequence 15317, A
586	6	0.8	174	4	US-09-270-767-55737	Sequence 55737, A	659	213	2	US-08-941-263-3	Sequence 3, Appli
587	6	0.8	175	4	US-09-252-991A-28806	Sequence 28806, A	660	213	3	US-09-227-178-3	Sequence 3, Appli
588	6	0.8	175	4	US-09-270-767-32224	Sequence 32224, A	661	213	3	US-08-397-411-12	Sequence 12, Appl
589	6	0.8	176	4	US-09-780-717-2	Sequence 2, Appll	662	213	3	US-09-470-449-3	Sequence 3, Appll
590	6	0.8	176	4	US-09-248-796A-20163	Sequence 20163, A	663	213	4	US-09-726-775-3	Sequence 3, Appli
591	6	0.8	176	4	US-09-248-796A-25947	Sequence 25947, A	664	213	4	US-09-252-991A-25866	Sequence 25866, A
592	6	0.8	177	4	US-09-248-796A-24917	Sequence 24917, A	665	213	4	US-08-529-055-47	Sequence 47, Appl
593	6	0.8	178	4	US-08-671-548C-14	Sequence 14, Appl	666	213	4	US-09-996-288-209	Sequence 209, App
594	6	0.8	178	4	US-09-732-210-1077	Sequence 1077, App	667	213	4	US-09-996-288-231	Sequence 231, App
595	6	0.8	180	4	US-09-252-991A-17913	Sequence 17913, A	668	213	4	US-09-996-288-255	Sequence 255, App
596	6	0.8	181	4	US-08-529-055-42	Sequence 42, Appl	669	213	4	US-09-603-208A-124	Sequence 124, App
597	6	0.8	182	2	US-08-353-476-93	Sequence 93, Appl	670	213	4	US-09-902-540-13705	Sequence 13705, A
598	6	0.8	182	3	US-08-958-207A-434	Sequence 434, App	671	214	4	US-09-543-681A-6408	Sequence 6408, Ap
599	6	0.8	183	4	US-08-529-055-50	Sequence 50, Appl	672	214	4	US-09-270-767-42972	Sequence 42972, A
600	6	0.8	184	3	US-09-122-443-13	Sequence 13, Appl	673	215	4	US-09-893-737-306	Sequence 306, App
601	6	0.8	184	4	US-09-558-089-13	Sequence 13, Appl	674	215	4	US-09-252-991A-22038	Sequence 22038, A
602	6	0.8	184	4	US-09-558-087-13	Sequence 13, Appl	675	216	4	US-09-543-681A-6921	Sequence 6921, Ap
603	6	0.8	184	4	US-09-558-474-13	Sequence 13, Appl	676	217	4	US-09-071-035-312	Sequence 312, App
604	6	0.8	185	4	US-08-529-055-46	Sequence 46, Appl	677	217	4	US-09-484-577A-30	Sequence 30, Appl
605	6	0.8	186	4	US-09-902-540-14912	Sequence 14912, A	678	217	4	US-09-391-606-7	Sequence 7, Appll
606	6	0.8	187	4	US-09-270-767-45734	Sequence 45734, A	679	218	4	US-09-270-767-43455	Sequence 43455, A
607	6	0.8	187	4	US-09-248-796A-19329	Sequence 19329, A	680	218	4	US-09-248-796A-16056	Sequence 16056, A
608	6	0.8	188	4	US-08-529-055-59	Sequence 59, Appl	681	218	4	US-09-107-433-3578	Sequence 3578, Ap
609	6	0.8	188	4	US-09-489-039A-13533	Sequence 13533, A	682	218	4	US-09-902-540-13913	Sequence 13913, A
610	6	0.8	188	4	US-09-902-540-12348	Sequence 12348, A	683	219	2	US-08-401-068-6	Sequence 6, Appll
611	6	0.8	189	4	US-09-252-991A-30049	Sequence 30049, A	684	219	2	US-08-846-338-6	Sequence 6, Appll

685	6	0.8	219	4	US-09-198-452A-634	Sequence 634, App	758	6	0.8	246	4	US-09-134-000C-5137	Sequence 5137, Ap
686	6	0.8	219	4	US-09-438-185A-593	Sequence 593, App	759	6	0.8	246	4	US-09-244-805-32	Sequence 32, Appl
687	6	0.8	220	4	US-09-853-450-38	Sequence 38, Appl	760	6	0.8	248	4	US-09-248-796A-18654	Sequence 18654, A
688	6	0.8	221	4	US-09-198-452A-292	Sequence 292, App	761	6	0.8	248	4	US-09-248-796A-18980	Sequence 18980, A
689	6	0.8	221	2	US-08-190-199A-67	Sequence 67, Appl	762	6	0.8	248	4	US-10-144-198-33	Sequence 33, Appl
690	6	0.8	222	4	US-09-232-991A-21377	Sequence 21377, A	763	6	0.8	248	4	US-09-302-540-11644	Sequence 11644, A
691	6	0.8	223	4	US-08-190-199A-63	Sequence 63, Appl	764	6	0.8	249	2	US-08-685-992-8	Sequence 8, Appli
692	6	0.8	223	4	US-09-252-991A-17072	Sequence 17072, A	765	6	0.8	249	2	US-09-144-925-8	Sequence 8, Appli
693	6	0.8	224	4	US-09-489-039A-13921	Sequence 13921, A	766	6	0.8	249	4	US-09-949-016-8151	Sequence 8151, Ap
694	6	0.8	224	4	US-09-248-796A-18609	Sequence 18609, A	767	6	0.8	249	4	US-09-489-039A-9843	Sequence 9843, Ap
695	6	0.8	224	4	US-09-438-185A-281	Sequence 281, App	768	6	0.8	250	4	US-09-134-000C-4602	Sequence 4602, Ap
696	6	0.8	225	4	US-09-270-767-3278	Sequence 3278, A	769	6	0.8	251	1	US-08-209-747-8	Sequence 8, Appli
697	6	0.8	225	4	US-09-270-767-47945	Sequence 47945, A	770	6	0.8	251	1	US-08-458-298-8	Sequence 8, Appli
698	6	0.8	226	4	US-09-710-279-1594	Sequence 1594, Ap	771	6	0.8	251	4	US-09-302-540-15293	Sequence 15293, A
699	6	0.8	226	4	US-09-252-991A-17294	Sequence 17294, A	772	6	0.8	252	4	US-09-252-991A-16901	Sequence 16901, A
700	6	0.8	226	4	US-09-270-767-60023	Sequence 60023, A	773	6	0.8	252	4	US-09-583-110-3303	Sequence 3303, Ap
701	6	0.8	227	4	US-09-252-991A-30027	Sequence 30027, A	774	6	0.8	252	4	US-09-370-767-47090	Sequence 47090, A
702	6	0.8	229	4	US-09-107-532A-6084	Sequence 6084, Ap	775	6	0.8	253	4	US-09-336-910A-7	Sequence 7, Appli
703	6	0.8	229	4	US-10-112-802-1	Sequence 1, Appli	776	6	0.8	253	4	US-09-302-540-14305	Sequence 14305, A
704	6	0.8	231	4	US-09-270-767-43196	Sequence 43196, A	777	6	0.8	253	4	US-09-252-991A-22771	Sequence 22771, A
705	6	0.8	232	4	US-08-529-055-70	Sequence 70, Appl	778	6	0.8	254	4	US-09-134-000C-4199	Sequence 4199, Ap
706	6	0.8	232	4	US-09-248-796A-14122	Sequence 14122, A	779	6	0.8	254	4	US-09-586-106D-159	Sequence 159, App
707	6	0.8	233	4	US-09-252-991A-20802	Sequence 20802, A	780	6	0.8	254	4	US-09-949-016-6948	Sequence 6948, Ap
708	6	0.8	233	4	US-09-252-991A-21274	Sequence 21274, A	781	6	0.8	255	3	US-09-353-498-8	Sequence 8, Appli
709	6	0.8	233	4	US-09-252-991A-23516	Sequence 23516, A	782	6	0.8	255	4	US-09-618-869-8	Sequence 8, Appli
710	6	0.8	233	3	US-09-270-767-43719	Sequence 43719, A	783	6	0.8	255	4	US-09-540-236-3420	Sequence 3420, Ap
711	6	0.8	234	3	US-08-836-236-4	Sequence 4, Appli	784	6	0.8	255	4	US-09-502-540-16637	Sequence 16637, A
712	6	0.8	234	3	US-08-836-236-5	Sequence 5, Appli	785	6	0.8	256	4	US-09-292-412-2	Sequence 2, Appli
713	6	0.8	234	3	US-08-715-628B-3	Sequence 3, Appli	786	6	0.8	256	4	US-09-252-991A-32307	Sequence 32307, A
714	6	0.8	234	4	US-09-535-679-4	Sequence 4, Appli	787	6	0.8	256	4	US-09-107-532A-3657	Sequence 3657, Ap
715	6	0.8	234	4	US-09-535-679-5	Sequence 5, Appli	788	6	0.8	256	4	US-09-583-110-4113	Sequence 4113, Ap
716	6	0.8	235	2	US-08-190-199A-61	Sequence 61, Appl	789	6	0.8	256	4	US-10-138-701-6	Sequence 6, Appli
717	6	0.8	235	2	US-08-303-569B-5	Sequence 5, Appli	790	6	0.8	256	4	US-09-292-411A-2	Sequence 2, Appli
718	6	0.8	235	2	US-08-116-247-5	Sequence 5, Appli	791	6	0.8	256	4	US-09-902-540-12724	Sequence 12724, A
719	6	0.8	235	4	US-09-795-515-5	Sequence 5, Appli	792	6	0.8	257	4	US-09-328-352-4324	Sequence 4324, Ap
720	6	0.8	235	4	US-09-270-767-48485	Sequence 48485, A	793	6	0.8	258	4	US-09-724-623-105	Sequence 105, App
721	6	0.8	235	4	US-09-248-796A-18489	Sequence 18489, A	794	6	0.8	258	4	US-09-023-942A-8	Sequence 8, Appli
722	6	0.8	235	4	US-09-348-224-5	Sequence 5, Appli	795	6	0.8	258	4	US-09-081-385-150	Sequence 150, App
723	6	0.8	235	4	US-09-949-016-7903	Sequence 7903, Ap	796	6	0.8	258	4	US-09-270-767-32398	Sequence 32398, A
724	6	0.8	236	2	US-08-190-199A-65	Sequence 65, Appl	797	6	0.8	258	4	US-09-270-767-43894	Sequence 43894, A
725	6	0.8	236	3	US-08-411-768B-8	Sequence 8, Appli	798	6	0.8	258	4	US-09-270-767-59125	Sequence 59125, A
726	6	0.8	236	4	US-09-543-681A-6359	Sequence 6359, Ap	799	6	0.8	259	4	US-09-270-767-45089	Sequence 45089, A
727	6	0.8	236	4	US-09-827-688-2	Sequence 2, Appli	800	6	0.8	260	3	US-09-134-001C-4009	Sequence 4009, Ap
728	6	0.8	237	3	US-09-320-878-11	Sequence 11, Appl	801	6	0.8	260	4	US-09-489-039A-7421	Sequence 7421, Ap
729	6	0.8	237	3	US-09-105-537-18	Sequence 18, Appl	802	6	0.8	260	4	US-09-270-767-33511	Sequence 33511, A
730	6	0.8	237	3	US-09-216-295-19	Sequence 19, Appl	803	6	0.8	260	4	US-09-270-767-46440	Sequence 46440, A
731	6	0.8	237	4	US-09-657-440-11	Sequence 11, Appl	804	6	0.8	260	4	US-09-248-796A-17592	Sequence 17592, A
732	6	0.8	237	4	US-09-232-991A-19656	Sequence 19656, A	805	6	0.8	261	4	US-09-489-039A-10725	Sequence 10725, A
733	6	0.8	237	4	US-09-543-681A-5471	Sequence 5471, Ap	806	6	0.8	261	4	US-09-252-991A-23754	Sequence 23754, A
734	6	0.8	237	4	US-09-632-570-19	Sequence 19, Appl	807	6	0.8	261	3	US-09-035-382-4	Sequence 4, Appli
735	6	0.8	237	4	US-09-632-575-49	Sequence 49, Appl	808	6	0.8	264	4	US-09-252-991A-27675	Sequence 27675, A
736	6	0.8	238	4	US-09-328-352-6703	Sequence 6703, Ap	809	6	0.8	264	4	US-09-134-000C-4403	Sequence 4403, Ap
737	6	0.8	238	4	US-09-543-681A-4429	Sequence 4429, Ap	810	6	0.8	264	4	US-09-302-540-16652	Sequence 16652, A
738	6	0.8	239	4	US-09-540-236-3366	Sequence 3366, Ap	811	6	0.8	266	4	US-09-050-739-153	Sequence 153, App
739	6	0.8	239	4	US-09-248-796A-15852	Sequence 15852, A	812	6	0.8	266	4	US-09-655-908-20	Sequence 20, Appl
740	6	0.8	239	4	US-09-107-433-3281	Sequence 3281, Ap	813	6	0.8	266	4	US-09-248-796A-20084	Sequence 20084, A
741	6	0.8	240	2	US-08-956-047-25	Sequence 25, Appl	814	6	0.8	266	4	US-09-902-540-13043	Sequence 13043, A
742	6	0.8	240	4	US-09-540-236-2994	Sequence 2994, Ap	815	6	0.8	267	4	US-09-489-039A-13450	Sequence 13450, A
743	6	0.8	240	4	US-09-270-767-48132	Sequence 48132, Ap	816	6	0.8	267	4	US-09-976-594-212	Sequence 212, App
744	6	0.8	241	4	US-09-370-838-194	Sequence 194, App	817	6	0.8	267	4	US-09-248-796A-18561	Sequence 18561, A
745	6	0.8	241	4	US-09-387-372-4	Sequence 4, Appli	818	6	0.8	267	4	US-09-302-540-14651	Sequence 14651, A
746	6	0.8	241	4	US-09-270-767-38616	Sequence 38616, A	819	6	0.8	268	4	US-09-328-352-8118	Sequence 8118, Ap
747	6	0.8	241	4	US-09-270-767-40578	Sequence 40578, A	820	6	0.8	268	4	US-09-540-236-3336	Sequence 3336, Ap
748	6	0.8	241	4	US-09-270-767-53833	Sequence 53833, A	821	6	0.8	269	4	US-09-583-110-3865	Sequence 3865, Ap
749	6	0.8	241	4	US-09-270-767-55794	Sequence 55794, A	822	6	0.8	269	4	US-09-270-767-42864	Sequence 42864, A
750	6	0.8	241	4	US-09-884-133-194	Sequence 133, App	823	6	0.8	270	3	US-08-878-474-1	Sequence 1, Appli
751	6	0.8	241	4	US-09-581-345-5	Sequence 5, Appli	824	6	0.8	270	4	US-09-107-433-5194	Sequence 5194, Ap
752	6	0.8	241	4	US-09-902-540-9790	Sequence 9790, Ap	825	6	0.8	271	4	US-09-540-236-2326	Sequence 2326, Ap
753	6	0.8	242	4	US-09-583-110-3522	Sequence 3522, Ap	826	6	0.8	271	4	US-09-270-767-46455	Sequence 46455, A
754	6	0.8	242	4	US-09-959-392-34	Sequence 34, Appl	827	6	0.8	271	6	5175255-1	Patent No. 5175255
755	6	0.8	242	4	US-09-949-016-10911	Sequence 10911, A	828	6	0.8	271	6	5175255-1	Patent No. 5175255
756	6	0.8	245	4	US-09-071-035-310	Sequence 310, App	829	6	0.8	272	4	US-09-902-540-16810	Sequence 16810, A
757	6	0.8	246	4	US-09-336-536-31	Sequence 31, Appl	830	6	0.8	273	4	US-09-252-991A-25600	Sequence 25600, A

831	6	0.8	274	4	US-09-489-039A-14339	Sequence 14339, A	904	6	0.8	305	4	US-09-248-796A-24107	Sequence 24107, A
832	6	0.8	276	3	US-08-961-083-134	Sequence 134, App	905	6	0.8	305	4	US-09-949-016-7706	Sequence 7706, Ap
833	6	0.8	276	4	US-09-232-991A-17951	Sequence 17951, A	906	6	0.8	306	4	US-09-489-039A-10306	Sequence 10306, A
834	6	0.8	276	4	US-09-536-784-134	Sequence 134, App	907	6	0.8	306	4	US-09-107-433-2663	Sequence 2663, Ap
835	6	0.8	276	4	US-09-902-540-15737	Sequence 15737, A	908	6	0.8	307	3	US-09-134-001C-3792	Sequence 3792, Ap
836	6	0.8	279	4	US-09-314-701-60	Sequence 60, Appl	909	6	0.8	307	4	US-09-270-767-44911	Sequence 44911, A
837	6	0.8	279	4	US-09-543-681A-4433	Sequence 4433, Ap	910	6	0.8	308	4	US-09-252-991A-27249	Sequence 27249, A
838	6	0.8	279	4	US-09-270-767-33415	Sequence 33415, A	911	6	0.8	308	4	US-09-328-352-6762	Sequence 6762, Ap
839	6	0.8	279	4	US-08-270-767-48632	Sequence 48632, A	912	6	0.8	309	4	US-09-270-767-44995	Sequence 44995, A
840	6	0.8	279	4	US-10-144-198-10	Sequence 10, Appl	913	6	0.8	310	4	US-09-543-681A-6858	Sequence 6858, Ap
841	6	0.8	280	4	US-09-489-039A-7715	Sequence 7715, Ap	914	6	0.8	310	4	US-09-538-092-690	Sequence 690, App
842	6	0.8	280	4	US-09-583-110-4231	Sequence 4231, Ap	915	6	0.8	311	4	US-09-107-532A-4438	Sequence 4438, Ap
843	6	0.8	281	4	US-09-252-991A-29199	Sequence 29199, A	916	6	0.8	311	4	US-09-107-532A-4439	Sequence 4439, Ap
844	6	0.8	282	4	US-09-248-796A-14445	Sequence 14445, A	917	6	0.8	311	4	US-09-107-433-2823	Sequence 2823, Ap
845	6	0.8	283	4	US-08-270-767-45300	Sequence 45300, A	918	6	0.8	312	4	US-09-538-092-42	Sequence 42, Appl
846	6	0.8	284	2	US-08-592-214A-24	Sequence 24, Appl	919	6	0.8	313	3	US-09-387-574-4	Sequence 4, Appli
847	6	0.8	284	3	US-08-659-188-20	Sequence 20, Appl	920	6	0.8	313	3	US-09-396-651B-3	Sequence 3, Appli
848	6	0.8	284	3	US-08-655-227-20	Sequence 20, Appl	921	6	0.8	313	3	US-09-668-096-4	Sequence 4, Appli
849	6	0.8	284	3	US-08-655-241-20	Sequence 20, Appl	922	6	0.8	313	3	US-09-470-512A-2	Sequence 2, Appli
850	6	0.8	284	3	US-09-149-976-24	Sequence 24, Appl	923	6	0.8	313	3	US-09-470-512A-10	Sequence 10, Appl
851	6	0.8	284	3	US-09-398-326-20	Sequence 20, Appl	924	6	0.8	313	4	US-09-543-681A-8278	Sequence 8278, Ap
852	6	0.8	284	4	US-09-134-000C-5638	Sequence 5638, Ap	925	6	0.8	313	4	US-09-248-796A-17065	Sequence 17065, A
853	6	0.8	284	4	US-09-853-450-20	Sequence 20, Appl	926	6	0.8	313	4	US-09-949-016-8602	Sequence 8602, Ap
854	6	0.8	285	4	US-09-540-236-2157	Sequence 2157, Ap	927	6	0.8	314	4	US-09-252-991A-33054	Sequence 33054, A
855	6	0.8	288	3	US-08-312-949-4	Sequence 4, Appli	928	6	0.8	314	4	US-09-270-767-32458	Sequence 32458, A
856	6	0.8	288	3	US-08-446-201-4	Sequence 4, Appli	929	6	0.8	314	4	US-09-270-767-42020	Sequence 42020, A
857	6	0.8	288	4	US-09-232-991A-20608	Sequence 20608, A	930	6	0.8	314	4	US-09-270-767-47675	Sequence 47675, A
858	6	0.8	288	4	US-09-949-016-10862	Sequence 10862, A	931	6	0.8	314	4	US-09-248-796A-18699	Sequence 18699, A
859	6	0.8	288	5	PCT-US95-04801-7	Sequence 7, Appli	932	6	0.8	315	1	US-08-118-270-28	Sequence 28, Appl
860	6	0.8	289	1	US-08-072-070-4	Sequence 4, Appli	933	6	0.8	315	4	US-09-252-991A-19140	Sequence 19140, A
861	6	0.8	289	1	US-08-469-434-4	Sequence 4, Appli	934	6	0.8	315	4	US-09-538-092-41	Sequence 41, Appl
862	6	0.8	289	1	US-08-214-222-4	Sequence 4, Appli	935	6	0.8	315	4	US-09-902-540-15838	Sequence 15838, A
863	6	0.8	289	2	US-08-467-852A-5	Sequence 5, Appli	936	6	0.8	315	5	PCT-US93-08528-28	Sequence 28, Appl
864	6	0.8	289	2	US-08-468-718-4	Sequence 4, Appli	937	6	0.8	316	3	US-09-504-358-10	Sequence 10, Appl
865	6	0.8	289	2	US-08-247-491A-5	Sequence 5, Appli	938	6	0.8	316	4	US-09-954-314-10	Sequence 10, Appl
866	6	0.8	289	4	US-09-543-681A-8235	Sequence 8235, Ap	939	6	0.8	316	4	US-09-328-352-6555	Sequence 6555, Ap
867	6	0.8	289	4	US-09-134-001C-3563	Sequence 3563, Ap	940	6	0.8	316	4	US-10-230-562-10	Sequence 10, Appl
868	6	0.8	290	3	US-09-134-001C-3841	Sequence 3841, Ap	941	6	0.8	316	4	US-09-902-540-12782	Sequence 12782, A
869	6	0.8	290	4	US-09-107-532A-3841	Sequence 3841, Ap	942	6	0.8	317	4	US-08-937-067-6	Sequence 6, Appli
870	6	0.8	290	4	US-09-743-847-2	Sequence 2, Appli	943	6	0.8	317	4	US-09-252-991A-29954	Sequence 29954, A
871	6	0.8	290	4	US-09-248-796A-18749	Sequence 18749, A	944	6	0.8	317	4	US-09-328-352-8169	Sequence 8169, Ap
872	6	0.8	291	4	US-09-134-000C-4458	Sequence 4458, Ap	945	6	0.8	317	4	US-09-583-110-3082	Sequence 3082, Ap
873	6	0.8	292	4	US-09-634-238-236	Sequence 236, App	946	6	0.8	317	4	US-09-949-016-6300	Sequence 6300, Ap
874	6	0.8	292	4	US-09-270-767-43846	Sequence 43846, A	947	6	0.8	318	4	US-09-252-991A-31545	Sequence 31545, A
875	6	0.8	292	4	US-09-107-433-4868	Sequence 4868, Ap	948	6	0.8	318	4	US-09-252-991A-32832	Sequence 32832, A
876	6	0.8	293	4	US-09-252-991A-27745	Sequence 27745, A	949	6	0.8	319	4	US-09-270-767-44572	Sequence 44572, A
877	6	0.8	293	4	US-09-949-016-8027	Sequence 8027, Ap	950	6	0.8	320	4	US-09-328-352-4526	Sequence 4526, Ap
878	6	0.8	294	4	US-09-252-991A-26450	Sequence 26450, A	951	6	0.8	320	4	US-09-328-352-4526	Sequence 4526, Ap
879	6	0.8	295	4	US-09-198-452A-268	Sequence 268, App	952	6	0.8	320	4	US-09-107-433-4531	Sequence 4531, Ap
880	6	0.8	295	4	US-09-270-767-45025	Sequence 45025, A	953	6	0.8	322	4	US-09-252-991A-32158	Sequence 32158, A
881	6	0.8	295	4	US-09-438-185A-258	Sequence 258, App	954	6	0.8	322	4	US-09-107-532A-4662	Sequence 4662, Ap
882	6	0.8	296	4	US-09-270-767-42478	Sequence 42478, A	955	6	0.8	322	4	US-09-949-016-8722	Sequence 8722, Ap
883	6	0.8	296	4	US-09-270-767-48808	Sequence 48808, A	956	6	0.8	322	4	US-09-949-016-8723	Sequence 8723, Ap
884	6	0.8	297	4	US-09-314-701-14	Sequence 14, Appl	957	6	0.8	323	4	US-09-134-000C-4836	Sequence 4836, Ap
885	6	0.8	297	4	US-09-252-991A-29778	Sequence 29778, A	958	6	0.8	323	4	US-09-248-796A-16307	Sequence 16307, A
886	6	0.8	297	4	US-09-489-039A-10089	Sequence 10089, A	959	6	0.8	323	4	US-09-248-796A-27766	Sequence 27766, A
887	6	0.8	298	4	US-09-543-681A-6110	Sequence 6110, Ap	960	6	0.8	323	4	US-09-902-540-14738	Sequence 14738, A
888	6	0.8	298	4	US-09-248-796A-27737	Sequence 27737, A	961	6	0.8	326	4	US-09-489-039A-11326	Sequence 11326, A
889	6	0.8	299	4	US-09-270-767-42307	Sequence 42307, A	962	6	0.8	326	6	5171684-7	Patent No. 5171684
890	6	0.8	299	4	US-09-710-279-1192	Sequence 1192, Ap	963	6	0.8	326	6	5171684-7	Patent No. 5171684
891	6	0.8	299	4	US-09-710-279-1768	Sequence 1768, Ap	964	6	0.8	327	4	US-09-270-767-42565	Sequence 42565, A
892	6	0.8	300	4	US-09-270-767-44496	Sequence 44496, A	965	6	0.8	328	4	US-09-187-999-31	Sequence 31, Appl
893	6	0.8	301	4	US-09-489-039A-10251	Sequence 10251, A	966	6	0.8	328	4	US-09-635-872A-8	Sequence 8, Appli
894	6	0.8	301	4	US-09-902-540-12303	Sequence 12303, A	967	6	0.8	328	4	US-09-636-077A-8	Sequence 8, Appli
895	6	0.8	302	3	US-08-303-861-20	Sequence 20, Appl	968	6	0.8	328	4	US-09-636-060C-8	Sequence 8, Appli
896	6	0.8	302	3	US-09-457-046B-24	Sequence 24, Appl	969	6	0.8	328	4	US-09-986-552-8	Sequence 8, Appli
897	6	0.8	302	4	US-09-232-991A-22159	Sequence 22159, A	970	6	0.8	328	4	US-09-636-596C-8	Sequence 8, Appli
898	6	0.8	302	4	US-09-107-532A-6924	Sequence 6924, Ap	971	6	0.8	328	4	US-10-023-894-10	Sequence 10, Appl
899	6	0.8	302	4	US-09-866-570B-24	Sequence 24, Appl	972	6	0.8	328	4	US-09-328-352-6400	Sequence 8, Appli
900	6	0.8	303	4	US-09-248-796A-15374	Sequence 15374, A	973	6	0.8	331	4	US-09-252-991A-21777	Sequence 21777, A
901	6	0.8	304	4	US-09-248-796A-15270	Sequence 15270, A	974	6	0.8	332	4	US-09-252-991A-24064	Sequence 24064, A
902	6	0.8	304	4	US-09-902-540-14051	Sequence 14051, A	975	6	0.8	332	4	US-09-252-991A-31956	Sequence 31956, A
903	6	0.8	305	4	US-09-248-796A-17837	Sequence 17837, A	976	6	0.8	332	4		

777 6 0.8 333 4 US-09-543-681A-4411 Sequence 4411, Ap
778 6 0.8 333 4 US-09-270-767-59028 Sequence 59028, A
779 6 0.8 334 1 US-08-279-058B-10 Sequence 10, Appl
780 6 0.8 334 4 US-08-828-323-10 Sequence 10, Appl
781 6 0.8 334 4 US-09-818-780-91 Sequence 91, Appl
782 6 0.8 334 4 US-09-270-767-33176 Sequence 33176, A
783 6 0.8 334 4 US-09-270-767-45019 Sequence 45019, A
784 6 0.8 334 4 US-09-248-796A-17169 Sequence 17169, A
785 6 0.8 334 4 US-09-438-185A-11 Sequence 11, Appl
786 6 0.8 335 4 US-09-482-273-118 Sequence 118, App
787 6 0.8 335 4 US-09-583-110-3726 Sequence 3726, Ap
788 6 0.8 336 3 US-08-804-166-8 Sequence 8, Appl
789 6 0.8 336 3 US-08-910-991-8 Sequence 8, Appl
790 6 0.8 336 4 US-09-543-681A-5330 Sequence 5330, Ap
791 6 0.8 336 4 US-09-489-039A-9200 Sequence 9200, Ap
792 6 0.8 336 4 US-09-756-186-8 Sequence 8, Appl
793 6 0.8 337 4 US-09-232-991A-17374 Sequence 17374, A
794 6 0.8 338 1 US-08-210-394-1 Sequence 1, Appl
795 6 0.8 338 3 US-09-134-001C-4795 Sequence 4795, Ap
796 6 0.8 338 4 US-09-248-796A-18170 Sequence 18170, A
797 6 0.8 338 4 US-09-538-092-144 Sequence 144, App
798 6 0.8 339 4 US-09-252-991A-26600 Sequence 26600, A
799 6 0.8 339 4 US-09-134-000C-4665 Sequence 4665, Ap
1000 6 0.8 341 4 US-09-336-536-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis

US-09-994-192-4
Query Match 100.0%; Score 797; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFPDVRVETADQQLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFPDVRVETADQQLLLTVIERPTGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SOYFNQATLNOAVAGLKEEYLGKLNQIQTIPKVTKLARNVDITDITDEKSAKITDIE 180
Db 121 SOYFNQATLNOAVAGLKEEYLGKLNQIQTIPKVTKLARNVDITDITDEKSAKITDIE 180

Qy 181 FEGNQVYSDRLKMQMSLITGGIWTWLTFRSNQFNEQKFAQDMKVDTFYQNGYDFDPRIL 240
Db 181 FEGNQVYSDRLKMQMSLITGGIWTWLTFRSNQFNEQKFAQDMKVDTFYQNGYDFDPRIL 240

Qy 241 DTDIQTWEDKTKQTIKIVTVEGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPKGWYERQQ 300

Db 241 DTDIQTWEDKTKQTIKIVTVEGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPKGWYERQQ 300
Qy 301 MTAVLGEIQNRMGSGAGYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSGAGYSEISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKT 360
Qy 361 RDVVRRELRLQMESAPYDTSKLQRSKERVELLGYFNVQFDPVPLAGTDPKVDLNNSLTE 420
Db 361 RDVVRRELRLQMESAPYDTSKLQRSKERVELLGYFNVQFDPVPLAGTDPKVDLNNSLTE 420
Qy 421 RSTGSLDLNAGWQDTGLVMSAGVSQDNLPGTCKSALRASRSKTTLNGSLSTDPYETA 480
Db 421 RSTGSLDLNAGWQDTGLVMSAGVSQDNLPGTCKSALRASRSKTTLNGSLSTDPYETA 480
Qy 481 DGVSGLGVYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGVYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPKHYADFIKKYKKTGDTGSGFKGWLKYKGTGVRNKTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKKTGDTGSGFKGWLKYKGTGVRNKTDSALWPTRGYLTGVNAEIA 600
Qy 601 LPQSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Db 601 LPQSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKADARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFOFQGLGTF 797
Db 781 KPEDEIQRFOFQGLGTF 797

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae

US-09-994-192-2
Query Match 19.7%; Score 157; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.6e-152;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDFVLHIEPGRKIYVNEIHTGNKKTDFVVRRELRLQMESAPYDTSKLQRSKERV 391
Db 332 TKTVDFVLHIEPGRKIYVNEIHTGNKKTDFVVRRELRLQMESAPYDTSKLQRSKERV 391
Qy 392 LGYFDNVQFDPVPLAGTDPKVDLNNSLTERSTGSLDLNAGWQDTGLVMSAGVSQDNLFG 451
Db 392 LGYFDNVQFDPVPLAGTDPKVDLNNSLTERSTGSLDLNAGWQDTGLVMSAGVSQDNLFG 451

US-09-270-767-45805
 ; Sequence 45805, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 45805
 ; LENGTH: 230
 ; TYPE: PRT
 ; ORGANISM: *Drosophila melanogaster*
 US-09-270-767-45805

Query Match 1.0%; Score 8; DB 4; Length 230;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 589 RGYLTGWN 596
 |||||
 Db 188 RGYLTGWN 195

RESULT 6
 US-09-902-540-15552
 ; Sequence 15552, Application US/09902540
 ; Patent No. 6833447
 ; GENERAL INFORMATION:
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Wiegand, Roger C.
 ; TITLE OF INVENTION: *Myxococcus xanthus* Genome Sequences and Uses Thereof
 ; FILE REFERENCE: 38-10(15849)B
 ; CURRENT APPLICATION NUMBER: US/09/902,540
 ; CURRENT FILING DATE: 2001-07-10
 ; PRIOR APPLICATION NUMBER: 60/217,883
 ; PRIOR FILING DATE: 2000-07-10
 ; NUMBER OF SEQ ID NOS: 16825
 ; SEQ ID NO 15552
 ; LENGTH: 274
 ; TYPE: PRT
 ; ORGANISM: *Myxococcus xanthus*
 US-09-902-540-15552

Query Match 1.0%; Score 8; DB 4; Length 274;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 281 KAELEKLL 288
 |||||
 Db 177 KAELEKLL 184

RESULT 7
 US-09-252-991A-24628
 ; Sequence 24628, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PSEUDOMONAS*
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142

; SEQ ID NO 24628
 ; LENGTH: 648
 ; TYPE: PRT
 ; ORGANISM: *Pseudomonas aeruginosa*
 US-09-252-991A-24628

Query Match 1.0%; Score 8; DB 4; Length 648;
 Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 VRVETADG 81
 |||||
 Db 94 VRVETADG 101

RESULT 8
 US-09-543-681A-4998
 ; Sequence 4998, Application US/09543681A
 ; Patent No. 6605709
 ; GENERAL INFORMATION:
 ; APPLICANT: GARY BRETON
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO *PROTEUS MIRABILIS*
 ; FILE REFERENCE: 2709.1002-001
 ; CURRENT APPLICATION NUMBER: US/09/543,681A
 ; CURRENT FILING DATE: 2000-04-05
 ; PRIOR APPLICATION NUMBER: US 60/128,706
 ; PRIOR FILING DATE: 1999-04-09
 ; NUMBER OF SEQ ID NOS: 8344
 ; SEQ ID NO 4998
 ; LENGTH: 1589
 ; TYPE: PRT
 ; ORGANISM: *Proteus mirabilis*
 US-09-543-681A-4998

Query Match 1.0%; Score 8; DB 4; Length 1589;
 Best Local Similarity 100.0%; Pred. No. 77;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 78 TADGQLLL 85
 |||||
 Db 563 TADGQLLL 570

RESULT 9
 US-09-674-973A-147
 ; Sequence 147, Application US/09674973A
 ; Patent No. 6759046
 ; GENERAL INFORMATION:
 ; APPLICANT: No. 6759046sk Hydro ASA
 ; TITLE OF INVENTION: Peptides
 ; FILE REFERENCE: 26625-296
 ; CURRENT APPLICATION NUMBER: US/09/674,973A
 ; CURRENT FILING DATE: 2001-06-04
 ; NUMBER OF SEQ ID NOS: 459
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 147
 ; LENGTH: 23
 ; TYPE: PRT
 ; ORGANISM: *Homo sapiens*
 US-09-674-973A-147

Query Match 0.9%; Score 7; DB 4; Length 23;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 283 ELEKLLT 289
 |||||
 Db 5 ELEKLLT 11

RESULT 10
 US-08-971-089-10

; Sequence 10, Application US/08971089
; Patent No. 6376174
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Scoles, Daniel R.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 58 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-971-089-10

Query Match 0.9%; Score 7; DB 3; Length 58;
Best Local Similarity 100.0%; Pred. No. 42; Mismatches 0; Indels 0; Gaps 0;
Matches 7; Conservative 0;

Qy 458 LRASRSK 464
| | | | |
Db 4 LRASRSK 10

RESULT 11
US-09-513-999C-7231
; Sequence 7231, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclert, A.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; Patent No. 6783961
; FILE REFERENCE: 59.US2.REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.Pm
; SEQ ID NO 7231
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

; NAME/KEY: UNSURE
; LOCATION: 51
; OTHER INFORMATION: Xaa-Ile or Leu or Val
; US-09-513-999C-7231

Query Match 0.9%; Score 7; DB 4; Length 60;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 458 LRASRSK 464
| | | | |
Db 38 LRASRSK 44

RESULT 12
US-09-328-352-6252
; Sequence 6252, Application US/09328352
; Patent No. 6562958
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 6252
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Acinetobacter baumannii
; US-09-328-352-6252

Query Match 0.9%; Score 7; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 654 GGLGSRV 660
| | | | |
Db 18 GGLGSRV 24

RESULT 13
US-09-489-039A-10485
; Sequence 10485, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 10485
; LENGTH: 86
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
; US-09-489-039A-10485

Query Match 0.9%; Score 7; DB 4; Length 86;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 483 VSLGYDV 489
| | | | |
Db 71 VSLGYDV 77

RESULT 14
US-09-461-325-325
; Sequence 325, Application US/09461325A

```
; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-325

Query Match      0.9%; Score 7; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      423 TGSIDL 429
      |||||
Db      36 TGSIDL 42

Search completed: July 6, 2005, 15:43:23
Job time : 62 secs

; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-012-542-325

Query Match      0.9%; Score 7; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      423 TGSIDL 429
      |||||
Db      36 TGSIDL 42

Search completed: July 6, 2005, 15:43:23
Job time : 62 secs

; Patent No. 6475753
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/09/461,325A
; CURRENT FILING DATE: 1999-12-14
; EARLIER APPLICATION NUMBER: PCT/US99/13418
; EARLIER FILING DATE: 1999-06-15
; EARLIER APPLICATION NUMBER: 60/089,507
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,508
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,509
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/089,510
; EARLIER FILING DATE: 1998-06-16
; EARLIER APPLICATION NUMBER: 60/090,112
; EARLIER FILING DATE: 1998-06-22
; EARLIER APPLICATION NUMBER: 60/090,113
; EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (21)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-461-325-325

Query Match      0.9%; Score 7; DB 4; Length 88;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      423 TGSIDL 429
      |||||
Db      36 TGSIDL 42

RESULT 15
US-10-012-542-325
; Sequence 325, Application US/10012542
; Patent No. 662741
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: 94 Human Secreted Proteins
; FILE REFERENCE: P2029P1
; CURRENT APPLICATION NUMBER: US/10/012,542
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/461,325
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-12-14
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,507
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,508
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,509
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/089,510
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/090,113
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-06-22
; NUMBER OF SEQ ID NOS: 532
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 325
; LENGTH: 88
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:20:52 ; Search time 44 Seconds
(without alignments)
1742.835 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEDEIQRFQGLGTF 797

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 283416 seqs, 96216763 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	752	94.4	797	D82000	outer membrane pro
2	752	94.4	797	G81228	outer membrane pro
3	9	1.1	328	T46206	hypothetical prote
4	9	1.1	435	T49132	hypothetical prote
5	8	1.0	129	A96984	hypothetical prote
6	8	1.0	225	E84423	hypothetical prote
7	8	1.0	335	B75057	glycerate dehydrog
8	8	1.0	337	C82190	formate dehydrogen
9	8	1.0	376	A71175	probable dehydroge
10	8	1.0	426	T04985	probable transamin
11	8	1.0	429	G42365	flagellar hook-len
12	8	1.0	474	IMBP4	site-specific reco
13	8	1.0	583	T283375	probable glycosyl
14	8	1.0	903	JE0337	dynammin-related pr
15	8	1.0	903	T50334	dynammin-related pr
16	8	1.0	1363	T43220	insulin-like growt
17	8	1.0	1577	T435140	hemolysin A precur
18	8	1.0	4919	T31105	hypothetical prote
19	7	0.9	75	E85707	hypothetical prote
20	7	0.9	75	F90849	probable regulator
21	7	0.9	76	1 CECCDC	cell division cont
22	7	0.9	95	T26611	hypothetical prote
23	7	0.9	101	T33316	hypothetical prote
24	7	0.9	101	T35232	hypothetical prote
25	7	0.9	109	E72527	hypothetical prote
26	7	0.9	118	T214079	pim1 protein - mou
27	7	0.9	131	T487461	hypothetical prote
28	7	0.9	148	T252550	probable transcrip
29	7	0.9	150	D81314	small protein B ho

30	7	0.9	171	2	C95143	hypothetical prote
31	7	0.9	175	2	T05669	hypothetical prote
32	7	0.9	184	2	C69142	hypothetical prote
33	7	0.9	184	2	S44652	f42h10.6 protein -
34	7	0.9	210	2	S36297	T-cell receptor ga
35	7	0.9	214	2	H86931	probable acyltrans
36	7	0.9	218	2	T45455	probable acyltrans
37	7	0.9	234	2	G71918	probable efflux tr
38	7	0.9	234	2	F64595	membrane fusion pr
39	7	0.9	238	2	A83224	probable ATP-bandi
40	7	0.9	255	2	F95228	hypothetical prote
41	7	0.9	255	2	B98093	hypothetical prote
42	7	0.9	264	2	A81668	conserved hypothet
43	7	0.9	264	2	E71509	hypothetical prote
44	7	0.9	288	2	T35568	probable lipoprote
45	7	0.9	269	2	T36001	probable integral
46	7	0.9	280	2	E87429	conserved hypothet
47	7	0.9	288	1	SNBYC1	proteasome endopep
48	7	0.9	305	2	A75334	lacyl-carrier-prot
49	7	0.9	305	2	T22009	hypothetical prote
50	7	0.9	306	2	T48715	hypothetical prote
51	7	0.9	306	2	AB2885	transcription regu
52	7	0.9	311	2	B97661	probable transcrip
53	7	0.9	311	2	H98278	hypothetical prote
54	7	0.9	311	2	AI3004	hypothetical prote
55	7	0.9	314	2	F96574	hypothetical prote
56	7	0.9	315	2	C96802	hypothetical prote
57	7	0.9	316	2	S61237	hypothetical prote
58	7	0.9	320	1	A43824	capsid protein - b
59	7	0.9	324	2	AC0548	delta-aminolevulin
60	7	0.9	336	2	G84562	hypothetical prote
61	7	0.9	347	2	T06671	hypothetical prote
62	7	0.9	349	2	G97121	scpE protein limpo
63	7	0.9	354	2	B89768	conserved hypothet
64	7	0.9	355	2	S29274	poly (3-hydroxybut
65	7	0.9	355	2	AC1925	cytochrome c oxida
66	7	0.9	359	2	T14742	hypothetical prote
67	7	0.9	363	2	S72209	hypothetical prote
68	7	0.9	366	2	C69391	3-isopropylmalate
69	7	0.9	373	2	S47911	enolase (eno) homo
70	7	0.9	373	2	A47380	PBS1 protein - yea
71	7	0.9	380	2	AC3494	RING finger-contai
72	7	0.9	380	2	T02968	oligopeptide trans
73	7	0.9	387	2	JC4578	cyclin A-type (clo
74	7	0.9	397	1	Z6BPT9	recombination prot
75	7	0.9	401	2	B83369	ribonucleoside-tri
76	7	0.9	416	2	F89779	conserved hypothet
77	7	0.9	417	2	JT0950	hypothetical prote
78	7	0.9	420	2	T43932	phosphoglycerate k
79	7	0.9	420	2	D64492	cell division cont
80	7	0.9	422	1	JGAGLR	N-ethylammelaine ch
81	7	0.9	428	2	S76184	lactose-binding pr
82	7	0.9	429	2	AB3574	hypothetical prote
83	7	0.9	432	2	G75199	multidrug resistan
84	7	0.9	437	1	B71233	probable cell divi
85	7	0.9	444	2	T27866	hypothetical prote
86	7	0.9	456	2	C71226	hypothetical prote
87	7	0.9	460	2	D90084	RNA-polymerase sig
88	7	0.9	464	2	A64974	hypothetical prote
89	7	0.9	464	2	B90989	hypothetical prote
90	7	0.9	464	2	E85834	probable membrane
91	7	0.9	469	2	T08310	probable membrane
92	7	0.9	471	2	AF1586	helicase homolog H
93	7	0.9	476	2	E97631	site-specific reco
94	7	0.9	489	1	H70729	probable membrane
95	7	0.9	497	2	D95102	cytochrome P450 Rv
96	7	0.9	497	2	F97970	hypothetical prote
97	7	0.9	498	2	B90456	site-specific DNA-
98	7	0.9	499	2	T34328	hypothetical prote
99	7	0.9	508	2	T20355	hypothetical prote
100	7	0.9	515	2	B90302	ATP-dependent RNA
101	7	0.9	518	2	JC4024	poliovirus recepto
102	7	0.9	518	2	F84391	orc / cell divisio

103	7	0.9	521	2	A86909	hypothetical prote	176	6	0.8	70	2	G91236	50S ribosomal subu
104	7	0.9	526	1	KRBOVI	keratin, 54K type	177	6	0.8	70	2	G86083	50S ribosomal subu
105	7	0.9	537	2	T38015	hypothetical prote	178	6	0.8	71	2	E69345	SSU ribosomal prot
106	7	0.9	545	2	AB0290	probable membrane	179	6	0.8	72	1	B24033	small acid-soluble
107	7	0.9	562	2	S61295	heat shock protein	180	6	0.8	74	2	AI0349	conserved hypothet
108	7	0.9	564	2	H82919	conserved hypothet	181	6	0.8	74	2	AB2071	hypothetical prote
109	7	0.9	587	2	JC5300	Ran GTPase activat	182	6	0.8	76	2	A48784	Ig kappa V regions
110	7	0.9	589	2	T52070	RNA1 protein homol	183	6	0.8	76	2	B88318	protein age-1 (imp
111	7	0.9	589	2	A36983	RNA1 homolog fugu	184	6	0.8	76	2	F70241	hypothetical prote
112	7	0.9	619	2	S40938	hypothetical prote	185	6	0.8	77	2	AC2101	lipoprotein (impor
113	7	0.9	620	2	S38994	origin recognition	186	6	0.8	78	2	A64450	ribosomal protein
114	7	0.9	623	2	AD2295	hypothetical prote	187	6	0.8	78	2	AF2345	hypothetical prote
115	7	0.9	625	2	A72592	glutamine-fructose	188	6	0.8	79	2	S68245	phosphatidylcholin
116	7	0.9	649	1	H64476	lipote protein li	189	6	0.8	79	2	F70013	hypothetical prote
117	7	0.9	656	2	H84649	probable DnaJ prot	190	6	0.8	80	2	G81108	hypothetical prote
118	7	0.9	666	2	D82386	methyl-accepting c	191	6	0.8	80	2	A32364	photosystem I iron
119	7	0.9	728	2	S71467	diacylglycerol kin	192	6	0.8	80	2	G97805	hypothetical prote
120	7	0.9	745	2	D96829	homeobox protein (193	6	0.8	81	1	FEPM1S	photosystem I iron
121	7	0.9	747	2	S71478	homeotic protein A	194	6	0.8	81	1	FEWTA	photosystem I iron
122	7	0.9	771	2	T01315	hypothetical prote	195	6	0.8	81	1	FEWT1	photosystem I iron
123	7	0.9	784	2	E82731	outer membrane ant	196	6	0.8	81	1	FEZM1C	photosystem I iron
124	7	0.9	797	2	H83190	probable outer mem	197	6	0.8	81	2	S07170	photosystem I iron
125	7	0.9	812	2	AH1049	ribonuclease R (RN	198	6	0.8	81	2	S73295	photosystem I iron
126	7	0.9	823	2	T52425	kinesin-like prote	199	6	0.8	81	2	T07571	photosystem I iron
127	7	0.9	827	1	S56404	virulence-associat	200	6	0.8	81	2	SI2198	photosystem I iron
128	7	0.9	827	2	C86114	probable enzyme va	201	6	0.8	81	2	AI3461	hypothetical prote
129	7	0.9	827	2	C91273	probable enzyme [i	202	6	0.8	81	2	A98247	hypothetical prote
130	7	0.9	856	2	F96998	phosphoenolpyruvat	203	6	0.8	81	2	H97567	hypothetical prote
131	7	0.9	881	2	L84737	kinesin heavy chai	204	6	0.8	83	2	F81267	30S ribosomal prot
132	7	0.9	888	2	D96619	protein T30E16.9 [205	6	0.8	83	2	S77417	prochlorophyllid
133	7	0.9	942	1	T31553	hypothetical prote	206	6	0.8	83	2	AI0032	probable type III
134	7	0.9	953	1	B30169	leukotoxin A - Pas	207	6	0.8	84	2	E97807	hypothetical prote
135	7	0.9	963	1	A41919	kinesin heavy chai	208	6	0.8	85	2	T08595	cysteine proteinas
136	7	0.9	983	2	AG2381	glycine cleavage s	209	6	0.8	85	2	AI0316	sec-independent pr
137	7	0.9	1054	2	D70425	conserved hypothet	210	6	0.8	86	2	H85939	type III secretion
138	7	0.9	1088	2	A69493	cysteine proteinas	211	6	0.8	86	2	D91094	type III secretion
139	7	0.9	1121	2	JC7329	WD-repeat protein	212	6	0.8	86	2	JQ0730	9K protein - Prote
140	7	0.9	1221	2	T25005	hypothetical prote	213	6	0.8	86	2	E82985	hypothetical prote
141	7	0.9	1222	2	B90593	hypothetical prote	214	6	0.8	86	2	AG3442	helix-turn-helix p
142	7	0.9	1234	2	T31623	hypothetical prote	215	6	0.8	87	2	T05709	auxin-induced prot
143	7	0.9	1259	2	T32901	hypothetical prote	216	6	0.8	88	2	C82468	hypothetical prote
144	7	0.9	1366	2	C85077	probable polyprote	217	6	0.8	88	2	E70880	hypothetical prote
145	7	0.9	1434	2	T30172	transmembrane prot	218	6	0.8	90	2	SI5149	hypothetical prote
146	7	0.9	1442	2	T18538	patched protein -	219	6	0.8	90	2	B82799	hypothetical prote
147	7	0.9	1449	2	B81963	IgA-specific serin	220	6	0.8	91	2	SI7627	Ig kappa chain V r
148	7	0.9	1457	2	D81019	adhesion and penet	221	6	0.8	91	2	SI7629	Ig kappa chain V r
149	7	0.9	1513	2	T44045	hypothetical prote	222	6	0.8	91	2	SI7638	Ig kappa chain V r
150	7	0.9	1520	2	T44231	hypothetical prote	223	6	0.8	91	2	SI7639	Ig kappa chain V r
151	7	0.9	1658	2	D75489	hypothetical prote	224	6	0.8	91	2	SI7628	Ig kappa chain V r
152	7	0.9	1943	2	B64596	toxin-like outer m	225	6	0.8	91	2	SI7637	Ig kappa chain V r
153	7	0.9	2174	2	E95965	hypothetical glyci	226	6	0.8	91	2	B69190	hypothetical prote
154	7	0.9	2274	2	T30258	adenomatous polyo	227	6	0.8	93	2	G71370	probable ribosomal
155	7	0.9	2431	1	KMWVSF	nonstructural poly	228	6	0.8	93	2	D70192	chaperonin (groES)
156	7	0.9	2478	2	AH2140	polyketide synthas	229	6	0.8	94	2	A60097	cortical cytoskele
157	7	0.9	3194	2	D71917	toxin-like outer m	230	6	0.8	94	2	S32105	chaperonin groES -
158	7	0.9	4385	2	T29042	hypothetical prote	231	6	0.8	94	2	JN0660	heat shock protein
159	7	0.9	4485	2	T08044	dynein gamma heavy	232	6	0.8	94	2	B40506	PRF2 protein - hum
160	7	0.9	5369	2	T44807	mycosubtilin synth	233	6	0.8	94	2	S75365	hypothetical prote
161	6	0.8	17	2	I55612	thyroid hormone re	234	6	0.8	95	2	T33730	Ig kappa chain V r
162	6	0.8	23	2	S45030	homeotic protein S	235	6	0.8	95	2	T03068	hypothetical prote
163	6	0.8	23	2	S60569	homeodomain protei	236	6	0.8	96	2	B26074	cysteine proteinas
164	6	0.8	25	2	D41606	homeotic protein M	237	6	0.8	96	2	S34937	heat shock protein
165	6	0.8	52	2	AI2399	hypothetical prote	238	6	0.8	96	2	C82048	chaperonin, 10 Kd
166	6	0.8	57	2	AB0373	hypothetical prote	239	6	0.8	96	2	JC4518	heat-shock protein
167	6	0.8	60	2	F75338	hypothetical prote	240	6	0.8	96	2	H97048	hypothetical prote
168	6	0.8	62	2	G70988	hypothetical prote	241	6	0.8	97	2	S26341	Ig light chain V r
169	6	0.8	65	2	HF2773	hypothetical prote	242	6	0.8	97	2	PH1084	Ig light chain V r
170	6	0.8	66	2	AF3083	hypothetical prote	243	6	0.8	97	2	C64029	hypothetical prote
171	6	0.8	67	2	F85904	hypothetical prote	244	6	0.8	97	2	F82416	hypothetical prote
172	6	0.8	68	2	H90086	hypothetical prote	245	6	0.8	98	2	H82577	hypothetical prote
173	6	0.8	68	2	F84002	hypothetical prote	246	6	0.8	99	2	S51210	Ig kappa chain V r
174	6	0.8	69	2	S33899	hypothetical prote	247	6	0.8	99	2	SS1224	probable ribosomal
175	6	0.8	70	1	R5EC31	ribosomal protein	248	6	0.8	100	2	S29590	Ig kappa chain V r

249	6	0.8	100	2	S03636	homeotic protein H	322	6	0.8	126	2	D95410	hypothetical prote
250	6	0.8	101	2	F82421	conserved hypothet	323	6	0.8	127	2	F75092	ssu ribosomal prot
251	6	0.8	101	2	C9076	hypothetical prote	324	6	0.8	127	2	D97381	methyglyoxal synt
252	6	0.8	102	2	S1115	Ig kappa chain v r	325	6	0.8	127	2	AC2599	methyglyoxal synt
253	6	0.8	102	2	SF3346	ssu ribosomal prot	326	6	0.8	127	2	A75086	translation initia
254	6	0.8	102	2	H87403	ribosomal protein	327	6	0.8	128	2	S39678	ywbH protein - Bac
255	6	0.8	102	2	A23931	anti-lipopolsacch	328	6	0.8	128	2	F84216	hypothetical prote
256	6	0.8	103	2	S29591	Ig kappa chain v r	329	6	0.8	128	2	S53584	probable membrane
257	6	0.8	103	2	G75237	hypothetical prote	330	6	0.8	129	2	B72853	AcMPV orf26 - Bom
258	6	0.8	104	2	B49040	Ig kappa chain v r	331	6	0.8	129	2	T41771	hypothetical prote
259	6	0.8	105	2	D95108	conserved hypothet	332	6	0.8	129	2	T46300	probable membrane
260	6	0.8	106	2	PS0071	Ig kappa chain v r	333	6	0.8	129	2	S45868	hypothetical prote
261	6	0.8	106	2	S11114	Ig kappa chain v r	334	6	0.8	129	2	T36916	hypothetical prote
262	6	0.8	106	2	S11120	Ig kappa chain v r	335	6	0.8	130	1	JI0079	Ig kappa chain pre
263	6	0.8	106	2	G27887	Ig kappa chain v r	336	6	0.8	130	1	JBAQ10	chorion class B pr
264	6	0.8	106	2	G28059	conserved hypothet	337	6	0.8	130	2	S01439	hypothetical prote
265	6	0.8	106	2	D86563	Ct466 hypothetical	338	6	0.8	130	2	H83150	lens fiber membran
266	6	0.8	106	2	T24774	hypothetical prote	339	6	0.8	131	1	S12972	hypothetical prote
267	6	0.8	107	1	XPSPSP	putidaredoxin [val	340	6	0.8	131	2	C87416	amicyanin - paraco
268	6	0.8	107	1	B36950	urease (EC 3.5.1.5	341	6	0.8	131	2	E71055	MutT/nudix family
269	6	0.8	107	2	S11112	Ig kappa chain v r	342	6	0.8	132	2	C70161	hypothetical prote
270	6	0.8	107	2	S11118	Ig kappa chain v r	343	6	0.8	132	2	D72583	hypothetical prote
271	6	0.8	107	2	S11116	Ig kappa chain v r	344	6	0.8	133	2	S39540	homeotic protein G
272	6	0.8	107	2	PD0011	Ig kappa chain v r	345	6	0.8	134	2	C69849	hypothetical prote
273	6	0.8	107	2	S11113	Ig kappa chain v r	346	6	0.8	134	2	T01042	hypothetical prote
274	6	0.8	107	2	PT0395	Ig kappa chain v r	347	6	0.8	135	2	AF2055	hypothetical prote
275	6	0.8	107	2	PT0402	Ig light chain v r	348	6	0.8	135	2	B72768	hypothetical prote
276	6	0.8	107	2	S11119	Ig kappa chain v r	349	6	0.8	136	2	AB1544	positive regulatio
277	6	0.8	107	2	PT0397	Ig kappa chain v r	350	6	0.8	136	2	T49582	hypothetical prote
278	6	0.8	107	2	S11123	Ig kappa chain v r	351	6	0.8	136	2	S04043	embryonic abundant
279	6	0.8	107	2	PT0398	Ig kappa chain v r	352	6	0.8	137	2	T45079	hypothetical prote
280	6	0.8	107	2	S11121	Ig kappa chain v r	353	6	0.8	138	1	A69219	conserved hypothet
281	6	0.8	107	2	S11117	Ig kappa chain v r	354	6	0.8	138	2	B83135	hypothetical prote
282	6	0.8	107	2	A30562	Ig kappa chain v r	355	6	0.8	138	2	G85806	hypothetical prote
283	6	0.8	107	2	PT0406	Ig kappa chain v r	356	6	0.8	139	2	A82140	hypothetical prote
284	6	0.8	107	2	B30562	Ig kappa chain v r	357	6	0.8	139	2	H97449	probable isomerase
285	6	0.8	107	2	PC4405	Ig kappa chain v r	358	6	0.8	139	2	S32510	homeobox-containin
286	6	0.8	107	2	C48078	biliary glycoprote	359	6	0.8	140	2	B97462	organic hydroperox
287	6	0.8	107	2	T17701	hypothetical prote	360	6	0.8	140	2	AG2680	hemoglobin alpha-I
288	6	0.8	108	2	G30560	Ig kappa chain v r	361	6	0.8	141	1	HAL2C	kinesin heavy chai
289	6	0.8	109	2	C30515	Ig heavy chain v r	362	6	0.8	143	2	C44259	hypothetical prote
290	6	0.8	109	2	D91085	hypothetical prote	363	6	0.8	143	2	A69115	hypothetical prote
291	6	0.8	109	2	F89330	hypothetical prote	364	6	0.8	143	2	E30338	DNA transport mach
292	6	0.8	109	2	D65061	hypothetical prote	365	6	0.8	143	2	B69267	transposase IS240-
293	6	0.8	109	2	AH3240	conserved hypothet	366	6	0.8	143	2	S58429	conserved hypothet
294	6	0.8	110	2	S51383	probable membrane	367	6	0.8	143	2	AG2682	hypothetical prote
295	6	0.8	111	2	G85974	probable proteinas	368	6	0.8	143	2	E97464	probable SdhD subu
296	6	0.8	111	2	G91129	suppressor protein	369	6	0.8	144	2	D70843	hypothetical prote
297	6	0.8	112	2	S51121	genome polyprotein	370	6	0.8	145	2	C72668	hypothetical prote
298	6	0.8	113	2	PQ0274	polyprotein - hepa	371	6	0.8	145	2	T36527	hypothetical prote
299	6	0.8	113	2	PQ0273	polyprotein - hepa	372	6	0.8	145	2	AD1447	major tail shaft p
300	6	0.8	113	2	A55205	xis 5'-region hypo	373	6	0.8	145	2	F69214	heat shock protein
301	6	0.8	113	2	I51025	transcription fact	374	6	0.8	145	2	F90185	conserved hypothet
302	6	0.8	114	2	E97976	conserved hypothet	375	6	0.8	145	2	S26443	hypothetical prote
303	6	0.8	115	2	T29883	hypothetical prote	376	6	0.8	146	2	T51473	calmodulin-like pr
304	6	0.8	117	2	H71431	hypothetical prote	377	6	0.8	146	2	T22474	hypothetical prote
305	6	0.8	117	2	T13096	probable minor cap	378	6	0.8	146	2	H64126	hypothetical prote
306	6	0.8	117	2	S75884	hypothetical prote	379	6	0.8	146	2	B82167	conserved hypothet
307	6	0.8	119	2	A64249	ribosomal protein	380	6	0.8	146	2	AE2935	conserved hypothet
308	6	0.8	119	2	B84407	hypothetical prote	381	6	0.8	146	2	B98347	hypothetical prote
309	6	0.8	120	2	S22049	reverse transcript	382	6	0.8	147	2	PH0127	Ig heavy chain pre
310	6	0.8	120	2	AH2668	conserved hypothet	383	6	0.8	147	2	PH0131	Ig heavy chain pre
311	6	0.8	120	2	AH1813	hypothetical prote	384	6	0.8	147	2	PH0123	Ig heavy chain pre
312	6	0.8	121	2	H70471	conserved hypothet	385	6	0.8	147	2	PH0125	Ig heavy chain pre
313	6	0.8	122	2	F97779	hypothetical prote	386	6	0.8	147	2	PH0124	Ig heavy chain pre
314	6	0.8	123	2	G71189	hypothetical prote	387	6	0.8	147	2	PH0130	Ig heavy chain pre
315	6	0.8	124	2	F82205	chemotaxis protein	388	6	0.8	147	2	A29910	myosin calcium-bin
316	6	0.8	124	2	G75172	hypothetical prote	389	6	0.8	147	2	T28131	hypothetical prote
317	6	0.8	124	2	AD3428	transposase BME14	390	6	0.8	150	2	A97536	hypothetical prote
318	6	0.8	124	2	S05005	homeotic protein H	391	6	0.8	150	2	T15428	hypothetical prote
319	6	0.8	125	2	C82831	ribosomal-binding	392	6	0.8	151	2	A75297	hypothetical prote
320	6	0.8	125	2	T16848	hypothetical prote	393	6	0.8	152	2	S29752	ubiquitin-activati
321	6	0.8	125	2	AC3195	hypothetical prote	394	6	0.8	153	1	JT0572	profilin - tetrahy

395	1	WRBP15	early protein gp17	468	6	0.8	178	2	E98050	hypothetical prote
396	153	G69847	conserved hypotet	469	6	0.8	179	2	A53522	peptidylprolyl iso
397	153	S63367	ribosomal protein	470	6	0.8	179	2	B69695	ribosomal protein
398	153	AH2203	bacterioferritin c	471	6	0.8	179	2	T48416	hypothetical prote
399	153	G70077	hypothetical prote	472	6	0.8	179	2	AD2427	hypothetical prote
400	153	S34255	hypothetical prote	473	6	0.8	181	2	E83436	probable oxidase p
401	153	C86324	protein Fl4D16.23	474	6	0.8	182	2	A02947	keratin, 60K type
402	154	T70681	hypothetical prote	475	6	0.8	182	2	A91031	probable fimbrial-
403	154	T34825	hypothetical prote	476	6	0.8	182	2	AH1579	hypothetical prote
404	155	T15379	hypothetical prote	477	6	0.8	182	2	G90235	hypothetical prote
405	156	F84356	hypothetical prote	478	6	0.8	183	2	S26961	H+-transporting tw
406	156	AG0243	probable exported	479	6	0.8	183	2	T37965	probable 40S ribos
407	157	F82390	methylated-DNA-lpr	480	6	0.8	183	2	A40360	hypothetical prote
408	159	T27686	hypothetical prote	481	6	0.8	183	2	C85786	hypothetical prote
409	160	T11949	hypothetical prote	482	6	0.8	183	2	G90937	hypothetical prote
410	161	JC7151	vacuolar H+-ATPase	483	6	0.8	183	2	B90092	hypothetical prote
411	161	F71860	biotin carboxyl ca	484	6	0.8	184	2	A05045	hypothetical prote
412	161	G71407	transcription fact	485	6	0.8	184	2	T33006	hypothetical prote
413	161	S50931	hypothetical prote	486	6	0.8	184	2	B71897	hypothetical prote
414	162	1 RFMWA	phycocyanin	487	6	0.8	185	2	G75379	conserved hypotet
415	162	H70314	hypothetical prote	488	6	0.8	185	2	AI3454	hypothetical prote
416	164	D69783	hypothetical regu	489	6	0.8	185	2	G71113	probable pyruvate
417	164	F71803	NADH dehydrogenase	490	6	0.8	186	2	T19073	hypothetical prote
418	164	D97283	ribosomal protein	491	6	0.8	186	2	AF3094	conserved hypotet
419	165	T27618	hypothetical prote	492	6	0.8	186	2	F90646	probable fimbrial
420	165	AG2428	hypothetical prote	493	6	0.8	186	2	F85497	probable drpp-4-de
421	166	S78003	cuticle structural	494	6	0.8	187	2	H95598	hypothetical prote
422	166	G90661	probable peptide c	495	6	0.8	187	2	D99192	hypothetical 21K p
423	166	E85512	translation releas	496	6	0.8	188	2	JU0451	myc protein - huma
424	166	E64748	ubiquinol-cytochro	497	6	0.8	188	2	I59116	myc protein - huma
425	167	C71803	fast skeletal trop	498	6	0.8	188	2	I79500	hypothetical prote
426	167	JW0065	early light-induce	499	6	0.8	188	2	C97438	conserved hypotet
427	167	S07473	probable gluconoki	500	6	0.8	188	2	AF2656	conserved IAA6 prot
428	167	AC0481	hypothetical prote	501	6	0.8	189	2	E96569	auxin-induced prot
429	167	D55224	NADH dehydrogenase	502	6	0.8	189	2	S58493	hypothetical prote
430	167	G90175	serine proteinase	503	6	0.8	189	2	S70104	acetylactate synth
431	168	S41973	phosphotransferase	504	6	0.8	190	2	AD3329	ribosomal protein
432	169	1 WQECF3	hypothetical prote	505	6	0.8	191	1	JH0585	adenylate kinase -
433	169	H69136	pTS system, glucos	506	6	0.8	191	2	B64597	recombination prot
434	169	D85894	glucose-specific p	507	6	0.8	191	2	C90518	probable phage-rel
435	169	A98040	molybdopterin co-f	508	6	0.8	191	2	H64887	probable phage-rel
436	169	T44852	type I interleukin	509	6	0.8	191	2	E64909	hypothetical prote
437	169	S151903	outer membrane pro	510	6	0.8	191	2	E74679	hypothetical prote
438	169	C70207	VPS29-like phospho	511	6	0.8	191	2	S74679	outer surface prot
439	170	C75184	hypothetical prote	512	6	0.8	191	2	I40153	hypothetical prote
440	170	S53648	hypothetical prote	513	6	0.8	191	2	E84375	hypothetical prote
441	170	F87482	hypothetical prote	514	6	0.8	191	2	A64704	hypothetical prote
442	171	1 JBA041	chorion class B pr	515	6	0.8	191	2	A71814	outer surface prot
443	171	G70883	probable lppu prot	516	6	0.8	192	2	S70267	hypothetical prote
444	171	E87459	cytochrome c famil	517	6	0.8	192	2	T05159	hypothetical prote
445	172	E81897	probable host-nucl	518	6	0.8	193	2	E85693	probable tail fibe
446	172	S07474	early light-induce	519	6	0.8	193	2	C90835	tail fiber assembl
447	172	E83696	hypothetical prote	520	6	0.8	193	2	D81009	conserved hypotet
448	173	B85875	probable minor fim	521	6	0.8	193	2	E82031	probable integral
449	173	A70914	hypothetical prote	522	6	0.8	193	2	S70276	outer surface prot
450	173	D90177	1S0 ribosomal prot	523	6	0.8	193	2	S70287	outer surface prot
451	174	T75176	hypothetical prote	524	6	0.8	194	1	R5PM24	ribosomal protein
452	174	T03056	hypothetical prote	525	6	0.8	194	2	T16556	hypothetical prote
453	174	T27552	hypothetical prote	526	6	0.8	194	2	S70277	dof zinc finger pr
454	174	D86239	protein T10024.23	527	6	0.8	194	2	T52044	hypothetical prote
455	175	C39141	transcription repr	528	6	0.8	194	2	T20322	hypothetical prote
456	175	A82297	conserved hypotet	529	6	0.8	195	2	AE1823	hypothetical prote
457	175	JC7274	DNA binding protei	530	6	0.8	195	2	G83170	hypothetical prote
458	176	AD1174	conserved hypotet	531	6	0.8	196	2	B86653	hypothetical prote
459	176	AE1531	conserved hypotet	532	6	0.8	196	2	C64891	ferripyochelin-bin
460	177	F83114	50S ribosomal prot	533	6	0.8	196	2	AH2441	hypothetical prote
461	178	G91182	probable fimbrial	534	6	0.8	196	2	G97964	conserved hypotet
462	178	C86029	probable major fim	535	6	0.8	196	2	AB3601	ctdtp-glucose 4-6-d
463	178	T01890	hypothetical prote	536	6	0.8	197	2	JC2339	neutrophil gelatin
464	178	T40104	outer surface prot	537	6	0.8	198	2	S72709	Lept1170 C3 229 pr
465	178	T40125	outer surface prot	538	6	0.8	198	2	A25706	sorcin - Chinese h
466	178	B95183	non-heme iron-cont	539	6	0.8	198	2	S52094	hypothetical prote
467	178	A47071	hypothetical prote	540	6	0.8	199	2	C96570	hypothetical prote

541	6	0.8	200	2	B96912	adenvylsulfate ki	614	221	2	A72097	probable ABC trans
542	6	0.8	200	2	S07397	lipocalin - mouse	615	221	2	G8525	probable ABC trans
543	6	0.8	200	2	S10946	transcription init	616	221	2	T15999	hypothetical prote
544	6	0.8	200	2	S10945	transcription init	617	222	2	F72572	probable TATA-box
545	6	0.8	200	2	AB1085	hypothetical prote	618	222	2	H82794	hypothetical prote
546	6	0.8	201	2	T38262	hypothetical prote	619	222	2	G87380	hypothetical prote
547	6	0.8	201	2	T49121	receptor like prot	620	222	2	S62001	MAIS protein - Yea
548	6	0.8	201	2	G85253	receptor like prot	621	223	2	A84436	probable glutathio
549	6	0.8	202	2	T35545	probable two-compo	622	223	2	T36952	conserved hypothet
550	6	0.8	202	2	T46515	probable two-compo	623	223	2	S73367	hypothetical prote
551	6	0.8	202	2	G90034	hypothetical prote	624	223	2	B89567	protein TOR9A.9 [i
552	6	0.8	202	2	T47319	hypothetical prote	625	224	2	S31845	chlorophyll a/b-bi
553	6	0.8	203	2	G86795	acetyltransferase	626	224	2	AG1196	ribose 5-phosphate
554	6	0.8	203	2	C97766	holliday junction	627	225	1	SYECDB	dethiobiotin synth
555	6	0.8	203	2	B72566	hypothetical prote	628	225	2	A99206	hypothetical prote
556	6	0.8	203	2	AD0223	probable glycosida	629	225	2	AH3080	RhtB family transp
557	6	0.8	203	2	S35563	sex-determining pr	630	226	2	G87518	lipote-protein li
558	6	0.8	204	2	S27526	5-bromo-4-chloroin	631	226	2	S23280	homeotic protein m
559	6	0.8	204	2	AI0542	probable peptide c	632	227	1	ADMSC	fructose-bisphosph
560	6	0.8	205	2	D90455	hypothetical prote	633	227	2	A38452	2-haloacid dehalog
561	6	0.8	206	2	AI0700	probable two-compo	634	227	2	T49711	hypothetical prote
562	6	0.8	206	2	AC2443	orotate phosphorib	635	227	2	E82408	ABC transporter, A
563	6	0.8	206	2	C82139	conserved hypothet	636	228	2	T37026	probable lipoprote
564	6	0.8	207	2	G71053	hypothetical prote	637	228	2	C90276	conserved hypothet
565	6	0.8	207	2	T1053	glutathione transf	638	230	2	T34822	ABC-transporter AT
566	6	0.8	208	1	A22045	interleukin-6 - sh	639	230	2	C64396	precorrin-2 methyl
567	6	0.8	208	2	C64657	2-dehydro-3-deoxy-	640	230	2	E71224	probable HESA prot
568	6	0.8	208	2	T71859	2-dehydro-3-deoxy-	641	231	2	AG2277	hypothetical prote
569	6	0.8	209	1	XUFF11	glutathione transf	642	231	2	AE2297	hypothetical prote
570	6	0.8	209	2	I40142	outer surface prot	643	232	2	S75699	cAMP receptor prot
571	6	0.8	209	2	D86882	hypothetical prote	644	232	2	H72807	gp65 protein - Myc
572	6	0.8	210	1	JN0277	DNA-directed DNA p	645	233	2	S15960	hypothetical prote
573	6	0.8	210	2	F71308	probable 2-dehydro	646	233	2	T28914	hypothetical prote
574	6	0.8	210	2	JC4381	imidazoleglycerol-	647	234	2	T06995	probable MADS box
575	6	0.8	210	2	T06864	transcription regu	648	234	2	H81669	conserved hypothet
576	6	0.8	210	2	H75599	probable acetyltra	649	234	2	T20933	hypothetical prote
577	6	0.8	210	2	T26154	hypothetical prote	650	235	2	E69814	conserved hypothet
578	6	0.8	210	2	I58391	sarcoma amplified	651	235	2	S25058	lg kappa chain - m
579	6	0.8	211	1	E71262	VPS29-like phospho	652	235	2	T36923	hypothetical prote
580	6	0.8	211	2	H64216	ribosomal protein	653	236	2	S16164	coat protein - pot
581	6	0.8	211	2	B89830	hypothetical prote	654	236	2	S35766	coat protein - pot
582	6	0.8	211	2	T49930	hypothetical prote	655	236	2	S41326	coat protein - pot
583	6	0.8	212	2	T44591	hypothetical prote	656	236	2	JQ2298	coat protein - pot
584	6	0.8	213	2	E71511	hypothetical prote	657	237	2	C84065	transcription regu
585	6	0.8	213	2	B72548	hypothetical prote	658	237	2	S47351	p30 B9.10 protein
586	6	0.8	213	2	A95863	hypothetical prote	659	238	2	A97336	Na+ ABC transporte
587	6	0.8	214	2	AB2195	serine esterase [i	660	238	2	AI0077	conserved hypothet
588	6	0.8	214	2	T51657	myb-related transc	661	239	2	A75293	amino acid ABC tra
589	6	0.8	214	2	A97540	hypothetical prote	662	239	2	T51534	hypothetical prote
590	6	0.8	214	2	AC2759	cytochrome b561 At	663	240	2	S75021	3-ketoacyl-acyl ca
591	6	0.8	215	2	A71541	hypothetical prote	664	240	2	H90778	DNA-binding protei
592	6	0.8	216	2	D75567	GTP cyclohydrolase	665	241	2	T00751	probable protein k
593	6	0.8	216	2	AI2635	two component resp	666	242	2	H69885	3-oxoacyl-acyl-ca
594	6	0.8	216	2	D86564	yage family [impor	667	242	2	C85640	hypothetical prote
595	6	0.8	216	2	G72060	yage family - Chla	668	242	2	G87696	hypothetical prote
596	6	0.8	216	2	C84900	hypothetical prote	669	242	2	A43904	homeotic protein G
597	6	0.8	216	2	S58100	ribosomal protein	670	243	1	B86746	probable phosphoe
598	6	0.8	216	2	F71378	hypothetical prote	671	243	2	B71512	hypothetical prote
599	6	0.8	217	1	KIBSAF	adenylate kinase (672	243	2	A43596	hypothetical prote
600	6	0.8	217	2	T16518	hypothetical prote	673	243	2	A69225	mip protein - Legi
601	6	0.8	218	2	T01076	transcription fact	674	243	2	JC7596	hypothetical prote
602	6	0.8	218	2	F84170	hypothetical prote	675	244	1	RDECPA	phosphoadenylyl-su
603	6	0.8	219	2	B82727	2-keto-3-deoxy-6-p	676	244	2	B64003	hypothetical prote
604	6	0.8	219	2	S52646	GTP-binding protei	677	244	2	B69381	conserved hypothet
605	6	0.8	219	2	T09720	conserved hypothet	678	245	2	AB2286	NADH dehydrogenase
606	6	0.8	219	2	T33190	hypothetical prote	679	245	2	B86738	hypothetical prote
607	6	0.8	220	2	T51827	MADS-box protein [680	246	2	AC3024	transcription regu
608	6	0.8	220	2	T05580	probable transcrip	681	246	2	T00704	hypothetical prote
609	6	0.8	220	2	D85991	potential acrif/en	682	246	2	S74961	hypothetical prote
610	6	0.8	220	2	B65119	probable transcrip	683	247	2	G83382	conserved hypothet
611	6	0.8	220	2	H91145	probable transcrip	684	247	2	D69453	hypothetical prote
612	6	0.8	220	2	T15275	hypothetical prote	685	247	2	G64788	ybcx protein, phag
613	6	0.8	220	2	T12474	hypothetical prote	686	248	2	F69449	tryptophan synthas

687	6	0.8	248	2	164230	sensory rhodopsin	760	6	0.8	266	2	T25230	hypothetical prote
688	6	0.8	249	1	A30113	NADH2 dehydrogenas	761	6	0.8	267	2	T22185	hypothetical prote
689	6	0.8	249	1	B30113	NADH2 dehydrogenas	762	6	0.8	267	2	H86320	probable MYB47 tra
690	6	0.8	249	2	AF1405	creatinine amidohy	763	6	0.8	267	2	E64175	hypothetical prote
691	6	0.8	249	2	AF1781	creatinine amidohy	764	6	0.8	267	2	E83232	probable ATP-bindi
692	6	0.8	250	2	H95161	conserved hypotet	765	6	0.8	267	2	S74998	hypothetical prote
693	6	0.8	250	2	G98037	conserved hypotet	766	6	0.8	267	2	E75471	transcription regu
694	6	0.8	250	2	G72650	hypothetical prote	767	6	0.8	267	2	A46122	homeotic protein H
695	6	0.8	250	2	D75119	hypothetical prote	768	6	0.8	267	2	A49068	cranosynotosis-as
696	6	0.8	251	2	I57668	luteinizing hormon	769	6	0.8	268	1	A49473	glutamate racemase
697	6	0.8	251	2	H65007	VacJ lipoprotein p	770	6	0.8	268	2	S31010	gene 65 protein -
698	6	0.8	251	2	E91032	lipoprotein precu	771	6	0.8	268	2	T46980	hypothetical prote
699	6	0.8	251	2	F85876	lipoprotein precu	772	6	0.8	268	2	AE0241	conserved hypotet
700	6	0.8	251	2	F70412	dihydrooorotate deh	773	6	0.8	268	2	S18814	homeotic protein H
701	6	0.8	252	2	C95183	triosephosphate is	774	6	0.8	269	2	T16115	hypothetical prote
702	6	0.8	252	2	A28449	tropomyosin, cytos	775	6	0.8	269	2	B84013	hypothetical prote
703	6	0.8	252	2	T10697	immature seed prot	776	6	0.8	269	2	T26504	hypothetical prote
704	6	0.8	253	2	H62919	pyrroline-5-carbox	777	6	0.8	270	1	CCECID	cell division inhi
705	6	0.8	253	2	JQ2255	triose-phosphate i	778	6	0.8	270	2	B84968	septum site-determ
706	6	0.8	253	2	S44053	structural protein	779	6	0.8	270	2	AH0724	septum site-determ
707	6	0.8	253	2	F69134	hypothetical prote	780	6	0.8	270	2	F85695	cell division inhi
708	6	0.8	253	2	G81311	probable ATP/Gnp-b	781	6	0.8	270	2	E90837	cell division inhi
709	6	0.8	253	2	AI3598	transposase BME10	782	6	0.8	270	2	AE0253	septum site-determ
710	6	0.8	254	2	B87396	DNA-binding respon	783	6	0.8	270	2	S71793	head-inducing fact
711	6	0.8	254	2	T08476	inclusion membrane	784	6	0.8	271	2	C81230	septum site-determ
712	6	0.8	254	2	E84382	hypothetical prote	785	6	0.8	271	2	JQ0950	ICP 18.5 protein -
713	6	0.8	254	2	C81208	ABC transporter, A	786	6	0.8	271	2	B60176	hypothetical prote
714	6	0.8	254	2	H81784	probable ABC trans	787	6	0.8	272	2	C75548	hypothetical prote
715	6	0.8	255	1	ISECT	triose-phosphate i	788	6	0.8	273	2	AH2709	transcription regu
716	6	0.8	255	2	A35255	chlorocatechol 1,2	789	6	0.8	273	2	S12637	transposase - Esch
717	6	0.8	255	2	AD0940	triosephosphate is	790	6	0.8	273	2	F69199	conserved hypotet
718	6	0.8	255	2	D91234	triosephosphate is	791	6	0.8	273	2	S23281	homeotic protein m
719	6	0.8	255	2	DB6081	triosephosphate is	792	6	0.8	274	2	A61030	nitrogenase (EC 1.
720	6	0.8	255	2	AE0011	triose-phosphate i	793	6	0.8	274	2	A43719	ured protein - pro
721	6	0.8	255	2	AI1374	conserved hypotet	794	6	0.8	275	1	S78606	probable transport
722	6	0.8	255	2	AG1744	conserved hypotet	795	6	0.8	275	2	S27805	porin - slime mold
723	6	0.8	255	2	C90431	conserved hypotet	796	6	0.8	275	2	S60662	signal peptidase 1
724	6	0.8	255	2	B87595	transcription regu	797	6	0.8	275	2	E83655	signal peptidase-1
725	6	0.8	256	2	C98969	trans-2-enoyl-ACP	798	6	0.8	275	2	S05299	hypothetical prote
726	6	0.8	256	2	A54322	corticotropin / li	799	6	0.8	276	1	S47640	adenylyl-sulfate k
727	6	0.8	256	2	H69348	hypothetical prote	800	6	0.8	276	2	T29125	ketoacyl reductase
728	6	0.8	256	2	E95936	hypothetical prote	801	6	0.8	276	2	T48842	halorhodopsin (aim
729	6	0.8	257	1	S22363	gufa protein homol	802	6	0.8	276	2	C82136	septum site-determ
730	6	0.8	257	2	H91119	gufa protein homol	803	6	0.8	276	2	T38825	hypothetical prote
731	6	0.8	257	2	G85964	gufa protein homol	804	6	0.8	276	2	E83922	hypothetical prote
732	6	0.8	258	1	C69175	heat shock protein	805	6	0.8	277	1	H71220	hypothetical prote
733	6	0.8	258	2	C84758	hypothetical prote	806	6	0.8	277	2	S32571	mald protein - Str
734	6	0.8	258	2	T27393	hypothetical prote	807	6	0.8	277	2	H87213	conserved hypotet
735	6	0.8	259	2	H86809	oxidoreductase ypa	808	6	0.8	277	2	S03240	hypothetical prote
736	6	0.8	259	2	G98050	triose-phosphate i	809	6	0.8	277	2	E72564	hypothetical prote
737	6	0.8	259	2	JS0660	homeotic protein H	810	6	0.8	277	2	G97783	hypothetical prote
738	6	0.8	259	2	A38284	homeotic protein Q	811	6	0.8	277	2	AD3386	phytoene synthase
739	6	0.8	260	2	S70589	cytochrome-c oxida	812	6	0.8	278	2	A84131	plant-metabolite d
740	6	0.8	260	2	AB2536	hypothetical prote	813	6	0.8	278	2	D64489	hypothetical prote
741	6	0.8	260	2	C95380	conserved hypotet	814	6	0.8	278	2	D75585	urease accessory p
742	6	0.8	261	2	S53423	major intrinsic pr	815	6	0.8	278	2	B70513	hypothetical prote
743	6	0.8	262	2	S72890	hypothetical prote	816	6	0.8	279	2	T09620	probable lectin 2
744	6	0.8	262	2	A70577	hypothetical prote	817	6	0.8	279	2	F84112	transcription regu
745	6	0.8	263	2	T12407	NADH2 dehydrogenas	818	6	0.8	279	2	AH1882	nitrate transport
746	6	0.8	263	2	G64085	triose-phosphate i	819	6	0.8	279	2	G70807	hypothetical prote
747	6	0.8	263	2	A55279	major intrinsic pr	820	6	0.8	279	2	C75538	hypothetical prote
748	6	0.8	263	2	S73314	hypothetical prote	821	6	0.8	279	2	AI1012	hypothetical prote
749	6	0.8	263	2	I54780	APK1 antigen - hum	822	6	0.8	279	2	A83148	conserved hypotet
750	6	0.8	264	2	B71362	probable exodeoxyr	823	6	0.8	280	2	T07741	nitrate reductase
751	6	0.8	264	2	T10155	hypothetical prote	824	6	0.8	280	2	H95246	maltodextrin ABC t
752	6	0.8	264	2	AI2667	conserved hypotet	825	6	0.8	280	2	A82185	glycerol-3-phospha
753	6	0.8	265	2	D83287	hypothetical prote	826	6	0.8	280	2	T24454	hypothetical prote
754	6	0.8	265	2	A75448	rRNA methylase - D	827	6	0.8	281	1	NMECUE	sn-Glycerol-3-phos
755	6	0.8	265	2	S62363	D-2-chloropropioni	828	6	0.8	281	1	B64227	hypothetical prote
756	6	0.8	265	2	H70858	probable electron	829	6	0.8	281	1	S73813	MG246 homolog H91
757	6	0.8	266	2	S51833	arcelin-4 precursor	830	6	0.8	281	2	AI1912	lysophospholipase-
758	6	0.8	266	2	C96913	sulfate adenylyate	831	6	0.8	281	2	A86012	hypothetical prote
759	6	0.8	266	2	P00393	genome polyprotein	832	6	0.8	281	2	A91166	hypothetical prote

833	6	0.8	281	2	C64241	hypothetical prote	906	0.8	296	2	F75209	hypothetical prote
834	6	0.8	281	2	T50208	yeast kt112 protei	907	0.8	297	2	G87187	phosphoribosylamin
835	6	0.8	281	2	T01445	hypothetical prote	908	0.8	297	2	G70708	probable purC prot
836	6	0.8	281	2	F89045	protein B0238.3 [l	909	0.8	297	2	A72130	hypothetical prote
837	6	0.8	281	2	AF3407	transporter, dme f	910	0.8	297	2	H87613	pilus assembly pro
838	6	0.8	282	2	T06637	hypothetical prote	911	0.8	297	2	G95384	probable LygA-fam
839	6	0.8	282	2	A75473	probable sigma fac	912	0.8	297	2	AF2980	conserved hypothet
840	6	0.8	282	2	F82851	conserved hypothet	913	0.8	297	2	H98302	hypothetical prote
841	6	0.8	282	2	D97442	hypothetical prote	914	0.8	297	2	A40560	homeobox protein H
842	6	0.8	283	1	I41318	fimbrial adhesin K	915	0.8	297	2	I54320	homeobox protein H
843	6	0.8	283	2	T12062	xpsK protein - xan	916	0.8	298	1	G69862	heat-shock protein
844	6	0.8	283	2	D83846	hypothetical prote	917	0.8	298	2	S12635	apolipoprotein E p
845	6	0.8	284	2	B46494	conserved hypothet	918	0.8	298	2	D87450	transcription regu
846	6	0.8	284	2	H83119	probable transcript	919	0.8	298	2	I40434	flagellar biosynth
847	6	0.8	284	2	A96604	hypothetical prote	920	0.8	298	2	T33220	hypothetical prote
848	6	0.8	284	2	T29001	hypothetical prote	921	0.8	298	2	T38937	rna binding protei
849	6	0.8	284	2	G71152	probable cobalt tr	922	0.8	298	2	T43542	rna-binding protei
850	6	0.8	285	2	A74742	flagellar motor sw	923	0.8	298	2	F84324	hypothetical prote
851	6	0.8	285	2	H71938	hydrolase [importe	924	0.8	299	2	PN0638	vgh protein - Stap
852	6	0.8	286	2	AF2829	thiosulfate sulfur	925	0.8	299	2	A99422	hypothetical prote
853	6	0.8	286	2	G59182	dihydrodipicolinat	926	0.8	299	2	E70737	hypothetical prote
854	6	0.8	286	2	H97341	probable aldehyde	927	0.8	299	2	AG2340	hypothetical prote
855	6	0.8	286	2	S72569	probable chromosom	928	0.8	299	2	S18813	homeotic protein H
856	6	0.8	287	1	A81969	hypothetical prote	929	0.8	300	2	AI3101	transcription regu
857	6	0.8	287	2	E98111	conserved hypothet	930	0.8	300	2	I40215	hypothetical prote
858	6	0.8	287	2	E82978	hypothetical prote	931	0.8	300	2	F75065	hypothetical prote
859	6	0.8	287	2	T24640	hypothetical prote	932	0.8	300	2	H75200	hypothetical prote
860	6	0.8	287	2	F64648	glycine betaine/l-	933	0.8	300	2	D71234	hypothetical prote
861	6	0.8	287	2	AE3578	pyruvate synthase	934	0.8	300	2	AF2846	permease [importe
862	6	0.8	288	2	E83946	7alpha-cephem-meth	935	0.8	300	2	F97623	hypothetical prote
863	6	0.8	288	2	C56281	sporulation protei	936	0.8	301	2	C69837	5-oxo-1,2,5-tricar
864	6	0.8	288	2	S18438	probable exported	937	0.8	301	2	S50377	probable membrane
865	6	0.8	288	2	AB0231	homeotic protein H	938	0.8	301	2	C96961	cell division prot
866	6	0.8	288	2	JS0659	probable glucosyl-1	939	0.8	302	1	WZBE9	gene 9 protein - h
867	6	0.8	289	1	S35294	deoxyuridine triph	940	0.8	302	2	T40490	probable 26S prote
868	6	0.8	289	1	S55649	homoserine kinase	941	0.8	302	2	F81016	conserved hypothet
869	6	0.8	289	2	A95158	homoserine kinase	942	0.8	302	2	F90158	DNA repair endo/ex
870	6	0.8	289	2	A98024	conserved hypothet	943	0.8	302	2	H87476	conserved hypothet
871	6	0.8	289	2	AB0282	Cr144 hypothetical	944	0.8	302	2	B82968	probable transcript
872	6	0.8	289	2	H86532	conserved hypothet	945	0.8	302	2	S75481	polysialic acid tr
873	6	0.8	289	2	B72099	probable outer mem	946	0.8	303	2	AC0092	probable chemotaxi
874	6	0.8	289	2	C71501	hypothetical prote	947	0.8	303	2	JC2410	ADP-ribosyl cyclas
875	6	0.8	289	2	B86794	ABC-type transport	948	0.8	303	2	F71680	hypothetical prote
876	6	0.8	289	2	S75197	phosphoribulokinas	949	0.8	303	2	H81818	conserved hypothet
877	6	0.8	290	1	KIRFAS	involved in lipopo	950	0.8	303	2	S75557	hypothetical prote
878	6	0.8	290	2	A86038	involved in lipopo	951	0.8	303	2	B47089	probable Arac-type
879	6	0.8	290	2	H91190	hypothetical prote	952	0.8	303	2	B96909	probable permease
880	6	0.8	290	2	S47839	short-chain dehydr	953	0.8	303	2	G71166	conserved hypothet
881	6	0.8	291	2	AH3074	probable short-cha	954	0.8	304	1	B69449	pyridoxine biosynt
882	6	0.8	291	2	A96212	conserved hypothet	955	0.8	304	2	T46647	ribonucleoside-dip
883	6	0.8	291	2	A81659	phosphoribulokinas	956	0.8	305	2	T03155	acyltransferase (E
884	6	0.8	292	1	E35819	probable membrane	957	0.8	305	2	JN0518	mrR restriction sy
885	6	0.8	292	2	D97199	4-hydroxybenzoate	958	0.8	305	2	AD2494	hypothetical prote
886	6	0.8	292	2	S23239	hypothetical prote	959	0.8	305	2	H75091	phosphoribosylamin
887	6	0.8	293	1	D69300	conserved hypothet	960	0.8	306	2	E64138	primosomal protein
888	6	0.8	293	2	A89818	rRNA methyltransfe	961	0.8	306	2	A89952	inosine-uridine pr
889	6	0.8	293	2	JH1095	conserved hypothet	962	0.8	306	2	AE3100	inosine-uridine pr
890	6	0.8	293	2	AN0651	hypothetical prote	963	0.8	306	2	E98186	transcriptional re
891	6	0.8	293	2	T75441	transcription regu	964	0.8	306	2	AF3230	probable ABC-type
892	6	0.8	293	2	T32229	probable membrane	965	0.8	306	2	T36764	cysteine synthase
893	6	0.8	293	2	A97313	tissue factor prec	966	0.8	307	2	H83660	primosome componen
894	6	0.8	293	2	AH0143	NADH2 dehydrogenas	967	0.8	307	2	AH1269	hypothetical prote
895	6	0.8	294	1	KRMS3	probable endonucle	968	0.8	307	2	AB1632	Na+/Ca2+ exchangin
896	6	0.8	294	2	T11379	Hs-transporting tw	969	0.8	307	2	S30432	conserved hypothet
897	6	0.8	294	2	T35492	hypothetical prote	970	0.8	307	2	G90270	hypothetical prote
898	6	0.8	294	2	B81427	conserved hypothet	971	0.8	307	2	G69211	ferrochelatase (EC
899	6	0.8	294	2	G97449	30S ribosomal prot	972	0.8	307	2	T24423	conserved hypothet
900	6	0.8	295	2	F69976	homeotic protein X	973	0.8	308	2	S70735	hypothetical prote
901	6	0.8	295	2	H97713	glucose-1-phosphat	974	0.8	308	2	D69348	tropinesterase (at
902	6	0.8	295	2	A60131	ribosomal protein	975	0.8	308	2	A99993	dihydrodipicolinat
903	6	0.8	296	2	D75597	hypothetical prote	976	0.8	309	2	D97607	probable epimerase
904	6	0.8	296	2	E71717	conserved hypothet	977	0.8	309	2	D64752	
905	6	0.8	296	2	S39746	30S ribosomal prot	978	0.8	309	2	C83136	

Db 201 GGIWTLTRSNQNEQKFAQDMKVDFYQNGGYDFPRILDTDIQTNEDKTKQTIKTVH 260
Qy 261 EGGFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOQMTAVLGBIQRNMGSAGYAYS 320
Db 261 EGGFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQOQMTAVLGBIQRNMGSAGYAYS 320
Qy 321 EISVQPLPNAETKTVDPLVHIEFGKRIYVNEIHTGNKTRDEVVRELQOMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDPLVHIEFGKRIYVNEIHTGNKTRDEVVRELQOMESAPYDTS 380
Qy 381 KLQSKKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDGLVM 440
Db 381 KLQSKKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDGLVM 440
Qy 441 SAGVSQNLFGTGSAAALRASRSKTTLLNGSLSTPDPYFTADGCVSLGVYDVYVKGAFDPRKAS 500
Db 441 SAGVSQNLFGTGSAAALRASRSKTTLLNGSLSTPDPYFTADGCVSLGVYDVYVKGAFDPRKAS 500
Qy 501 TS1KQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPHYADFIKKYKGTIDG 560
Db 501 TS1KQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNAKPHYADFIKKYKGTIDG 560
Qy 561 TDGSFQKWLKYGTVGWRNKTDTSALWPTRGYLTVGNAEIALPGSKLQYYSATHTQWTFPP 620
Db 561 TDGSFQKWLKYGTVGWRNKTDTSALWPTRGYLTVGNAEIALPGSKLQYYSATHTQWTFPP 620
Qy 621 LSKTFTMLGGEVGIAGGYQRTKEIPFENFYGGGLGVRGYSGLTGPVKPYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYQRTKEIPFENFYGGGLGVRGYSGLTGPVKPYDEYGEKIS 680
Qy 681 YGNGKANVAEALLFPMGAKDARTVRLSLFADAGSVWMDKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNGKANVAEALLFPMGAKDARTVRLSLFADAGSVWMDKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSAAGGAVTWLSPGLPMKF 772

RESULT 3
T46206
hypothetical protein T8P19.130 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 09-Jul-2004
R;Choi, N.; Robert, C.; Brottier, P.; Wincker, P.; Cattolico, L.; Artiguenave, F.; Sa
submitted to the Protein Sequence Database, December 1999
A;Reference number: Z23008
A;Accession: T46206
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-328 <CHO>
A;Cross-references: UNIPROT:Q9SMN7; EMBL:AL13315
A;Experimental source: cultivar Columbia; BAC clone T8P19
C;Genetics:
A;Map position: 3
A;Introns: 39/2; 62/3; 94/3; 133/2; 179/3; 277/1
A;Note: T8P19.130

Query Match 1.1%; Score 9; DB 2; Length 328;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 654 GGLGSVRGY 662
Db 152 GGLGSVRGY 160

RESULT 4
T49132
hypothetical protein F26G5.110 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Feb-2000 #text_change 09-Jul-2004

C;Accession: T49132
R;D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Rudd, S.; Le
submitted to the Protein Sequence Database, April 2000
A;Reference number: Z25017
A;Accession: T49132
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-435 <DAN>
A;Cross-references: UNIPROT:Q9LXP7; EMBL:AL1353814; GSPDB:GN00061; ATSP:F26G5.110
A;Experimental source: cultivar Columbia; BAC clone F26G5
C;Genetics:
A;Gene: ATSP:F26G5.110
A;Map position: 3
A;Introns: 12/1; 34/2; 135/3; 188/3; 212/2; 238/3; 277/2; 326/3; 350/1; 395/1

Query Match 1.1%; Score 9; DB 2; Length 435;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 654 GGLGSVRGY 662
Db 296 GGLGSVRGY 304

RESULT 5
A96984
hypothetical protein CAC0683 [imported] - Clostridium acetobutylicum
C;Species: Clostridium acetobutylicum
C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
C;Accession: A96984
R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A;Reference number: A96900; MUID:21359325; PMID:21359325
A;Accession: A96984
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-129 <KUR>
A;Cross-references: UNIPROT:Q97L79; GB:AE001437; PIDN:AAK78660.1; PID:gl5023560; GSPDB:G
A;Experimental source: Clostridium acetobutylicum ATCC824
C;Genetics:
A;Gene: CAC0683

Query Match 1.0%; Score 8; DB 2; Length 129;
Best Local Similarity 100.0%; Pred. No. 5.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 670 KYVDEYGE 677
Db 17 KYVDEYGE 24

RESULT 6
E84423
hypothetical protein At2g01340 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: E84423
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: E84423
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-225 <STO>
A;Cross-references: UNIPROT:Q9ZU33; GB:AE002093; NID:g4262241; PIDN:AAD14534.1; GSPDB:GN
C;Genetics:
A;Gene: At2g01340
A;Map position: 2

```

Query Match      1.0%; Score 8; DB 2; Length 225;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 280 PKAELEKL 287
    |||||
Db 144 PKAELEKL 151

RESULT 7
B75057
glycerate dehydrogenase PAB2374 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C:Accession: B75057
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: B75057
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <RAW>
A:Cross-references: UNIPROT:Q9UYR1; GB:AJ248287; GB:AL096836; NID:G5458657; PIDN:CAB5035
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: gdh-like; PAB2374
C:Superfamily: phosphoglycerate dehydrogenase

Query Match      1.0%; Score 8; DB 2; Length 335;
Best Local Similarity 100.0%; Pred. No. 14;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 LGYDVYVK 492
    |||||
Db 145 LGYDVYVK 152

RESULT 8
C82190
formate dehydrogenase accessory protein VC1519 [imported] - Vibrio cholerae (strain N169
C:Species: Vibrio cholerae
C>Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C:Accession: C82190
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A:Reference number: A82035; MUID:20406833; PMID:10952301
A:Accession: C82190
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <HEI>
A:Cross-references: UNIPROT:Q9KRW5; GB:A5004230; GB:A5003852; NID:G9656018; PIDN:AAP9467
A:Experimental source: serogroup O1; strain N16961; biotype El Tor
C:Genetics:
A:Gene: VC1519
A:Map position: 1
C:Superfamily: formate dehydrogenase accessory protein FdhD

Query Match      1.0%; Score 8; DB 2; Length 337;
Best Local Similarity 100.0%; Pred. No. 14;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 671 VYDEYGEK 678
    |||||
Db 81 VYDEYGEK 88

RESULT 9
A71175
probable dehydrogenase - Pyrococcus horikoshii
C:Species: Pyrococcus horikoshii
C>Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 12-Jul-2004
C:Accession: A71175
R:Kawarabayashi, Y.; Sawada, M.; Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekine
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi,
DNA Res. 5, 55-76, 1998
A:Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A:Reference number: A71000; MUID:98344137; PMID:9679194
A:Accession: A71175
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-376 <RAW>
A:Cross-references: UNIPROT:O58320; GB:AP000002; NID:G3236129; PIDN:BAA29686.1; PID:G325;
A:Experimental source: strain OT3
A:Note: this accession replaces an interim accession for a sequence replaced by GenBank
C:Genetics:
A:Gene: PH0597

Query Match      1.0%; Score 8; DB 2; Length 376;
Best Local Similarity 100.0%; Pred. No. 15;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 LGYDVYVK 492
    |||||
Db 186 LGYDVYVK 193

RESULT 10
T04985
probable transaminase (EC 2.6.1.-) T16L1.170 [similarity] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
C:Accession: T04985
R:Bevan, M.; Obermaier, B.; Deutschenbaur, S.; Piravandi, E.; Hoheisel, J.; Mewes, H.W.;
submitted to the Protein Sequence Database, November 1998
A:Reference number: Z15393
A:Accession: T04985
A:Molecule type: DNA
A:Residues: 1-426 <BEV>
A:Cross-references: UNIPROT:O81895; EMBL:AL031394
A:Experimental source: cultivar Columbia; BAC clone T16L1
C:Genetics:
A:Map position: 4
A:Introns: 19/1; 41/3; 80/3; 101/3; 136/3; 153/3; 260/3; 329/3
A:Note: T16L1.170
C:Superfamily: aspartate transaminase
C:Keywords: aminotransferase

Query Match      1.0%; Score 8; DB 2; Length 426;
Best Local Similarity 100.0%; Pred. No. 17;
Matches      8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 484 SLGYDVYK 491
    |||||
Db 351 SLGYDVYK 358

RESULT 11
G42365
flagellar hook-length control protein fliK - Bacillus subtilis
N:Alternate names: hypothetical protein 7 (flaA operon)
C:Species: Bacillus subtilis
C>Date: 24-Jul-1992 #sequence_revision 24-Jul-1992 #text_change 09-Jul-2004
C:Accession: G42365; G59624; S14500
R:Albertini, A.M.; Caramori, T.; Crabb, W.D.; Scoffone, F.; Galizzi, A.
J. Bacteriol. 173, 3573-3579, 1991
A:Title: The flaA locus of Bacillus subtilis is part of a large operon coding for flagell
A:Reference number: A42365; MUID:91258343; PMID:1828465
A:Accession: G42365
A:Molecule type: DNA
A:Residues: 1-429 <ALB>
A:Cross-references: UNIPROT:P23451; EMBL:X56049; NID:G39904; PIDN:CAA39526.1; PID:G39910

```

R;Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galle
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maues
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Roche, B.; Rose, B.; Sadale, Y.; Sato, T.; Scanlon,
A;Authors: Schleicher, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A;Reference number: A69580; MUID:98044033; PMID:9384377

A;Accession: G69624
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-429 <KUN>
A;Cross-references: GB:AL009126; NID:G26333902; PIDN:CAB13500.1; PID:ell85218;
A;Experimental source: strain 168
C;Genetics:
A;Gene: flik

Query Match 1.0%; Score 8; DB 2; Length 429;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 328 PNAETKTV 335
|||||
DB 286 PNAETKTV 293

RESULT 12

IMBP4
site-specific recombinase for integration and excision - *Bacillus* phage phi-105
N;Alternate names: immunity region protein 3, 4, 5, 6
C;Species: *Bacillus* phage phi-105

C;Date: 31-Dec-1998 #sequence_revision 22-Oct-1999 #text_change 09-Jul-2004

C;Accession: T13541; C24521; D24521; E24521; F24521

R; Kobayashi, K.; Okamura, K.; Inoue, T.; Sato, T.; Kobayashi, Y.

submitted to the EMBL Data Library, July 1998

A;Description: Complete nucleotide sequence of *Bacillus subtilis* phage phi-105.

A;Reference number: Z17688

A;Accession: T13541

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-474 <KOB>

A;Cross-references: UNIPROT:Q9T200; EMBL:AB016282; PIDN:BA036658.1

R;Cully, D.F.; Garro, A.J.

A;Title: Nucleotide sequence of the immunity region of *Bacillus subtilis* bacteriophage phi

Gene 38, 153-164, 1985

A;Reference number: A91535; MUID:96056972; PMID:3934047

A;Accession: C24521

A;Molecule type: DNA

A;Residues: 1-78, 'MTHC' <CUL>

A;Cross-references: GB:M11920; NID:G215477; PIDN:AAA88399.1; PID:g1196717

A;Accession: D24521

A;Molecule type: DNA

A;Residues: 149-160, 'AR', 163, 'H', 'HSDSQRRVR', 381-383, 'RIQRRARS', 392 <CU2>

A;Cross-references: GB:M11920; NID:G215477; PIDN:AAA88401.1; PID:g1196719

A;Accession: E24521

A;Molecule type: DNA

A;Residues: 189-318, 'HAP', <CU3>

A;Cross-references: GB:M11920

A;Accession: F24521

A;Molecule type: DNA

A;Residues: 'MP', 319-376, 'RNTK', 381, 'PGPWS', <CU4>

A;Cross-references: GB:M11920

C;Superfamily: phage phi-105 site-specific recombinase

C;Keywords: early protein

Query Match 1.0%; Score 8; DB 1; Length 474;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 168 IDEGKSAK 175
|||||
DB 53 IDEGKSAK 60

RESULT 13

G83375

probable glycosyl hydrolase PA2164 [imported] - *Pseudomonas aeruginosa* (strain PA01)

C;Species: *Pseudomonas aeruginosa*

C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004

C;Accession: G83375

R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Bri

adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,

Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of *Pseudomonas aeruginosa* PA01, an opportunistic patho

A;Reference number: A82950; MUID:20437337; PMID:10984043

A;Accession: G83375

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-583 <STO>

A;Cross-references: UNIPROT:Q9I1V1; GB:AE004643; GB:AE004091; NID:G9948178; PIDN:AA0555;

A;Experimental source: strain PA01

C;Genetics:

A;Gene: PA2164

C;Superfamily: glycosyltrehalose trehalohydrolase

Query Match 1.0%; Score 8; DB 2; Length 583;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 74 VRVETADG 81
|||||
DB 29 VRVETADG 36

RESULT 14

JE0327

dynamin-related protein MSP1 - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C;Accession: JE0327

R;Pellegrini, L.; Belenguer, P.; Menon, Y.; Ducommun, B.

Biochem Biophys Res Commun 251, 720-726, 1998

A;Title: Identification of a fission yeast dynamin-related protein involved in mitochondr

A;Reference number: JE0327; MUID:99008891; PMID:9790976

A;Accession: JE0327

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-903 <PEL>

A;Cross-references: UNIPROT:P87320; GB:Y07891; NID:G2231081; PIDN:CAA69196.1; PID:G223108

C;Genetics:

A;Gene: MSP1

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 SAALRASR 462
|||||
DB 417 SAALRASR 424

RESULT 15

T50334

dynamin-related protein [imported] - fission yeast (*Schizosaccharomyces pombe*)

C;Species: *Schizosaccharomyces pombe*

C;Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jul-2004

C;Accession: T50334

R;Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Brown, S.; Harris, D.
submitted to the EMBL Data Library, February 2000
A;Reference number: Z25062
A;Accession: T50334
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-903 <LYN>
A;Cross-references: UNIPROT:P87320; EMBL:AL157874; PIDN:CAB75996.1; GSPDB:GN00067; SPDB:
A;Experimental source: strain 972h(-); cosmid c1718
C;Genetics:
A;Gene: SPDB:SPBC1718.06
A;Map position: 2

Query Match 1.0%; Score 8; DB 2; Length 903;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 SAALRASR 462
Db 417 SAALRASR 424
|||||

Search completed: July 6, 2005, 15:44:23
Job time : 66 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 49.7902 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMWLGISPLAF.....RNRVDITIDECKSAKITD 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	797	2	O30912
2	879	99.3	797	2	O9KIH0
3	875	98.9	797	2	O9JX31
4	863	97.5	792	2	P95359
5	469	53.0	771	2	O7NVY6
6	390	44.1	758	2	O82U03
7	375	42.4	769	2	O63T20
8	374	42.3	769	2	O62JD2
9	371.5	42.0	778	2	O7VYC2
10	371.5	42.0	778	2	O7WA52
11	371.5	42.0	778	2	O7WJ86
12	356	40.2	818	2	O8PAW1
13	355.5	40.2	788	2	O8PWL3
14	354	40.0	785	2	O8XZ13
15	346	39.1	784	2	O9PB12
16	345	39.0	784	2	O87B11
17	313.5	35.4	804	2	O7MTG8
18	313.5	35.4	804	2	O8DBF3
19	305.5	34.5	803	2	O8ZPA3
20	304.5	34.5	804	2	O8ZRP0
21	304.5	34.4	795	2	O667J7
22	304.5	34.4	795	2	O8ZH58
23	299.5	33.8	808	2	O6Q8T1
24	298.5	33.7	804	2	O87ME5
25	297.5	33.6	797	2	O9S341
26	297.5	33.6	797	2	O7N8N9
27	295.5	33.4	797	2	O9HXY4
28	295.5	33.4	810	1	UP05 ECOLI
29	292.5	33.1	786	2	O8BMH2
30	292.5	33.1	803	2	O9KPW0
31	292.5	33.1	810	2	O8KR94

32 292.5 33.1 814 2 O6D8D5
33 291.5 32.9 805 2 O6LN32
34 289 32.7 795 2 O886N5
35 281 31.8 785 2 O9R2E3
36 281 31.8 787 2 O88H14
37 262 29.6 826 2 O8EGG7
38 255 28.8 825 2 O6FCG7
39 244 27.6 789 2 O51930
40 244 27.6 803 2 O83DT2
41 243 27.5 791 2 O9CJL1
42 242 27.3 790 2 O8GBX8
43 239 27.0 768 2 O9ZE03
44 236.5 26.7 792 2 O32625
45 236.5 26.7 793 1 D153_HAEIN

ALIGNMENTS

RESULT 1

O30912 ID O30912 PRELIMINARY; PRT; 797 AA.
AC O30912;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=HH;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Oma87.";
RL Microb. Pathog. 25;11-21(1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg_Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;

Query Match 100.0%; Score 885; DB 2; Length 797;

Best Local Similarity 100.0%; Pred. No. 3.7e-64;

Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDVTYNDTHGSA 60

Db 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDVTYNDTHGSA 60

OY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120

OY 121 SQYFNQATLNQAVAGLKEEYLRGKLNITPKVTKLARNVDITIDECKSAKITD 178

Db 121 SQYFNQATLNQAVAGLKEEYLRGKLNITPKVTKLARNVDITIDECKSAKITD 178

RESULT 2

O9KIH0 ID O9KIH0 PRELIMINARY; PRT; 797 AA.

AC O9KIH0;

DT 01-OCT-2000 (TrEMBLrel. 15, Created)

DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)

DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Outer membrane protein Omp85.

```

GN OrderedLocusNames=NWB0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tetelini H., Saunders N.J., Heideberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwin M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Hatt D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Cittone H., Clark E.B., Cotton M.D., Uterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain
RT MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AE002375; AAF40639.1; -.
DR PIR: G81228; G81228.
DR TIGR: NWB0182; -.
DR InterPro: IPR000184; Bac_surfAg_D15.
DR InterPro: IPR010827; Surf_Ag_VNR.
DR Pfam: PF01103; Bac_surface_Ag; 1.
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A43D22EB8 CRC64;

Query Match 99.3%; Score 879; DB 2; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-63;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178

RESULT 3
Q9JX31 PRELIMINARY; PRT; 797 AA.
AC Q9JX31;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein OMP85.
GN Name=OMP85;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Z2491 / Serogroup A / Serotype 4A;
RX MEDLINE=2022556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrell B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria
RT meningitidis Z2491."

```

```

RL Nature 404:502-506(2000).
DR EMBL: AL162752; CAB83401.1; -.
DR PIR: D82000; D82000.
DR InterPro: IPR000184; Bac_surfAg_D15.
DR InterPro: IPR010827; Surf_Ag_VNR.
DR Pfam: PF01103; Bac_surface_Ag; 1.
DR Pfam: PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DB47E0C9E1D1F CRC64;

Query Match 98.9%; Score 875; DB 2; Length 797;
Best Local Similarity 98.9%; Pred. No. 2.4e-63;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178

RESULT 4
P95359 PRELIMINARY; PRT; 792 AA.
AC P95359;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein.
GN Name=omp85;
OS Neisseria gonorrhoeae.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=485;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FA19;
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis
RT are similar to Haemophilus influenzae D-15-Ag and Pasteurella
RT multocida Omp87."
RL Microb. Pathog. 25:11-21(1998).
DR EMBL: U81959; AAC17600.1; -.
DR InterPro: IPR000184; Bac_surfAg_D15.
DR InterPro: IPR010827; Surf_Ag_VNR.
DR Pfam: PF01103; Bac_surface_Ag; 1.
DR Pfam: PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 792 AA; 87868 MW; 90E32D24AA0513D8 CRC64;

Query Match 97.5%; Score 863; DB 2; Length 792;
Best Local Similarity 98.3%; Pred. No. 2.3e-62;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDEGKSAKITD 178

```

```
RESULT 5
Q7NVY6 PRELIMINARY; PRT; 771 AA.
AC Q7NVY6;
DT 01-MAR-2004 (Tremblrel. 26, Created)
DT 01-MAR-2004 (Tremblrel. 26, Last sequence update)
DE Probable outer membrane protein.
GN OrderedLocusNames=CV2204;
OS Chromobacterium violaceum.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Chromobacterium.
OX NCBI_TaxID=536;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 12472 / DSM 30191;
RX MEDLINE=22882880; PubMed=14500782; DOI=10.1073/pnas.1832124100;
RA Vasconcelos A.T.R., de Almeida D.F., Hungria M., Guimaraes C.T.,
RA Antonio R.V., Almeida F.C., de Almeida L.G.P., de Almeida R.,
RA Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA Astolfi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA Batista J.S., Belo A.C., van den Berg C., Bogo M., Bonatto S.,
RA Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burity H.A.,
RA Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA Creczynski-Pasa T.B., Cunha-Junior N.C., Fagundes N., Falcao C.L.,
RA Fantinatti F., Farias I.P., Felipe M.S.S., Ferrari L.P., Ferro J.A.,
RA Ferro M.I.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA Grattapaglia D., Grissard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA Leoi L.C.T., Lima L.P.A., Loureiro M.P., Lyra M.C.C.P.,
RA Madeira H.M.F., Manfio G.P., Maranhao A.Q., Martins W.S.,
RA di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA Nascimento F.F., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA Pereira M., Pinto L.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA Santos E.B.P., Santos F.R., Schneider M.P.C., Seunanz H.N.,
RA Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA Souza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA Vettore A., Wassem R., Zaha A., Simpson A.J.G.;
RA "The complete genome sequence of Chromobacterium violaceum reveals
RT remarkable and exploitable bacterial adaptability."
RL Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR EMBL; AB016917; AAQ59877.1; -
DR InterPro; IPR000184; Bac surfag D15.
DR Pfam; PF01103; Surf Ag VNR.
DR Pfam; PF07244; Surf Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 771 AA; 85250 MW; 272FA6D8B5F03BE8 CRC64;

Query Match 53.0%; Score 469; DB 2; Length 771;
Best Local Similarity 54.4%; Pred. No. 5.3e-30;
Matches 98; Conservative 28; Mismatches 52; Indels 2; Gaps 1;

QY 1 MKLQIASALMMLGIGSLAFA--DFTIQDIRVEGLQRTPESTVFNLYPKVGDYNDTHG 58
DB 1 MKLRLVAAMGLTMTAVMAADPFVVKDIRVEGLQRTPESTVFNLYPKVGDYNDTHG 60
QY 59 SALKSLYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGL 118
DB 61 KEAIAKALFGTGFNDVRVESRGDTLTVTAERPVTQLNINGAKEPSKQALKKNDNGF 120
QY 119 AOSYFNQATLNOAVAGLKEEYLGKLNITQTPKTKLARNVDTITIDGSKSAKITD 178
DB 121 AESLIFDQALLDGAQVQLKRYYSRGSISVEITPTVTKLRNRAVTLIDINEGVTAIRE 180

RESULT 6
Q82U03 PRELIMINARY; PRT; 758 AA.
ID Q82U03
```

```
AC Q82U03;
DT 01-JUN-2003 (Tremblrel. 24, Created)
DT 01-JUN-2003 (Tremblrel. 24, Last sequence update)
DE Bacterial surface antigen (D15).
GN OrderedLocusNames=NE1710;
OS Nitrosomonas europaea.
OC Bacteria; Proteobacteria; Betaproteobacteria; Nitrosomonadales;
OC Nitrosomonadaceae; Nitrosomonas.
OX NCBI_TaxID=915;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 19718 / IPO 14298;
RX MEDLINE=22586410; PubMed=12700255;
DOI=10.1128/JB.185.9.2759-2773.2003;
RA Chain P., Lamerdin J.E., Larimer F.W., Regala W., Lao V., Land M.L.,
RA Hauser L., Hooper A.B., Klotz M.G., Norton J., Sayavedra-Soto L.A.,
RA Arciero D.M., Hommes N.G., Whittaker M.M., Arp D.J.;
RT "Complete genome sequence of the ammonia-oxidizing bacterium and
RT obligate chemolithoautotroph Nitrosomonas europaea."
RL J. Bacteriol. 185:2759-2773(2003).
DR EMBL; BX321862; CAD85621.1; -
DR InterPro; IPR000184; Bac surfag D15.
DR Pfam; PF01103; Bac surfag Ag; 1.
DR Pfam; PF07244; Surf Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 758 AA; 85016 MW; 6B9630B7124B06C9 CRC64;

Query Match 44.1%; Score 390; DB 2; Length 758;
Best Local Similarity 44.3%; Pred. No. 1.6e-23;
Matches 78; Conservative 37; Mismatches 61; Indels 0; Gaps 0;

QY 1 MKLQIASALMMLGIGSLAFA--DFTIQDIRVEGLQRTPESTVFNLYPKVGDYNDTHGSA 60
DB 1 MKLRLVLLPFLSLSLGLCMANDSLVVRDIRVEGLQRTPESTVFNLYPKVGDVLDKSKASA 60
QY 61 IKSILYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQ 120
DB 61 AIKALYATGFPDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKNLESFGLAQ 120
QY 121 SOYFNQATLNOAVAGLKEEYLGKLNITQTPKTKLARNVDTITIDGSKSAKI 176
DB 121 SIFRSRLLEKAEQELKRYYSRGSISVEITPTVTKLRNRAVTLIDINEGVTAIRE 176

RESULT 7
Q63T20 PRELIMINARY; PRT; 769 AA.
ID Q63T20
AC Q63T20;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DE Putative outer membrane protein.
GN ORFNames=BFSL2151;
OS Burkholderia pseudomallei K96243.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Burkholderia.
OX NCBI_TaxID=272560;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K96243;
RX PubMed=15377794;
RA Holden M.T.G., Titball R.W., Peacock S.J., Cerdeno-Tarraga A.M.,
RA Atkins T., Crossman L.C., Pitt T., Churcher C., Mungall K.,
RA Bentley S.D., Sebahia M., Thomson N.R., Bason N., Beacham I.R.,
RA Brooks K., Brown K.A., Brown N.F., Challis G.L., Cherevach I.,
RA Chillingworth T., Cronin A., Crosset B., Davis P., Deshazer D.,
RA Feltwell T., Fraser A., Hance Z., Hauser H., Holroyd S., Jagels K.,
RA Keith K.E., Maddison M., Moule S., Price C., Quail M.A.,
RA Rabinowitz E., Rutherford K., Sanders M., Simmonds M.,
RA Songvilai S., Stevens K., Tumapa S., Vesaratchave M.,
RA Whitehead S., Yeats C., Barrell B.G., Oyston P.C.F., Parkhill J.;
```


RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640427; CAE36837.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; Cphg synth L D2.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; SurfAg_VNR; 5.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 778 AA; 86342 MW; 15C8F0F43B865298 CRC64;
Query Match 42.0%; Score 371.5; DB 2; Length 778;
Best Local Similarity 41.8%; Pred. No. 5.5e-22;
Matches 72; Conservative 40; Mismatches 60; Indels 1; Gaps 1;
QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTNDTHGSAIKSL 65
DB 18 LAALLAPALAH-AFEFFVVRDIRVEGIQRTDAGTVFGLPVKVGKFTDEEATEAVRRL 76
QY 66 YATGFDDVRVETADGQLLTIVERTPTGSLNTGAKMLQNDIAKKNLESFGLAQSOYFN 125
DB 77 YGTGFSDVQIQTDNNVVVVQVQERTIASISFNGRPFDSKAITKSLAQVGGEGRIFD 136
QY 126 QATLQNAVAGLKEEYLGKGLNIQTPKVKTLARNRVDITITDEGSAKITD 178
DB 137 QSMLEAEYELKEQYLAAGKYGVEVTATVTPLRNRVGVSGFDVFEGEVAKIRE 189
RESULT 11
Q7WJ86 ID Q7WJ86 PRELIMINARY; PRT; 778 AA.
AC Q7WJ86;
DT 01-OCT-2003 (T-EMBLrel. 25, Created)
DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Probable surface antigen.
GN OrderedLocusNames=BB2613;
OC Bordetella bronchiseptica (Alcaligenes bronchisepticus).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=518;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271; DOI=10.1038/ng1227;
RA Parkhill J., Sebaihia M., Preston A., Murphy L.D., Thomson N.R.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.-M., Temple L., James K.D., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitz E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.,
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR ENBL; BX640444; CAE33106.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR005479; Cphg synth L p2.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; SurfAg_VNR; 5.
DR PROSITE; PS00867; CPSASE_2; UNKNOWN_1.

KW Complete proteome.
SQ SEQUENCE 778 AA; 86352 MW; BF0CA34EFP501CCF CRC64;
Query Match 42.0%; Score 371.5; DB 2; Length 778;
Best Local Similarity 41.6%; Pred. No. 5.5e-22;
Matches 72; Conservative 40; Mismatches 60; Indels 1; Gaps 1;
QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTNDTHGSAIKSL 65
DB 18 LAALLAPALAH-AFEFFVVRDIRVEGIQRTDAGTVFGLPVKVGKFTDEEATEAVRRL 76
QY 66 YATGFDDVRVETADGQLLTIVERTPTGSLNTGAKMLQNDIAKKNLESFGLAQSOYFN 125
DB 77 YGTGFSDVQIQTDNNVVVVQVQERTIASISFNGRPFDSKAITKSLAQVGGEGRIFD 136
QY 126 QATLQNAVAGLKEEYLGKGLNIQTPKVKTLARNRVDITITDEGSAKITD 178
DB 137 QSMLEAEYELKEQYLAAGKYGVEVTATVTPLRNRVGVSGFDVFEGEVAKIRE 189
RESULT 12
Q8PAW1 ID Q8PAW1 PRELIMINARY; PRT; 818 AA.
AC Q8PAW1;
DT 01-OCT-2002 (T-EMBLrel. 22, Created)
DT 01-OCT-2002 (T-EMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Outer membrane antigen.
GN Name=oma; OrderedLocusNames=XCC1365;
OS Xanthomonas campestris (pv. campestris).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=340;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 33913 / NCPPB 528;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Ciapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorri H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.C., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martine-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spinola L.A.F., Takica M.A., Tamura R.E., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi D., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR ENBL; AE012236; AAM40663.1; --
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; SurfAg_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 818 AA; 90685 MW; B4770C972C08FA26 CRC64;
Query Match 40.2%; Score 356; DB 2; Length 818;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 74; Conservative 33; Mismatches 64; Indels 0; Gaps 0;
QY 6 IASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGTNDTHGSAIKSL 65
DB 43 LAAGLSLPAALAAAEPPFVSDIRVDGLQRIASGTVFTYLPVNRGTVDGKVASIRAL 102
QY 66 YATGFDDVRVETADGQLLTIVERTPTGSLNTGAKMLQNDIAKKNLESFGLAQSOYFN 125

```
Db 103 YRTGFFEDVQDRQGNILVTVKERPAINKLVTGKNKDKISEBLLKGLGDIUTEGGTFD 162
QY 126 QATLNOAVAGLKEEYLGRGKLNQITPKVTKLARNRVDDITIDEGKSAKI 176
Db 163 RLSDLRVQELTQYNNRGKYNVEIPTVSPLDNRVDVAIAIKEGKAABI 213

RESULT 13
Q8PML3 PRELIMINARY; PRT; 788 AA.
AC Q8PML3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane antigen.
GN Names: OrderedLocusNames=XAC1413;
OS Xanthomonas axonopodis (pv. citri);
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xanthomonas.
OX NCBI_TaxID=92829;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=306 / ATCC 13902 / XV 101;
RX MEDLINE=22022145; PubMed=12024217; DOI=10.1038/417459a;
RA da Silva A.C.R., Ferro J.A., Reinach F.C., Farah C.S., Furlan L.R.,
RA Quaggio R.B., Monteiro-Vitorello C.B., Van Sluys M.A., Almeida N.F.,
RA Alves L.M.C., do Amaral A.M., Bertolini M.C., Camargo L.E.A.,
RA Camarotte G., Cannavan F., Cardozo J., Chambergo F., Clapina L.P.,
RA Cicarelli R.M.B., Coutinho L.L., Cursino-Santos J.R., El-Dorry H.,
RA Faria J.B., Ferreira A.J.S., Ferreira R.C.C., Ferro M.I.T.,
RA Formighieri E.F., Franco M.C., Greggio C.C., Gruber A.,
RA Katsuyama A.C., Kishi L.T., Leite R.P., Lemos E.G.M., Lemos M.V.F.,
RA Locali E.C., Machado M.A., Madeira A.M.B.N., Martinez-Rossi N.M.,
RA Martins E.C., Meidanis J., Menck C.F.M., Miyaki C.Y., Moon D.H.,
RA Moreira L.M., Novo M.T.M., Okura V.K., Oliveira M.C., Oliveira V.R.,
RA Pereira H.A., Rossi A., Sena J.A.D., Silva C., de Souza R.F.,
RA Spínola L.A.F., Takita M.A., Tamura R.B., Teixeira E.C., Tezza R.I.D.,
RA Trindade dos Santos M., Truffi J., Tsai S.M., White F.F.,
RA Setubal J.C., Kitajima J.P.;
RT "Comparison of the genomes of two Xanthomonas pathogens with differing
RT host specificities.";
RL Nature 417:459-463(2002).
DR EMBL; AE011773; NAM36284.1; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 788 AA; 87704 MW; C76CB1E017A4B224 CRC64;

Query Match 40.2%; Score 355.5; DB 2; Length 788;
Best Local Similarity 43.3%; Pred. No. 1.1e-20;
Matches 74; Conservative 35; Mismatches 61; Indels 1; Gaps 1;

QY 6 IASALMMLGISPLAFDFTIQDIRVEGLQRTPESTFVFNLPVKVGDYNDTHGSIAIKSL 65
Db 14 LAAGLSLPAVA-LAVEPFVASDIRVDGLQRIASGTFTYLPVNRGDTVDKADVAIRAL 72
QY 66 YATGFFDDVVEVETADGQLLTIVERTIGSLNTGAKMLNDIAIKNLSFGLAQSOYFN 125
Db 73 YRTGFFEDVQDRQGNILVTVKERPAINKLVTGKNKDKISEBLLKGLGDIUTEGGTFD 132
QY 126 QATLNOAVAGLKEEYLGRGKLNQITPKVTKLARNRVDDITIDEGKSAKI 176
Db 133 RLSDLRVQELTQYNNRGKYNVEIPTVSPLDNRVDVAIAIKEGKAABI 183

RESULT 14
Q8XZ13 PRELIMINARY; PRT; 765 AA.
AC Q8XZ13;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
```

```
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PUTATIVE OUTER MEMBRANE SIGNAL PEPTIDE PROTEIN.
GN Name=RS05280; OrderedLocusNames=RS01412;
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21681879; PubMed=11823852; DOI=10.1038/415497a;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.C., Catolico L.,
RA Chandler M., Choisne N., Claudel-Renard C., Cunnac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Signier P., Thebault P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
DR EMBL; AL646064; CAD15114.1; -.
DR Pfam; PF01103; Bac_surfAg; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
DR PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
KW Complete proteome.
SQ SEQUENCE 765 AA; 85878 MW; 378641FB9F247C68 CRC64;

Query Match 40.0%; Score 354; DB 2; Length 765;
Best Local Similarity 40.1%; Pred. No. 1.5e-20;
Matches 73; Conservative 34; Mismatches 67; Indels 8; Gaps 1;

QY 3 LKQIASALMMLGISPL-----APADFTIQDIRVEGLQRTPESTFVFNLPVKVGDYND 54
Db 2 IRQHRPPLSMLAASVLTVCAGQAHAVEPFVIKDIRVEGVQVPEPTVFGYLPVKVGETFT 61
QY 55 DTHGSIAIKSLYATGFFDDVVEVETADGQLLTIVERTIGSLNTGAKMLNDIAIKNLE 114
Db 62 DKGAESIRALYNTGFFKDVQIRAEGNVLVVRVEERPAISLEFIIKGFDKDRLRSUR 121
QY 115 SFLGAQSOYFNQATLNOAVAGLKEEYLGRGKLNQITPKVTKLARNRVDDITIDEGKSA 174
Db 122 GVGVAEARYDKSLIDRAEQELKRVSVSGYAADVQTTVPDANRVSVTFIVDSGPA 181
QY 175 KI 176
Db 182 KI 183

RESULT 15
Q9PEI2 PRELIMINARY; PRT; 784 AA.
AC Q9PEI2;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane antigen.
GN OrderedLocusNames=Xfi1046;
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Xanthomonadales;
OC Xanthomonadaceae; Xylella.
OX NCBI_TaxID=2371;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=9a5C;
RX MEDLINE=20365717; PubMed=10910347; DOI=10.1038/35018003;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvaranga R., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.,
RA Colauto N.B., Colombo C., Costa F.P., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
RA Pacincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
```

Search completed: July 6, 2005, 15:18:05
Job time : 52.7902 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 223.733 Seconds

(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 4152

Sequence: 1 MKLKQASALMMLGISPLAF.....LKKKPEIQRFQQLGTF 757

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_5/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4152	100.0	797	9	US-09-994-192-4
2	4152	100.0	797	17	US-10-606-618-4
3	4140	99.7	797	14	US-10-181-660-3
4	4140	99.7	797	15	US-10-320-800-6
5	4140	99.7	797	16	US-10-181-600-3
6	4136	99.6	797	14	US-10-181-660-11
7	4136	99.6	797	16	US-10-181-660-11
8	4049	97.5	776	14	US-10-181-660-5
9	4049	97.5	776	14	US-10-181-660-13
10	4049	97.5	776	16	US-10-181-600-5
11	4049	97.5	776	16	US-10-181-600-13

12	3956.5	95.3	792	14	US-10-181-660-7	Sequence 7, Appli
13	3956.5	95.3	792	16	US-10-181-660-7	Sequence 7, Appli
14	3937.5	94.8	792	9	US-09-994-192-2	Sequence 2, Appli
15	3937.5	94.8	792	16	US-10-467-534-92	Sequence 92, Appli
16	3937.5	94.8	792	17	US-10-606-618-2	Sequence 2, Appli
17	3859.5	93.0	771	14	US-10-181-660-9	Sequence 9, Appli
18	3859.5	93.0	771	16	US-10-181-660-9	Sequence 9, Appli
19	1109	26.7	813	16	US-10-896-725-2	Sequence 4, Appli
20	1109	26.7	813	16	US-10-896-725-4	Sequence 4, Appli
21	703	16.9	896	14	US-10-210-296-5	Sequence 5, Appli
22	703	16.9	896	15	US-10-449-462-5	Sequence 5, Appli
23	532	12.7	847	10	US-09-988-067B-8	Sequence 8, Appli
24	526	12.7	925	15	US-10-335-977-4919	Sequence 4919, Ap
25	454.5	10.9	795	15	US-10-289-762-314	Sequence 314, App
26	452.5	10.9	790	15	US-10-312-273-147	Sequence 147, App
27	433	10.4	792	16	US-10-467-534-25	Sequence 25, Appli
28	431	10.4	792	17	US-10-498-327-55	Sequence 55, Appli
29	400.5	9.6	614	15	US-10-335-977-4918	Sequence 4918, Ap
30	286	6.9	252	16	US-10-437-963-114029	Sequence 114029,
31	253	6.1	889	16	US-10-878-939-4	Sequence 4, Appli
32	253	6.1	919	16	US-10-878-939-2	Sequence 2, Appli
33	251	6.0	609	16	US-10-833-884-2	Sequence 2, Appli
34	251	6.0	609	16	US-10-833-884-4	Sequence 4, Appli
35	246	5.9	665	16	US-10-437-963-126949	Sequence 126949,
36	241.5	5.8	512	16	US-10-425-115-317331	Sequence 317331,
37	237	5.7	587	16	US-10-833-884-6	Sequence 6, Appli
38	209	5.0	602	14	US-10-010-160-16	Sequence 16, Appli
39	200	4.6	469	15	US-10-166-349-7	Sequence 7, Appli
40	190	4.6	469	15	US-10-678-986-1	Sequence 1, Appli
41	190	4.6	469	16	US-10-408-765A-2300	Sequence 2300, Ap
42	189	4.6	469	16	US-10-408-765A-1346	Sequence 1346, Ap
43	188.5	4.5	463	15	US-10-166-349-9	Sequence 9, Appli
44	186	4.5	469	15	US-10-166-349-8	Sequence 8, Appli
45	184.5	4.4	468	16	US-10-408-765A-1807	Sequence 1807, Ap

ALIGNMENTS

RESULT 1

US-09-994-192-4
; Sequence 4, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UMSBCL47AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 4152; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 2,1e-295;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MKLKQASALMMLGISPLAFDETIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA	60
Db	1	MKLKQASALMMLGISPLAFDETIQDIRVEGLQRTPESTVFNYPVKVGDTYNDTHGSA	60
QY	61	IIKSLVATGFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ	120
Db	61	IIKSLVATGFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDIAIKKNLESFGLAQ	120

```
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNLIQITPKVTKLARNRVDITIDTIDSGKSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNLIQITPKVTKLARNRVDITIDTIDSGKSAKITDIE 180
Qy 181 FEGNOVYSRDLKRMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGVDFPRIL 240
Db 181 FEGNOVYSRDLKRMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGVDFPRIL 240
Qy 241 DTDIQTNEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Qy 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Db 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Qy 361 RDEVVRELQMESAPYDTSKLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRELQMESAPYDTSKLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
Qy 481 DGVSGLDYVYVKAFDPRPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLDYVYVKAFDPRPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPHYADFIKKYKTKDGTGSGFKGWLKGTGVMGRNKTDSALWPTRCYLGTVNAEIA 600
Db 541 YNKAPHYADFIKKYKTKDGTGSGFKGWLKGTGVMGRNKTDSALWPTRCYLGTVNAEIA 600
Qy 601 LPSGKLQYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
Db 601 LPSGKLQYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQFQLGTTTF 797
Db 781 KPEDEIQRFQFQLGTTTF 797
RESULT 2
US-10-606-618-4
; Sequence 4, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBCL47AUSA
; CURRENT FILING DATE: 2003-06-26
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 2001-11-26
; PRIOR FILING DATE: 2001-11-26
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4
```

```
Query Match 100.0%; Score 4152; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.1e-295;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MKLKQJASALMLGIGISPLAFADFTIODIRVEGQRTPESTVFYVLPVKVGDYNDTHGSA 60
Db 1 MKLKQJASALMLGIGISPLAFADFTIODIRVEGQRTPESTVFYVLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDDVRVETADGQQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQQLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNLIQITPKVTKLARNRVDITIDTIDSGKSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNLIQITPKVTKLARNRVDITIDTIDSGKSAKITDIE 180
Qy 181 FEGNOVYSRDLKRMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGVDFPRIL 240
Db 181 FEGNOVYSRDLKRMQMSLTGEGGIWTLTRSNQFNEQKFAQDMKVTDFYQNGVDFPRIL 240
Qy 241 DTDIQTNEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Qy 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Db 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHIITGNKKT 360
Qy 361 RDEVVRELQMESAPYDTSKLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
Db 361 RDEVVRELQMESAPYDTSKLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSL 420
Qy 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFCTGKSAALRASRSKTTTLNGSLSFDPYFTA 480
Qy 481 DGVSGLDYVYVKAFDPRPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLDYVYVKAFDPRPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Qy 541 YNKAPHYADFIKKYKTKDGTGSGFKGWLKGTGVMGRNKTDSALWPTRCYLGTVNAEIA 600
Db 541 YNKAPHYADFIKKYKTKDGTGSGFKGWLKGTGVMGRNKTDSALWPTRCYLGTVNAEIA 600
Qy 601 LPSGKLQYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
Db 601 LPSGKLQYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVR 660
Qy 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Qy 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
Qy 781 KPEDEIQRFQFQLGTTTF 797
Db 781 KPEDEIQRFQFQLGTTTF 797
RESULT 3
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
```

; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

```
Query Match      99.7%; Score 4140; DB 14; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQVFNQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SQVFNQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180

Qy 181 FEGNQVYSDRKLNRQMSLTGEGITWLTTRSNORNEQFAQDMKVTDYQNGYFDFRIL 240
Db 181 FEGNQVYSDRKLNRQMSLTGEGITWLTTRSNORNEQFAQDMKVTDYQNGYFDFRIL 240

Qy 241 DTDIQTNEDKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300

Qy 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

Qy 361 RDEVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTPDKVLDNLSL 420
Db 361 RDEVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTPDKVLDNLSL 420

Qy 421 RSTGSLDLSAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFDPDYFTA 480
Db 421 RSTGSLDLSAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFDPDYFTA 480

Qy 481 DGVS LGDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVS LGDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Qy 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600

Qy 601 LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
Db 601 LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANVAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVAEALLFPMGAKADARTVRLSLFADAGSVWDG 720

Qy 721 KTYDDNSSATGRRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFFYAYPLKK 780
Db 721 KTYDDNSSATGRRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPGLPMKFFYAYPLKK 780

Qy 781 KPEDEIQRFOFQLGTTFF 797
Db 781 KPEDEIQRFOFQLGTTFF 797
```

RESULT 4

US-10-320-800-6

; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

```
Query Match      99.7%; Score 4140; DB 15; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQVFNQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180
Db 121 SQVFNQATLNOAVAGLKEEYLGKLNITQTPKVTKLARNRVDITIDEGKSAKITDIE 180

Qy 181 FEGNQVYSDRKLNRQMSLTGEGITWLTTRSNORNEQFAQDMKVTDYQNGYFDFRIL 240
Db 181 FEGNQVYSDRKLNRQMSLTGEGITWLTTRSNORNEQFAQDMKVTDYQNGYFDFRIL 240

Qy 241 DTDIQTNEDKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300

Qy 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

Qy 361 RDEVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTPDKVLDNLSL 420
Db 361 RDEVVRRELROMESAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTPDKVLDNLSL 420

Qy 421 RSTGSLDLSAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFDPDYFTA 480
Db 421 RSTGSLDLSAGVQDGTGLVMSAGVSQDNLFQTKGSAALRASRSKTTLLNGSLSFDPDYFTA 480

Qy 481 DGVS LGDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVS LGDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Qy 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPKHYADFIKKYKGTGDTGSGFKGWLKYGTVGWRNKTTDSALWPTRGYLTGVNAEIA 600

Qy 601 LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660
Db 601 LPGSKLQYYSATHNQTFWFFPLSKTFTMLGGEVGIAGGYGRKTEIPEFFENFYGGGLGSVR 660

Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANVAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVAEALLFPMGAKADARTVRLSLFADAGSVWDG 720
```

QY 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPKFRYAYPLKK 780
QY 781 KPEDEIQRFOFQLGTTTF 797
Db 781 KPEDEIQRFOFQLGTTTF 797
RESULT 5
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3
Query Match 99.7%; Score 4140; DB 16; Length 797;
Best Local Similarity 99.7%; Pred. No. 1.6e-294;
Matches 795; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYVNDTHGSA 60
Db 1 MKLQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYVNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDIDEGSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDIDEGSAKITDIE 180
QY 181 FEGNOVYSDRKLAROMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
Db 181 FEGNOVYSDRKLAROMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEWVRELQMSAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEWVRELQMSAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
QY 421 RSTGSLDLSAGVQDITGLVMSAGVSDNLFCTGKSAALRASRSKTTLINGSLSFTDPVETA 480
Db 421 RSTGSLDLSAGVQDITGLVMSAGVSDNLFCTGKSAALRASRSKTTLINGSLSFTDPVETA 480
QY 481 DGVSGLGVYVYKAPDRPKASTSIKQYKTTTAGACIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGVYVYKAPDRPKASTSIKQYKTTTAGACIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPHYADFIKKYKTKDGTGDSFGKWLKYGTVGGRNKTDSALWPTRCYLTGVNAEIA 600

Db 541 YNKAPHYADFIKKYKTKDGTGDSFGKWLKYGTVGGRNKTDSALWPTRCYLTGVNAEIA 600
QY 601 LPGSKLQYYSATHNQWFFPLSKTFTMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR 660
Db 601 LPGSKLQYYSATHNQWFFPLSKTFTMLGGEVGIAGGYGRTKEIPEFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELLFPMPGAADARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAAELLFPMPGAADARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVONIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPKFRYAYPLKK 780
QY 781 KPEDEIQRFOFQLGTTTF 797
Db 781 KPEDEIQRFOFQLGTTTF 797
RESULT 6
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11
Query Match 99.6%; Score 4136; DB 14; Length 797;
Best Local Similarity 99.6%; Pred. No. 3.1e-294;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MKLQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYVNDTHGSA 60
Db 1 MKLQIASALMWLGISPLAFADFTIODIRVEGLQRTPESTVFVNYLPVKVGDYVNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDIDEGSAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDIDEGSAKITDIE 180
QY 181 FEGNOVYSDRKLAROMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
Db 181 FEGNOVYSDRKLAROMSLTEGGIWTWLTNRNQFNEQKFAQDMKVTDIFYQNNGYDFPRIL 240
QY 241 DTDIQTNEDEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
Db 241 DTDIQTNEDEKTKQTIKITVHEGGRFRGWKVSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMGSAAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
QY 361 RDEWVRELQMSAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420
Db 361 RDEWVRELQMSAPYDTSKLORSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNSLTE 420


```
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
QY 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHADFIKKYKTKDGTGDSFGKWLKGTGNGRNKTDLSALWPTRGVLTGVNAEIA 600
DB 541 YNKAPKHADFIKKYKTKDGTGDSFGKWLKGTGNGRNKTDLSALWPTRGVLTGVNAEIA 600
QY 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
DB 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQGLGTTTF 797
DB 781 KPEDEIQRFQFQGLGTTTF 797

RESULT 7
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; TYPE: PRT
; LENGTH: 797
; ORGANISM: Neisseria meningitidis
; US-10-181-600-11

Query Match 99.6%; Score 4136; DB 16; Length 797;
Best Local Similarity 99.6%; Pred. No. 3.1e-294;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSA 60
DB 1 MKLQIASALMVLGISPLAFADFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120
DB 61 IIKSLYATGFFDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQ 120
QY 121 SQYFNQATLQNAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDTIDSGSAKITDIE 180
DB 121 SQYFNQATLQNAVAGLKEEYLGKLNQITPKVTKLARNRVDITIDTIDSGSAKITDIE 180
QY 181 PEGNOVYSDRKLQMSLITGGIITWLTNRQNFNEQKFAQOMKQVDFYQNGYFDFRIL 240
DB 181 PEGNOVYSDRKLQMSLITGGIITWLTNRQNFNEQKFAQOMKQVDFYQNGYFDFRIL 240
QY 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
DB 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
```

```
DB 241 DTDIQTNEDEKTKQTIKITVHEGGRFRWKVYSIEGDTNEVPKAELEKLLTMKPGKWYERQ 300
QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVPVLHIEPGRKIYVNEIHIITGNKT 360
DB 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVPVLHIEPGRKIYVNEIHIITGNKT 360
QY 361 RDEVVRRELQMSAPYDTSKLORSKERVELLGVFDNVQPDVAVPLAGTDPKVDLNMSLTE 420
DB 361 RDEVVRRELQMSAPYDTSKLORSKERVELLGVFDNVQPDVAVPLAGTDPKVDLNMSLTE 420
QY 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
DB 421 RSTGSLDLSAGWQDTGLVMSAGVSQDNLFGTGSAAALRASRSKTTTLNGSLSFDPYFTA 480
QY 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSLGVDVYKAFDPKPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHADFIKKYKTKDGTGDSFGKWLKGTGNGRNKTDLSALWPTRGVLTGVNAEIA 600
DB 541 YNKAPKHADFIKKYKTKDGTGDSFGKWLKGTGNGRNKTDLSALWPTRGVLTGVNAEIA 600
QY 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
DB 601 LPGSKLQYYSATHNQTFPPLSKTFTLMLGGEVGIAGYGRTKETKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDG 720
DB 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSALLFPMPGAKDARTVRLSLFADAGSVMDG 720
QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFQFQGLGTTTF 797
DB 781 KPEDEIQRFQFQGLGTTTF 797

RESULT 8
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; TYPE: PRT
; LENGTH: 776
; ORGANISM: Neisseria meningitidis
; US-10-181-660-5

Query Match 97.5%; Score 4049; DB 14; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSAIKSLYATGFFDVRVETADG 81
DB 1 DFTIQDIRVEGLQRTPESTVFNFYLPVKVGDYNDTHGSAIKSLYATGFFDVRVETADG 60
QY 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQSQYFNQATLQNAVAGLKEEYL 141
DB 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFLAQSQYFNQATLQNAVAGLKEEYL 120
```

```
Qy 142 GRGKLNQITPKVTKLARNRVDIDITIDEKSAKITDIEFEGNQVSDRKLQMQLTEG 201
|
|
|
Db 121 GRGKLNQITPKVTKLARNRVDIDITIDEKSAKITDIEFEGNQVSDRKLQMQLTEG 180
|
|
|
Qy 202 GIWTLTRSNQNEQFAQDMKVTDFYQNGYDFRILDTDIQTNEDEKTKQIKITVHE 261
|
|
|
Db 181 GIWTLTRSNQNEQFAQDMKVTDFYQNGYDFRILDTDIQTNEDEKTKQIKITVHE 240
|
|
|
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSAGYAYSE 321
|
|
|
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSAGYAYSE 300
|
|
|
Qy 322 ISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 381
|
|
|
Db 301 ISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 360
|
|
|
Qy 382 LQSKERVVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLVMS 441
|
|
|
Db 361 LQSKERVVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLVMS 420
|
|
|
Qy 442 AGVSQDNLFQTKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKPKAST 501
|
|
|
Db 421 AGVSQDNLFQTKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKPKAST 480
|
|
|
Qy 502 SIQKYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT 561
|
|
|
Db 481 SIQKYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT 540
|
|
|
Qy 562 DGSFKGWLKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYSATHNQTFWFFPL 621
|
|
|
Db 541 DGSFKGWLKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYSATHNQTFWFFPL 600
|
|
|
Qy 622 SKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKISY 681
|
|
|
Db 601 SKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKISY 660
|
|
|
Qy 682 GGNKANVSAEILLFPMPEGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
|
|
|
Db 661 GGNKANVSAEILLFPMPEGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
|
|
|
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIORFQFOLGTTTF 797
|
|
|
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKFSYAYPLKXKPEDEIORFQFOLGTTTF 776
|
|
|
RESULT 9
US-10-181-660-13
; Sequence 13, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-10-181-660-13
Query Match 97.5%; Score 4049; DB 14; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFNLYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETADG 81
|
|
|
```

```
Db 1 DFTIQDIRVEGLQRTPESTVFNLYPVKVGDTYNDTHGSAIIKSLYATGFFDDVRVETADG 60
|
|
|
Qy 82 QLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLQAQVAGLKEEYL 141
|
|
|
Db 61 QLLLTVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLQAQVAGLKEEYL 120
|
|
|
Qy 142 GRGKLNQITPKVTKLARNRVDIDITIDEKSAKITDIEFEGNQVSDRKLQMQLTEG 201
|
|
|
Db 121 GRGKLNQITPKVTKLARNRVDIDITIDEKSAKITDIEFEGNQVSDRKLQMQLTEG 180
|
|
|
Qy 202 GIWTLTRSNQNEQFAQDMKVTDFYQNGYDFRILDTDIQTNEDEKTKQIKITVHE 261
|
|
|
Db 181 GIWTLTRSNQNEQFAQDMKVTDFYQNGYDFRILDTDIQTNEDEKTKQIKITVHE 240
|
|
|
Qy 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSAGYAYSE 321
|
|
|
Db 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMSAGYAYSE 300
|
|
|
Qy 322 ISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 381
|
|
|
Db 301 ISVQPLPNAETKTVDVFLHIIEPGRKIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 360
|
|
|
Qy 382 LQSKERVVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLVMS 441
|
|
|
Db 361 LQSKERVVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVQDTGLVMS 420
|
|
|
Qy 442 AGVSQDNLFQTKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKPKAST 501
|
|
|
Db 421 AGVSQDNLFQTKSAALRASRSKTTLNGSLSFDPYFTADGVSIGYDVYKAFDPKPKAST 480
|
|
|
Qy 502 SIQKYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT 561
|
|
|
Db 481 SIQKYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTKDGT 540
|
|
|
Qy 562 DGSFKGWLKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYSATHNQTFWFFPL 621
|
|
|
Db 541 DGSFKGWLKGTGWRGNKTDLSALWPTRGYLTGVNAEIALPGSKLOYSATHNQTFWFFPL 600
|
|
|
Qy 622 SKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKISY 681
|
|
|
Db 601 SKTFTLMLGGEVGIAGGYGRTKEIIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKISY 660
|
|
|
Qy 682 GGNKANVSAEILLFPMPEGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 741
|
|
|
Db 661 GGNKANVSAEILLFPMPEGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYGA 720
|
|
|
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIORFQFOLGTTTF 797
|
|
|
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKFSYAYPLKXKPEDEIORFQFOLGTTTF 776
|
|
|
RESULT 10
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRN
; ORGANISM: Neisseria meningitidis
US-10-181-600-5
```

Query Match 97.5%; Score 4049; DB 16; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFPDDVRVETADG 81
DB 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFPDDVRVETADG 60

QY 82 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 141
DB 61 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 120

QY 142 GRGKLNIIQITPKVTYKLNARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLMEQMSLTEG 201
DB 121 GRGKLNIIQITPKVTYKLNARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLMEQMSLTEG 180

QY 202 GIWTLTRSNQNFQKPAQDMKVTDYQNNGYDFRILDTDIQTNEDEKTKQIKITVHE 261
DB 181 GIWTLTRSNQNFQKPAQDMKVTDYQNNGYDFRILDTDIQTNEDEKTKQIKITVHE 240

QY 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGEIQNRMGSGAGYAYSE 321
DB 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGEIQNRMGSGAGYAYSE 300

QY 322 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 381
DB 301 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 360

QY 382 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGWQDTGLVMS 441
DB 361 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGWQDTGLVMS 420

QY 442 AGVSQDNLFCTGKSAALRASRSKTTNLGSLSFDPYFTADGVSIGLYDVYKAFDPKRAST 501
DB 421 AGVSQDNLFCTGKSAALRASRSKTTNLGSLSFDPYFTADGVSIGLYDVYKAFDPKRAST 480

QY 502 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 561
DB 481 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 540

QY 562 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 621
DB 541 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 600

QY 622 SKTFTLMLGGEVGIAGGYGRTKEIIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 681
DB 601 SKTFTLMLGGEVGIAGGYGRTKEIIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 660

QY 682 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 741
DB 661 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 720

QY 742 GNTHKSTFTNELRYLSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIQRFOFQLGTTTF 797
DB 721 GNTHKSTFTNELRYLSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIQRFOFQLGTTTF 776

RESULT 11

US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02

RESULT 12

US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31

; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-13

Query Match 97.5%; Score 4049; DB 16; Length 776;
Best Local Similarity 99.9%; Pred. No. 7.2e-288;
Matches 775; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFPDDVRVETADG 81
DB 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFPDDVRVETADG 60

QY 82 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 141
DB 61 QLLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEYL 120

QY 142 GRGKLNIIQITPKVTYKLNARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLMEQMSLTEG 201
DB 121 GRGKLNIIQITPKVTYKLNARNVDIITIDEGKSAKITDIEFEGNOVYSDRKLMEQMSLTEG 180

QY 202 GIWTLTRSNQNFQKPAQDMKVTDYQNNGYDFRILDTDIQTNEDEKTKQIKITVHE 261
DB 181 GIWTLTRSNQNFQKPAQDMKVTDYQNNGYDFRILDTDIQTNEDEKTKQIKITVHE 240

QY 262 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGEIQNRMGSGAGYAYSE 321
DB 241 GGRFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOQMTAVLGEIQNRMGSGAGYAYSE 300

QY 322 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 381
DB 301 ISVQPLPNAETKTVDVFLHI EPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSK 360

QY 382 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGWQDTGLVMS 441
DB 361 LQSSKERVLLGYFDNVQFPAVPLAGTDPKVDLNMSLTERSTGSLDL SAGWQDTGLVMS 420

QY 442 AGVSQDNLFCTGKSAALRASRSKTTNLGSLSFDPYFTADGVSIGLYDVYKAFDPKRAST 501
DB 421 AGVSQDNLFCTGKSAALRASRSKTTNLGSLSFDPYFTADGVSIGLYDVYKAFDPKRAST 480

QY 502 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 561
DB 481 SIQOYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHVADFIKYGKTDGT 540

QY 562 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 621
DB 541 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTFWFFPL 600

QY 622 SKTFTLMLGGEVGIAGGYGRTKEIIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 681
DB 601 SKTFTLMLGGEVGIAGGYGRTKEIIPFENFYGGGLSGVRGYESGTLGPKVYDEYGEKISY 660

QY 682 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 741
DB 661 GGNKANVSALLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGA 720

QY 742 GNTHKSTFTNELRYLSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIQRFOFQLGTTTF 797
DB 721 GNTHKSTFTNELRYLSAGGAVTWLSPGLPMKFRYAYPLKXKPEDEIQRFOFQLGTTTF 776

```

; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7

Query Match          95.3%; Score 3956.5; DB 14; Length 792;
Best Local Similarity 95.4%; Pred. No. 4.5e-281;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

Qy 1 M K L K Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Db 1 M K L K Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Qy 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T T G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Db 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T T G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Qy 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Qy 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S N O F N E Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Db 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S D R F D R Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Qy 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Db 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Qy 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A G T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Qy 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Db 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Qy 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Qy 481 D G V S L G Y D V Y G K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
Db 481 D G V S L G Y D I Y G K A F D P R K A S T S V K Q Y K T T T A G G V R M G I P V T E Y D R V N F G L A A E H L T V N T 540
Qy 541 Y N K A P K H Y A D F I K Y G K T D G T D G S F K G M L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
Db 541 Y N K A P K Y A D F I R K Y K T D G A D G S F K G L Y K G T V G W G R N K T D S A S W P T R G Y L T G V N A E I A 600
Qy 601 L P G S K L Q Y Y S A T H N Q T W F F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Db 601 L P G S K L Q Y Y S A T H N Q T W F F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R 660
Qy 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Qy 721 K T Y D N S S S A T G R V Q N I Y C A G N T H K S T F T N E L R Y S A G G A V T W L S P L G P M K F Y A Y P L K K 780
Db 721 R T Y - - - - T A E N G N N K S V Y - S E N A H K S T F T N E L R Y S A G G A V T W L S P L G P M K F S I A Y P L K K 775
Qy 781 K P E D E I Q R F Q L G T T F 797
Db 776 K P E D E I Q R F Q L G T T F 792
```

```

RESULT 13
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match          95.3%; Score 3956.5; DB 16; Length 792;
Best Local Similarity 95.4%; Pred. No. 4.5e-281;
Matches 760; Conservative 16; Mismatches 16; Indels 5; Gaps 2;

Qy 1 M K L K Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Db 1 M K L K Q I A S A L M M L G I S P L A F A D T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y N D T H G S A 60
Qy 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T T G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Db 61 I I K S L Y A T G F D D V R V E T A D G Q L L L T V I E R P T T G S L N I T G A K M L Q N D A I K K N L E S F G L A Q 120
Qy 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Db 121 S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T D E G S A K I T D I E 180
Qy 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S N O F N E Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Db 181 F E G N Q V Y S D R K L M R Q M S L T E G G I T W L T R S D R F D R Q K F A D M E K V T D F Y Q N N G Y F D F R I L 240
Qy 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Db 241 D T D I Q T N E D K T R Q T I K I T V H E G G R F R W G K V S I E G D T N E V P K A E L K L L T M K P G K W Y E R Q Q 300
Qy 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Db 301 M T A V L G E I Q N R M G S A G Y A Y S E I S V Q P L P N A G T K T V D F V L H I E P G R K I Y N E I H I T G N N K T 360
Qy 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Db 361 R D E V V R R E L R Q M S A P Y D T S K L Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T E 420
Qy 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Db 421 R S T G S L D L S A G W Q D T G L V M S A G V S Q D N L F G T G K S A A L R A S R S K T T L N G S L S F T D P Y F T A 480
Qy 481 D G V S L G Y D V Y G K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P T E Y D R V N F G L V A E H L T V N T 540
Db 481 D G V S L G Y D I Y G K A F D P R K A S T S V K Q Y K T T T A G G V R M G I P V T E Y D R V N F G L A A E H L T V N T 540
Qy 541 Y N K A P K H Y A D F I K Y G K T D G T D G S F K G M L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E I A 600
Db 541 Y N K A P K Y A D F I R K Y K T D G A D G S F K G L Y K G T V G W G R N K T D S A S W P T R G Y L T G V N A E I A 600
Qy 601 L P G S K L Q Y Y S A T H N Q T W F F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G G L G S V R 660
Db 601 L P G S K L Q Y Y S A T H N Q T W F F P L S K T F T L M L G G E V G I A G G Y G R T K E I P F F E N F Y G G L G S V R 660
Qy 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
Db 661 G Y E S G T L G P K V Y D E Y G E K I S Y G N K K A N V S A E L L F P M P G A K A R T V R L S L F A D A G S V W D G 720
```


Qy	361	RDEVVRELQMESAPYDTSKLORSKERVLLGYFDNVQFDVPLACTPKVDLNMSLTE	420
Db	361		
Qy	421	RSTGSLDLSAGWQDTCGLVMSAGVSQDNLFGTGKSAALRASRSKTTLNGSLSTDPYFTA	480
Db	421		
Qy	481	DGVSGLGYDVYTKAFDPRKASTSIKQYKTTTATAGIRMSVPVTEYDRVNFGLVAEHLTVNT	540
Db	481		
Qy	541	YNKAPKHYADFIKKYKTDGDSFKGWLKGTVGWGRNKTDLSALWPTRGYLTGVNAEIA	600
Db	541		
Qy	601	LPGSKLOYYSATHNOTWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFPENFYGGGLGSVR	660
Db	601		
Qy	661	GYESGTLGPKVYDEYGEKISYGGNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDG	720
Db	661		
Qy	721	KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK	780
Db	721		
Qy	781	KPEDEIORFQFOLGTTTF	797
Db	776	KPEDEIORFQFOLGTTTF	792

Search completed: July 6, 2005, 15:42:19
Job time : 227.733 secs

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 51.7532 seconds
(without alignments)
1481.738 Million cell updates/sec

Title: US-10-606-618-4
Perfect score: 4152
Sequence: 1 MKLKQIASALMMLGISPLAF.....LKKKPEDEIQRFQGLGTTTF 797

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: Pirl:*
2: Pirl:*
3: Pirl:*
4: Pirl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	4140	99.7	797	2 G81228	outer membrane pro
2	4136	99.6	797	2 D82000	outer membrane pro
3	1279.5	30.8	797	2 H83190	probable outer mem
4	1241	29.9	784	2 H82731	outer membrane ant
5	1212	29.2	803	2 AB0530	outer membrane pro
6	1197	28.8	795	2 AC0129	probable surface a
7	1178.5	28.4	810	2 A64742	hypothetical prote
8	1178.5	28.4	810	2 C90651	hypothetical prote
9	1178.5	28.4	810	2 C85502	hypothetical prote
10	1168	28.1	803	2 B82099	surface antigen VC
11	1136	27.4	797	2 JC4078	protective surface
12	1135	27.3	808	2 F64102	protective surface
13	906	21.8	774	2 D97527	empl protein precu
14	906	21.8	774	2 AE2746	group 1 outer memb
15	877.5	21.1	769	2 F87486	outer membrane pro
16	850.5	20.5	781	2 AH3355	outer membrane pro
17	785	18.9	768	2 D71266	outer membrane pro
18	766	18.4	768	2 B97725	outer membrane pro
19	649	15.6	778	2 C70412	outer membrane pro
20	639.5	15.4	739	2 A81430	outer membrane pro
21	582.5	14.0	617	2 H84957	hypothetical prote
22	533	12.8	916	2 G64601	protective surface
23	526	12.7	906	2 F71910	probable outer mem
24	452.5	10.9	790	2 D86528	omp85 analog (limp
25	452.5	10.9	790	2 D72094	omp85 analog - Chl
26	446	10.7	792	2 H81693	outer membrane pro
27	433	10.4	792	2 B71539	probable omp85 ana
28	393.5	9.5	853	2 A71339	probable outer mem
29	364.5	8.8	821	2 B70199	outer membrane pro

30	348	8.4	846	2 F75525	outer membrane pro
31	307	7.4	833	2 AF2089	hypothetical prote
32	306.5	7.4	579	2 F83327	conserved hypotet
33	299.5	7.2	861	2 S77409	hypothetical prote
34	283.5	6.8	617	2 AF2897	conserved hypotet
35	283.5	6.8	641	2 H97672	hypothetical prote
36	272.5	6.6	853	2 D70304	hypothetical prote
37	254.5	6.1	578	2 B64012	hypothetical prote
38	239	5.8	615	2 A82025	probable outer mem
39	237	5.7	635	2 G81003	conserved hypotet
40	232	5.6	676	2 AE2417	hypothetical prote
41	220	5.3	623	2 A13488	outer membrane pro
42	218	5.3	628	2 B87448	conserved hypotet
43	212.5	5.1	577	2 F86119	hypothetical prote
44	211.5	5.1	577	2 F91278	hypothetical prote
45	211.5	5.1	577	2 S56445	hypothetical 64.8K

ALIGNMENTS

RESULT 1

G81228
outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 ser C;Species: Neisseria meningitidis
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C;Accession: G81228
R;Tetcelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A;Reference number: AB1000; MUID:20175755; PMID:10710307
A;Accession: G81228
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <RET>
A;Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; MID:g7225394; PIDN:AAF4063;
A;Experimental source: serogroup B, strain MC58
C;Genetics:
A;Gene: NMB0182
C;Superfamily: protective surface antigen D-15

Query Match	99.7%	Score	4140;	DB	2;	Length	797;
Best Local Similarity	99.7%	Pred. No.	1.6e-240;				
Matches	795;	Conservative	0;	Mismatches	2;	Indels	0;
						Gaps	0;
QY	1	1	1	1	1	1	1
Db	1	1	1	1	1	1	1
QY	61	1	1	1	1	1	1
Db	61	1	1	1	1	1	1
QY	121	1	1	1	1	1	1
Db	121	1	1	1	1	1	1
QY	181	1	1	1	1	1	1
Db	181	1	1	1	1	1	1
QY	241	1	1	1	1	1	1
Db	241	1	1	1	1	1	1
QY	301	1	1	1	1	1	1
Db	301	1	1	1	1	1	1
QY	361	1	1	1	1	1	1
Db	361	1	1	1	1	1	1


```
Db 361 RDEVREBELQMESAPYDTSKLQSKRVERVELLGYFDNVQFDVPLAGTDPDKVDLNLMSLTE 420
QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTDLSALWPTRGYLGVAEHLTVNT 600
Db 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTDLSALWPTRGYLGVAEHLTVNT 600
QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIORFQFQGLGTTTF 797
Db 781 KPEDEIORFQFQGLGTTTF 797

RESULT 2
D82000
outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491)
C;Species: Neisseria meningitidis
C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C;Accession: D82000
R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morel
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A;Reference number: A81775; MUID:20222556; PMID:10761919
A;Accession: D82000
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Cross-references: UNIPROT:Q9JX31; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8340
A;Experimental source: serogroup A, strain Z2491
C;Genetics:
A;Gene: omp85; NMA0085
C;Superfamily: protective surface antigen D-15

Query Match 99.6%; Score 4136; DB 2; Length 797;
Best Local Similarity 99.6%; Pred. No. 2.8e-240;
Matches 794; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MKLQJASALMWLGISPLAFADFTIQDIRVEGQRTPESTFVNYLPVKVGDYNDTHGSA 60
Db 1 MKLQJASALMWLGISPLAFADFTIQDIRVEGQRTPESTFVNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYVLRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180
Db 121 SQYFNQATLNQAVAGLKEEYVLRGKUNIQITPKVTKLARNRVIDITIDEGKSAKITDIE 180

QY 181 FEGNOVYSRDKLRQMSLTEGGIWTLTRSQNEQKFAQDMKVTDFYQNNGYDFPRIL 240
Db 181 FEGNOVYSRDKLRQMSLTEGGIWTLTRSQNEQKFAQDMKVTDFYQNNGYDFPRIL 240
```

```
QY 241 DTDIQTNEDKTKQTIKITVHEGGRFRAGKVSIEGDTNEVPKAELEKLLTMKPGKYERQQ 300
Db 241 DTDIQTNEDKTKQTIKITVHEGGRFRAGKVSIEGDTNEVPKAELEKLLTMKPGKYERQQ 300

QY 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
Db 301 MTAVLGEIQNRMSAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360

QY 361 RDEVREBELQMESAPYDTSKLQSKRVERVELLGYFDNVQFDVPLAGTDPDKVDLNLMSLTE 420
Db 361 RDEVREBELQMESAPYDTSKLQSKRVERVELLGYFDNVQFDVPLAGTDPDKVDLNLMSLTE 420
QY 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
Db 421 RSTGSLDLGAGWQDTGLVMSAGVSQDNLFQGTGSAALRASRSKTTLLNGSLSFDPYFTA 480
QY 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGYDVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTDLSALWPTRGYLGVAEHLTVNT 600
Db 541 YNKAPKHYADFIKKYKGTGDTGDSFGKWLKYGTVGWRNKTDLSALWPTRGYLGVAEHLTVNT 600
QY 601 LPGSKLOYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
Db 601 LPGSKLOYYSATHNQWTFPPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGGNKKANVSAELLFPMGAKDARTVRLSLFADAGSVWDG 720
QY 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIORFQFQGLGTTTF 797
Db 781 KPEDEIORFQFQGLGTTTF 797

RESULT 3
H83190
probable outer membrane protein PA3648 [imported] - Pseudomonas aeruginosa (strain PA01)
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 09-Jul-2004
C;Accession: H83190
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Brj
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho
A;Reference number: A82950; MUID:20437337; PMID:10984043
A;Accession: H83190
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <STO>
A;Cross-references: UNIPROT:Q9HXY4; GB:AE004784; GB:AE004091; NID:g9949799; PIDN:AAG0703
A;Experimental source: strain PA01
C;Genetics:
A;Gene: PA3648
C;Superfamily: protective surface antigen D-15

Query Match 30.8%; Score 1279.5; DB 2; Length 797;
Best Local Similarity 33.3%; Pred. No. 7e-69;
Matches 273; Conservative 157; Mismatches 338; Indels 51; Gaps 7;

QY 3 LKQIASALMWLGISPLAFADFTIQDIRVEGQRTPESTFVNYLPVKVGDYNDTHGSAII 62
Db 6 LPAALLSALM--IAEVHAESFTVSDIRVNLQQRVSAGSVFAALPLNVEGTIDIDQALVQAT 62

QY 63 KSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 122
Db 63 KSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 122
```


Db 63 RSLFKTGFQDIQGRDGNVLVTVVERPSSISIEBGNKAISKEDLLKGLKQSLAEGE 122
Qy 123 YFNQATLNOAVAGLKEBYLGRGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIEPE 182
Db 123 IFORATLGVNRELQRYVAQGRYSAAEVIQPPNRVALKININEGTVAASHINVV 182
Qy 183 GNOVYSRDKLMRQMSLTGEGITWLTNRSNQNEOKFAQDMEKVTDFYONNGYDFPRLDT 242
Db 183 GNVVSEEDLTDLPFLKTTNWLSPFFKNDKDYAREKLSGDLRLRSYLDLRYINMDIAT 242
Qy 243 DIQNEKTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMPKGRWYERQOMT 302
Db 243 QVSTTPDKKHVITVNIKEGKVTIRDVKLTGDL-KVPEEVEKRLLLVQKQFVSRRKVM 301
Qy 303 AVLGEIQNRMGSGAGYASEISVQPLPNAETKTVDFVLHIEPGRKIYNEIHTGNKTRD 362
Db 302 TTSDLITRRLNGEGYTVANVNGPEAHDDDKTTSVTFVDPGKRAYVNRINFRGNTKTD 361
Qy 363 EVVRELROMESAPYDTSKLORSKERVLLGYFDNVQFADVPLAGTDPKVDLNNSLTERS 422
Db 362 EVLRENRQEGGWASTYILDQSKARLERLGYFKEVNVETPAVPGTDDQVDVNVSEEQP 421
Qy 423 TGSLLDSAGVQDTGLVMSAGVSDNLFCTGSKAALRASRSTKTLNGLSFTDPYFTADG 482
Db 422 SSGTASVGFQAQAGLLGSGISQNNFLGTGNKVSIGLTRSEYQTRVNFGEVDPYWTVDG 481
Qy 483 VSLGYDVYKAFPRKASTSIGKYKTTAGATIRMSVPVTEYDRVNFGLVAEHLTVNTYN 542
Db 482 VSLGYNAYFRKTDYDELVDVVASVNSLGAAGSIGYPISETSRLTYGLSVQRDQDTGR 541
Qy 543 KAPHYADFTKYKGTGDTGSGFKGWLKCTGVGWRNKTDLSALWPTFGYLTGVNAETALP 602
Db 542 YTVDIEIYDFLDKGG-----DNFTN--FKASIGSESTLNGVLATRGHQSGLTLETL 593
Qy 603 GSKLQYVSATHNQTWFFPLSKTFTMLGGBGVAGYGRTEKPEIFFNFYGGGLGSRVGY 662
Db 594 GSDLFFKYIDYRGOVFAPLDNTYMRPHTELGYDGVGSTERLPFFENYTAGFNSVRGF 653
Qy 663 ESGTLGP-----KVDYGEKISYGGNKKANVSAAELFPMP 698
Db 654 KDSTLGRPSTPSVARNPDGTPMKNQGPDSKGRVTDPDQDPEAFGNNILITGGAELLP 713
Qy 699 GAKDARTVRLSLFADAGSVNDGTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSG 758
Db 714 FVKDQRLVTLFWDVGS-----TFDTCPTKTTNCDGIX-----TDNLASSVG 758
Qy 759 GAVTWLSPGLPMKFRYAYPLKXKPEDEIQRFQFOLGTF 797
Db 759 VGLTWITALGFLSFLATPIKPDNAETQVQFSLGQTF 797

RESULT 4
E82731
outer membrane antigen XF1046 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
R;Accession: E82731
Nature 406, 151-157, 2000
A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STM>
A;Cross-references: UNIPROT:Q9BEI2; GB:A8003941; GB:A8003849; NID:g91059978; PIDN:AAF8385
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carrier, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Pacinani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Frohm

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laigre
Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A.
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveira
M.; Tsubako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1046
C;Superfamily: protective surface antigen D-15

Query Match 29.9%; Score 1241; DB 2; Length 784;
Best Local Similarity 33.7%; Pred. No. 1.4e-66;
Matches 272; Conservative 163; Mismatches 319; Indels 52; Gaps 10;

Qy 8 SALMLGIGSLAPADFTIODIRVEGLQRTPEPSVFVNYLPVKVGDVTYNDTHGSAIKSLYA 67
Db 15 AANFSLPVLTOAESFVANDIRVDGLQRIASGTVFYLPVNRGDTVDADAKVAIRALXR 74
Qy 68 TGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQSQYNQOA 127
Db 75 TGFENVIRDRQGNILVWVKERPAINKLTITGNKDIKSEELLKGLSEIGLSEGGTFDRL 134
Qy 128 TLNQAVAGLKEEYLGKLNIOITPKVTKLARNRVDIDITIDEGSKAKITDIEFGNQVY 187
Db 135 SLDRVTOELKQYNNRGYNVQMTTTPLDNRNVDTTAKEGKAARHINLIGTEKF 194
Qy 188 SDRKLQMSLTGGITWLTNRSNQNEOKFAQDMEKVTDFYONNGYDFPRLDTDTQTN 247
Db 195 NNDVMSANESKEHNWASWYRDDQYSKEKLSGDEKLNSWYLDGVDFVNDISTQVVIS 254
Qy 248 EDTKOTIKITVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTMPKGRWYERQOMTAVLGE 307
Db 255 PEKHNFFITAGVTEGQYKISSIKVTGNT-VLPQEKIEKLVIPKTDIPFSLVEYSAA 313
Qy 308 IQNRMGSGAGYASEISVQPLPNAETKTVDFVLHIEPGRKIYNEIHTGNKTRDEVVRR 367
Db 314 IINTLSNIGYAFSKVNPITANRADRTVAVNLHVPGRVTVRQILFKGNTRTSDEVLR 373
Qy 368 ELRQMSAPYDTSKLORSKERVLLGYFDNVQFADVPLAGTDPKVDLNNLSLTERSTGSLD 427
Db 374 EMQFNSWSQAIDRSKIRLQRLGTFEADVSTPVGSDNQVDLVYTKETTSQSFQ 433
Qy 428 LSAGWQDTGLVMSAGVSDNLFCTGSKAALRASRSTKTLNGLSFTDPYFTADGVSGLY 487
Db 434 VGLGSKTYGVTTSVQLSQNNFLGSGNRVSDASRSRYQDRYSFSYTNPFTDNGVSLGY 493
Qy 488 DVYKAFPRKASTSIGKYKTTAGATIRMSVPVTEYDRVNFGLVAEHLTVNTY-NKAPK 546
Db 494 NLAYQKLD--YSDFNAAYNSKRMSCGQITFGIPITENDTVSWVIGADSDNQITTFPGSTPK 551
Qy 547 HYADFTKYKGTGDTGSGFKGWLKCTGVGWRNKTDLSALWPTFGYLTGVNAETALPCKSL 606
Db 552 AIIDYIDAVGQR-----TFRAW--RTELGWARTDRNDYFNPNGMYQRIAGAEVTLPGSTI 604
Qy 607 QYVSATHNQTWFFPLSKTFTMLGGBGVAGYGRTE-----KEIPFFENFYG 653
Db 605 KYKYNQVISKYWPPIPALVNLRLVLEVGDDYGVKSHTRILPDGTVATASGLPFFENFYA 664
Qy 654 GGLGVSRYGESGTLGPK--VYDEYGEKISYGGNKKANVSAAELFPMPGAKARTVRLSLF 711
Db 665 GGTVSVGRFRDNLGPRSEVTLVYNQQLGSGFKTVGSTEMYFPK--LFDSPSARISAF 722
Qy 712 ADAGSVWDGKTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSGAGVATWLSPLGPMK 771
Db 723 LDFGNFYNGV-----NNFKA---NELRASSGVALLWRAPIGPIS 758
Qy 772 FRVAYPLKXKPEDEIQRFQFOLGTF 797
Db 759 ISYAFFIKKENDEIRLQTFFGQF 784

Qy	536	LTVTYNKAPKHYADFIKKYKTKDGTGDSFGKWLKYKTVGWGRNKTDSALMPTRGVLTCV	599
Db	536	LSDDLMPQVAMRWRYLESVGRPGYDREG-FTTDDFTLLMLGWTYNNLDRGFFFTSGVKSSV	594
Qy	596	NAEIALPGSKLOYYSATHNQTWFRPLS--KTYFTMLGGEVGIAGCYGRTKEIPPFENFYG	653
Db	595	NTKLTVPESDNEFFKYVTPDTSAYQPLNDRSVMLLGRGLGYGDGIG-SKEMPFYENFYA	653
Qy	654	GGLGSVRGYSBGTGLGPKV--YDEYGEKI-----SYGNNKCANVSAELLFPMP--GAKDAR	704
Db	654	GGSTVRGFRSNNIGPKAAYANGGATVNTSDAVGGNAMAVASIELITPTPFISEKYN	713
Qy	705	TVRLSLFADAGSVNDKTYTDNNSSATG-----GRVQNIYAGNTHKSTFTNELRYSAGA	760
Db	714	SVRTSIETSDGTVDNTWNTAKTRAAGIPDYGKASNI-----RVSAGVA	758
Qy	761	VTWLSPGPKMFRYAYPLKKPEDEIQRFQFOLGTTFF	797
Db	759	LQWMSPLGLPVFSYAKPVKDYEGDKSEQFQFNIGKTW	795
Qy	797	RESULT 7	
Db	795	A64742	
Qy	795	hypothetical protein b0177 - Escherichia coli (strain K-12)	
Db	795	C:Species: Escherichia coli	
Qy	795	C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004	
Db	795	C:Accession: A64742	
Qy	795	R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Rile	
Db	795	A.; Rose, D.J.; Mau, B.; Saaio, Y.	
Qy	795	Science 277, 1453-1462, 1997	
Db	795	A:Title: The complete genome sequence of Escherichia coli K-12.	
Qy	795	A:Reference number: A64720; MUID:97426617; PMID:9278503	
Db	795	A:Accession: A64742	
Qy	795	A:Status: nucleic acid sequence not shown; translation not shown	
Db	795	A:Molecule type: DNA	
Qy	795	A:Residues: 1-810 <BLAT>	
Db	795	A:Cross-references: UNIPROT:P39170; GB:AE000127; GB:U00096; NID:gl786370; PIDN	
Qy	795	A:Experimental source: strain K-12, substrain MG1655	
Db	795	C:Superfamily: protective surface antigen D-15	
Qy	795	Query Match 28.4%; Score 1178.5; DB 2; Length 810;	
Db	795	Best Local Similarity 32.8%; Pred. No. 8.3e-63;	
Qy	795	Matches 273; Conservative 154; Mismatches 348; Indels 57; Gaps 15	
Db	795	1 MKLKOIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPEPSTVFNVLPVKVGDTYNDTHGS	59
Db	795	1 MAMKKLLIASLFFSATYVGAEGFVKDIIHEGLQORVAVGAALLSPMVRTGDTVDNDEIS	60
Qy	795	60 AIIKSLYATGFDDRVRVETADGQLLLTVIERPTTGLSNITGAKMLQNDAIKNLESFGLA	119
Db	795	61 NTIRALFATGNFEDRVRLRDGDTLLVQVKERTIASITFSGNKS VKDDMLKQNLASGVR	120
Qy	795	120 QSQYFNQATLNOAVAGLKEEYLGRLGKLNIOITPKVTKLARNRVDIITIDECKSAKITDI	179
Db	795	121 VGESLDRTTIADIEKGLDFYYSVGKYSASVAKVVTPLPRNRVDLKLVPQEGVSAEQI	180
Qy	795	180 EFEGNQVYSDRKLARQMSLTGGGIWTWLTNRNFOEQKFAODMEKVTDFYQNNGVDFDRI	239
Db	795	181 NIVGNHAFTTDELISHFQLRDVPMVWNVGDKYQKQKLAGLEFIRSYLDRGVARFNI	240
Qy	795	240 LDTDIQTNEDTKQTIKITIVHEGGRFRGKYSIEGDTNEVPKAELEKLLTKPKGKWYERQ	299
Db	795	241 DSTQVSLTPDKKGIYVTVNITGDDQYKLSGVEVSNL--AGHSAETIEQLTKIEPGLYNGT	299
Qy	795	300 QMTAVLGBIQNRMSGAGYAYSEISVQPLPNAETKTVDFVLHIEPGRKIVYVNEIHTGNKK	359
Db	795	300 KVTWEMDDIKLLGRYGAYPRVQSPMPINDADKTVKLRVNVNADGNRFYVRKIRFEQNDT	359
Qy	795	360 TRDEVRRELROMESAPYDTSKLQRSKERVELLYGFDVNVQDPAVLACTPDKVDLNMSLT	419
Db	795	360 SKQAVLRREMEQMEGANLWGSDLVQDGKRLNRLGFFETVDTQTRVPSQDQVVVYKVK	419
Qy	795	420 ERSTGSLDLSAGWQDITGLVMSAGVSODNLFGTGKSAALRASRSKTTILNGSLFSDTDPFT	479

[illegible]

```
QY 300 QMTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKK 359
Db 300 KVTXMEDDIKLLGRYGYAYPRVQSMPEINDAKTVKLRVNVNDAGRFYVRKIRFEGNDT 359
QY 360 TRDEVVRELRQMESAPYDTSKLORSKERVVELLGYFDNQVDFAVPLAGTDPDKVDLNNSLT 419
Db 360 SKDAVLRREMRQMEGAWLGSDLVQDQKERLNRGLGFETVDTDTQRPVPSDPQDVVYKVK 419
QY 420 ERSTGSLDLGAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTTLNGSLSTFTDPYFT 479
Db 420 ERNTGSFNGIGYGTESGVSFQAGVQDQNLWLGTYGAVGINGTKNDYQTYAELSVTNPYFT 479
QY 480 ADGVSIGYDVYKAF--DPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
Db 480 VDGVSIG---GRLFYNDQFQADDADLSDTNKSYSYGTDTVLGFPINEYNSLRAGLGYVHNS 535
QY 538 VNTYNAKPK---HYADFIKKYKTDGTSFGKWLKGYGVHGRNKTDLSALMPTRGYLT 593
Db 536 LS--NMQPVAMRWLYLSMGEHPSTSDQNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRV 593
QY 594 GVNAETALPGSKLOYYSATHNQWFFPLSKTFTMLMGGEV--GIAGGYGRTEKIPFFENF 651
Db 594 NLTKVVTIPGSDNEYKVTLDATYVPIDDHKWVVLGRTFWGVGDGLG--GKEMPPYENF 652
QY 652 YGGGLGSRVYEGSTLGP-K-VY-----DEYGEKISY-----GKNKKA 687
Db 653 YAGGSSTVRGFSQNTIGPKAVYVPHQASNYDPDYDECATQDQAKOLCKSDDDAVAGGNAMA 712
QY 688 NVSAELLFPMGAKD--ARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGAGNTH 745
Db 713 VASLEFITTPTFISDKYANSVRSTFFMDMGTVMD--TNWSSQYS-----GYPD 759
QY 746 KSTFTNELRYSGAGVATWLSPLGPKMFRYAYPLKKKPEDEIQRFOQLGTTFF 797
Db 760 YSDPSN--IRMSAGIALQWMSPLGLPVSFAQPFKKYDGDKAQEQFQFNIGKTW 810

RESULT 9
C85502
hypothetical protein yaeT [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C;Species: Escherichia coli
C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C;Accession: C85502
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A;Reference number: A85480; MUID:21074935; PMID:11206551
A;Accession: C85502
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-810 <STO>
A;Cross-references: UNIPROT:P39170; GB:AE005174; NID:g12512902; PIDN:AAG54479.1; GSPDB:C
A;Experimental source: strain O157:H7, substrain EDL933
C;Genetics:
A;Gene: yaeT
C;Superfamily: protective surface antigen D-15

Query Match 28.4%; Score 1178.5; DB 2; Length 810;
Best Local Similarity 32.8%; Pred. No. 8.3e-63;
Matches 273; Conservative 154; Mismatches 348; Indels 57; Gaps 15;

QY 1 MKLKQIASALMWLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNTDTHGS 59
Db 1 MANKULLIASLPPSSATVYGAEGFVVKDTHFEGLRQVAVGCAALLSNPVRTGDTVNDSDIS 60
QY 60 AI1KSLYATGFFDDRVETADGOLLTVIERPTIGSLNITGAKMLQNDAIKKNLSEFGLA 119
Db 61 NTIRALFATGNFEDRVLRGDTLLVQVKERPTIASITFSGNKSXVQDDMLKQLEASGVR 120
QY 120 OSQYFNQATLNQAVAGKEEYLRGKLNIOITPKYTKLARNRVLDITIDEGSAKITDI 179
Db 121 VGESLDRTTIADIEKGLDFYYSVGKYSASVKAIVTPLPRNRVDLKLVFQEGVSABIQI 180
```

```
QY 180 EPEGNQVSDRKLMRQMSLTBGGIWTWLTSRNQFBNQKFAQDMKEVTDYFQNNGYDFRI 239
Db 181 NIVGNEHAFTTDELISHFQLRDEVPWNVVDGRKYQKQKLAGDLLETLSRYLDRGYARFNI 240
QY 240 LQDTQITNEDKTKQTKITVHEGGRFRWGVKSIEGDTNEVPKAELEKLLTMKPGKKYERQ 299
Db 241 DSTQVSLTDPKGIYVTVNITEGDQYKLSGVEVSGNL--AGHSAEIBQLTKIEFELYNGT 299
QY 300 QMTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKK 359
Db 300 KVTXMEDDIKLLGRYGYAYPRVQSMPEINDAKTVKLRVNVNDAGRFYVRKIRFEGNDT 359
QY 360 TRDEVVRELRQMESAPYDTSKLORSKERVVELLGYFDNQVDFAVPLAGTDPDKVDLNNSLT 419
Db 360 SKDAVLRREMRQMEGAWLGSDLVQDQKERLNRGLGFETVDTDTQRPVPSDPQDVVYKVK 419
QY 420 ERSTGSLDLGAGVQDTGLVMSAGVSQDNLFGTGKSAALRASRSKTTTLNGSLSTFTDPYFT 479
Db 420 ERNTGSFNGIGYGTESGVSFQAGVQDQNLWLGTYGAVGINGTKNDYQTYAELSVTNPYFT 479
QY 480 ADGVSIGYDVYKAF--DPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLT 537
Db 480 VDGVSIG---GRLFYNDQFQADDADLSDTNKSYSYGTDTVLGFPINEYNSLRAGLGYVHNS 535
QY 538 VNTYNAKPK---HYADFIKKYKTDGTSFGKWLKGYGVHGRNKTDLSALMPTRGYLT 593
Db 536 LS--NMQPVAMRWLYLSMGEHPSTSDQNSFKTDDFTFNYGWTYNKLDRGYFPTDGSRV 593
QY 594 GVNAETALPGSKLOYYSATHNQWFFPLSKTFTMLMGGEV--GIAGGYGRTEKIPFFENF 651
Db 594 NLTKVVTIPGSDNEYKVTLDATYVPIDDHKWVVLGRTFWGVGDGLG--GKEMPPYENF 652
QY 652 YGGGLGSRVYEGSTLGP-K-VY-----DEYGEKISY-----GKNKKA 687
Db 653 YAGGSSTVRGFSQNTIGPKAVYVPHQASNYDPDYDECATQDQAKOLCKSDDDAVAGGNAMA 712
QY 688 NVSAELLFPMGAKD--ARTVRLSLFADAGSVMDGKTYDDNSSATGGRVQNIYGAGNTH 745
Db 713 VASLEFITTPTFISDKYANSVRSTFFMDMGTVMD--TNWSSQYS-----GYPD 759
QY 746 KSTFTNELRYSGAGVATWLSPLGPKMFRYAYPLKKKPEDEIQRFOQLGTTFF 797
Db 760 YSDPSN--IRMSAGIALQWMSPLGLPVSFAQPFKKYDGDKAQEQFQFNIGKTW 810

RESULT 10
B82099
surface antigen VC2252 [imported] - Vibrio cholerae (strain N16961 serogroup O1)
C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: B82099
R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.;
chardson, D.; Ermolaeva, M.D.; Vamathavan, J.; Babs, S.; Qin, H.; Dragoi, I.; Sellers, P.
1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
A;Reference number: A82035; MUID:20406833; PMID:10952301
A;Accession: B82099
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-803 <HEI>
A;Cross-references: UNIPROT:Q9KPW0; GB:AE004297; GB:AE003852; NID:g9656810; PIDN:AAF95396
A;Experimental source: serogroup O1; strain N16961; biotype El Tor
C;Genetics:
A;Gene: VC2252
C;Map position: 1
C;Superfamily: protective surface antigen D-15

Query Match 28.1%; Score 1168; DB 2; Length 803;
Best Local Similarity 32.4%; Pred. No. 3.5e-62;
Matches 265; Conservative 166; Mismatches 352; Indels 34; Gaps 13;
```

Qy 1 M K L I Q J A S A - L M M L G I S P L A F A D T T I O D I R V E G L Q R T E P S T V F N Y L P V K V G D T Y D N T H G S 59
:
Db 1 M A M E Q I L L A T L A T S V S A N G A E K F W V O D I Q I D G L Q R V A L G A A L L K M P V R V G D S V D S Q D V A 60
:
Qy 60 A I I K S L Y A T G P F D D R V R V E T A D G O L L L T V I E R P T T G S L N I T C A K M L Q N D A T K N L S F G L A 119
:
Db 61 N I I K A L Y S G N F E D V K U L R D G N T L M V Q K E R P T T A S F S G N K A I K E Q L Q N L A E S S I R 120
:
Qy 120 Q S O Y F N Q A T L N Q A V A G L K E E Y L G R G K L N I Q I T P K V T K L A R N R V D I D I T I D E G S A K I T D I 179
:
Db 121 V G E A L D R T T L S N I E K G L E D F Y S V G K Y N A T V K A V V T P L P R N R A D L K F V F T E G V S A K I Q Q I 180
:
Qy 180 E F E G N O Y V S D R K L M Q M S L T E G G I W T M L T R S N Q N E Q K F A O D M E K V T D F Q N G N Y F D F R I 239
:
Db 181 N F I G N Q V S D E E L S R F N L N V D V A W N F L A D D K Y K Q V L A G D I E A L R T Y Y L D R G Y L A F O V 240
:
Qy 240 L D T Q I T N E D K T K O I K I T H E G G R F W G K V S I E G D T N E V P K A E L K L T M K C K W Y E R Q 299
:
Db 241 D S T O V A I S P D K K G V I T I N L N E G P Y T V S K V Q F R G E L M G - K E A E F T S L I F E I G E T Y N G S 299
:
Qy 300 Q M T A V L G E I Q N R M S G A G Y S E I S V Q P L P N A E T K T V D F V L H I E P G R K I Y Y N E I H I T G N N K 359
:
Db 300 A V T E L S S V K V L G E S G A Y P Q V P T I F E F D D E K Q V S L V H V E A G K V Y R D I R F V G N N S 359
:
Qy 360 T R D V R R E L R Q M E S A P Y D T S K Q R S K E R V E L L G Y F D N V Q F D A V P L A G T P D K V D L N M S L T 419
:
Db 360 T R D V L R E M Q R M E G S L M K S D I E T G K T R L N R L G F F E T V E Q T V R V P G S E D Q V D L V Y S V K 419
:
Qy 420 E R S T G S L D L S A G W V Q D T G L V M S A G V S O D N L F G T C K S A A L R A S R S K T T L N G S L F T D P Y F T 479
:
Db 420 E A N S G N Y N F G V G Y G T E S G V S F Q V G L O Q D N F L G S G N R V G V N A M I N D Y O K N I L T E Y R D P Y W N 479
:
Qy 480 A D G V S L G Y D V Y K A F D P R K A S T S I K O Y K T T T A G A G I R M S V P V T E Y D R V N F G L V A E H L T V N 539
:
Db 480 L D G V S L G C K Y F Y N Q F A S E A - G I V D Y T N E S Y G T S L T W G F F D E L N R F E F I G Y T H N K I G 537
:
Qy 540 T Y N K A P - K H Y A D F I K Y G K T D G T D G S F K G W L Y K G T V G W G R N K T D S A L W P T R G Y L T G V N A E 598
:
Db 538 -- N L T P Y L Q V E N F L A A Q A S N I D S G N L L T D D F D I N L S W T R N L N L N S Y F P T A G N H Q R A F Y K 595
:
Qy 599 I A L P G S K L O Y Y S A T H N Q T W F P P L S K -- T P T L M L G G E V G I A G G Y G R T ---- K E I P F F E N F Y 652
:
Db 596 M T V P G S D A Q Y F K L Q Y D V R Q Y F P L T K H E F T L L R G L G Y G N G Y G O T D G K D N L F P P Y E N F Y 655
:
Qy 653 G G G L G S V R G Y E S G T L G P K - V Y D E Y ----- G E K I S Y G N K K A N V S A E L L P M P - G A K 701
:
Db 656 A G G F T S L R G F G S N S A G K A V I R Y S G S N G S D T A T D D S V G G N A I A L A S V E L I V P T P F A S E 715
:
Qy 702 D A R T - V R L S L F A D A G S Y M D G K T Y D D N S S S A T G G R V Q N I Y A G A N T H K S T F T N E L R Y S A G G A 760
:
Db 716 E A R N Q I R T S I F Y D M A S W D T E - F D Y R G A D Y G N Q Y Y D Y S D P T N Y R S S Y ----- G V A 766
:
Qy 761 V T W L S P L G P M K F R Y A Y P L K K X P E D E T Q R F O L G T T F 797
:
Db 767 L O W V S P M G P L V F S L A K P I K K Y E G D D E F F T T I G R T F 803

RESULT 11

JC4078

C;Protective surface antigen D-15 precursor - Haemophilus influenzae (type b)

C;Species: Haemophilus influenzae

A;Variety: type b

C;Date: 30-Jun-1995 #sequence_revision 14-Jul-1995 #text_change 09-Jul-2004

C;Accession: JC4078

R;Flack, F.S.; Loosmore, S.; Chong, P.; Thomas, W.R.

Gene 156, 97-99, 1995

A;Title: The sequencing of the 80-kDa D15 protective surface antigen of Haemophilus influenzae

A;Reference number: JC4078; PMID:95255676; PMID:7737523

A;Accession: JC4078

A;Molecule type: DNA

A;Residues: 1-797 <FLA>

A;Cross-references: UNIPROT:P46024; GB:U13961; NID:G537447; PIDN:AAA85645.1; PID:G537448

A;Experimental source: tvoc b

C:Superfamily: protective surface antigen D-15
C:Keywords: surface antigen
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-797/Product: protective surface antigen D-15 #status predicted <MAT>

Query Match 27.4%; Score 11361; DB 2; Length 797;
Best Local Similarity 31.6%; Pred. No. 2.9e-60;
Matches 263; Conservative 166; Mismatches 332; Indels 70; Gaps 19;

Qy	3	LKOITASALMLMGISPLAF-ADETODLRVREGLQRTPESTVFNYLVPVKVGDYNTDTHGSAI	61
Db	1	MKLLIASLFGITTTVFAAFVAKDIRVDGVQGDLEQQIRASLPVRAGQRTVDNDVANI	60
Qy	62	IKSLYATGFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDIAIKKNLEFGLAQ	121
Db	61	VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVITEALKQNLDANGFKVKG	120
Qy	122	QYFNQATLNOAVAGLKEEYIGRGLNLIQITPKVTYGLARNRVDDITIDDEGKSAKITDIEF	181
Db	121	DVLIRKLENFAXSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQNEODDKAKLASLTF	180
Qy	182	EGNQVYSDRKLMQMSLTTEGGIW-TWLTNRNQFNEQKFAQMEKVITDFYQNNGYFDFRIL	240
Db	181	KGNESVSSSTLQSQMELQDPSWWKLM--GNKPEGAQFEKLOSIRDYLYNNGYAKAQIT	237
Qy	241	DTDIQTNEKTKOTIKITVHEGGRFRMGKVISIEGDTNEVPKAELEKLLT-MKPGKWTERQ	299
Db	238	KTDVQLNDEKTKVNVITDVNEGLOYDLRSARIIGNLGM-SAELEPILLSALHLNDTFERS	296
Qy	300	QMTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDVLHI BPRKIYVNEIHITGNKK	359
Db	297	DIADVENAIKAKLGERGYGSATVNSVPDFDDANKTLAITLWVDAGRLTVRQRFEGTV	356
Qy	360	TRDEVVRRELROMESAPYDTSKLQSKERVVELLGYPDNVQFADVPLACTPKDVKDLNMSLT	419
Db	357	SADSTLRQEMRQEGTWYNSQLVELGKIRLDRTGFETVENRDPINGSNDEVVVYKVK	416
Qy	420	ERSTGSLDLISAGWQDTGLVMSAGVSQDNLFGTGSAALRASRSKTTLNGLSLFTDPVFT	479
Db	417	ERNYGSINFGIYGTSESGISYQASVQDNFLGTGAAVSIAGTKNDYGTSVNLGYTEPYFT	476
Qy	480	ADGVSLGYDYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRWFNGLVAEHLTVN	539
Db	477	KDGVSLGGNVFFENYDNSKSDTS-SNYKRTTYSNVTLGFVPVNNNSYVVGL-----GH	529
Qy	540	TYNKAAPH-----YADFIKYG---KTDGTDGFKGWLKYGTVGWGRNKTDTSALWPT	588
Db	530	TYNKISNFALERNRNLIIOSMKFKGNIGIKTNDPDPF-----GWNTYNSLNRGFYPT	580
Qy	589	RGVLTGVNAEIALPGSKLOYYSATHNQTFPFLKTFLLMLGGE--VGIAGGYGRTRKEIP	646
Db	581	KGVASLGRKVTIIPGSDNKIYKULSADVQGFPLDRDHLWVWSAKASAGYANGFG-NKRLP	639
Qy	647	FFENFYGGGLGSVRGYESGTLGPK-VYDEYG-----EKIS---YGGNKKANVSALL	694
Db	640	FYQTYTAGGIGSLRGFAYSGISIGNAIYAEYNGSGGTCTFKKISSDVI GGNAIATASAEI	699
Qy	695	FMP--GAKDARTVRISLFPADAGSVWDGKYTDNSSSATCGRVONI-----YGAGNTHK	746
Db	700	VPTFPFVSDKSQNTVRTSLFVDAASVWNTKWSDKN-----GLESDVLKRLPDYCK-----	749
Qy	747	STFTNELRYSAGGAVTWLSPGLGPKMERYAPLKKKPEDEIQRQFOLGTTTF	797
Db	750	---SSRIRASTGVGFQWQPIGLVFSYAKPIKKYENDDDVEQOFQSIGGSF	797

RESULT 12
F64102
protective surface antigen D-15 - Haemophilus influenzae (strain Rd KW20)
C:Species: Haemophilus influenzae
C:Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Sep-1998
C:Accession: F64102
R:Flieschmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Ker

Db 646 NLLVDFQFKFG-RQVRGFKNDGIGPRIGSD-----SIGGTTTFAASAETAMPGPVDP 699
QY 704 RTVRLSLFADAGSVDCKTVDNNSSTATGGRVQNIYAGNTHKSTFTNELRYAGGAVTW 763
Db 700 FGLRLAGFVAGTGMGNKV-----STGTVKD-----DNSIRASAGIGVMW 740
QY 764 LSPGLPMKFRYAYPLKKKPEDEIQRFQGLGTTTF 797
Db 741 ASPFGPIRVDAIPIAKEDYDEQRFQFGSNTF 774

RESULT 14
AE2746
group 1 outer membrane protein precursor ompl [imported] - Agrobacterium tumefaciens (se
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 09-Jul-2004
C;Accession: AE2746
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2746
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-774 <KUR>
A;Cross-references: UNIPROT:OBUFL6; GB:AE008688; PIDN:AAL42387.1; PID:g17739796; GSPDB:G
A;Experimental source: strain C58 (Dupont)
C;Genetics:
A;Gene: ompl
A;Map position: circular chromosome
C;Superfamily: protective surface antigen D-15

Query Match 21.8%; Score 906; DB 2; Length 774;
Best Local Similarity 28.5%; Pred. No. 1.7e-46;
Matches 232; Conservative 161; Mismatches 341; Indels 80; Gaps 18;

QY 7 ASALMMLGISPLADAF-----TIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAII 62
Db 18 AGVSSVAGLVLASAGVANAASVSKIDVRCASGSDSVRSNITIAPKNFNSDIDESV 77
QY 63 KSLYATGFFDDVRVETADGQLLTIVIERPTTGLSLNITGAKMLQNDIAKKNLESFGLAQSQ 122
Db 78 KRLYATGYFENVMRVSGLTAVTNENQLVQWFGNKRKIDDKLA-----GIVQIQ 131
QY 123 ---YFNOATLNOAVAGLKEEYLRGKLNITQITPKVTKLARNVDIDITIDEGSAKITDI 179
Db 132 PMGFFNQAIIVTADIAIRIKEAYSAGRSDBEITTTQTVSVGGQGVNIAFVINEGERTKIGRI 191
QY 180 EFGNQVYSDRKLROMSLTEGGITWLTTRSNQFNQKPAQDMKEKVTDFYONNGYDFRI 239
Db 192 DFGNNSYSDCLAAVNTKSNMLFTRIKOVYNEKLRADAEALRQFYNNRGYADFRV 251
QY 240 LDTDIQTNEDKTKQITKITVHEGGRFWGKSTEGDNEVPKAELEKLLTMKPGKWERQ 299
Db 252 VSSDAVLDESKEVNTISITVDEGKYDFGNVAVESTVPGVDSGLQGLVETRGASYSAK 311
QY 300 QMTAVLGEIQNRMGSAIYSEISVQPLPNAETKTVDFVLHIEPGRIKYVNEIHTGNK 359
Db 312 EVQQSMEAISKRVAGEGYPARVTPRGDRMSGNTIGVTIVDQGERAVVERIEIRGNTR 371
QY 360 TRDEVVRRELROMESAPYDTSKLQSKERVLLGYFDNVQFQDAVPLAG--TPDKVDLMS 417
Db 372 TRDYVIRREFDISGDAFNQITITAKRLEALGYSKVN---ISTAGSAPRVVIVVD 428
QY 418 LTERSTGSLDSAGVQDITGLVMSAGVSQDNLPFGTKSAALRASRKTLLNG--SLSFTDP 476
Db 429 VEDQSTGSGFAGYQNDGVLEASVEEKNFLGRQYIRVAACAGEDDARTVLSFTFEP 488
QY 477 YFTADGVSIGYVYGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHL 536

Db 489 YFLGYRLAGFDLP-----KNQSKSEYNYNDEQGFALRVTAPIYE-----NLSTTFKY - 537
QY 537 TVNTYNKAPKHYADFIKKYKTKTDGDSFGKMLYKGTV-----GWGR-----NKTDSA 584
Db 538 ---TYKQ-----INVEGKGDQNNANLAEPYQALIRGEDWTQSILSNTLNVNTLDDR 586
QY 585 LWPTRGYLTGVNAEIALPGSKLOYYSATHNQIWFPLSKTFTLMLGVEGVIAGGYGTKE 644
Db 587 NMPREGQAAALTNEFAGLGDSEYKYIYAKARYYTLTSDIYD-VIGSLTQGAQGVVMP 645
QY 645 -IPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKISYGGNKKANYSAELLFPMPGAKDA 703
Db 646 NLLVDFQFKFG-RQVRGFKNDGIGPRIGSD-----SIGGTTTFAASAETAMPGPVDP 699
QY 704 RTVRLSLFADAGSVDCKTVDNNSSTATGGRVQNIYAGNTHKSTFTNELRYAGGAVTW 763
Db 700 FGLRLAGFVAGTGMGNKV-----STGTVKD-----DNSIRASAGIGVMW 740
QY 764 LSPGLPMKFRYAYPLKKKPEDEIQRFQGLGTTTF 797
Db 741 ASPFGPIRVDAIPIAKEDYDEQRFQFGSNTF 774

RESULT 15
F87486
outer membrane protein CC1915 [imported] - Caulobacter crescentus
C;Species: Caulobacter crescentus
C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
C;Accession: F87486
R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A;Title: Complete Genome Sequence of Caulobacter crescentus.
A;Reference number: AB7249; MUID:21173698; PMID:11259647
A;Accession: F87486
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-769 <STO>
A;Cross-references: UNIPROT:Q9A711; GB:AE005673; NID:g13423368; PIDN:AAK23890.1; GSPDB:G
C;Genetics:
A;Gene: CC1915
C;Superfamily: protective surface antigen D-15

Query Match 21.1%; Score 877.5; DB 2; Length 769;
Best Local Similarity 28.2%; Pred. No. 8.8e-45;
Matches 226; Conservative 157; Mismatches 369; Indels 49; Gaps 17;

QY 11 MMLGISPL-----AFADF-----TIQDIRVEGLQRTPESTVFNYLPVKVGTVDYNDTHGSAI 61
Db 3 LLLGSTALVAPQQAFAQAQTGVQVQRIQVQGNRIEQGTVLSYLPQPGDVTDSQRLDLA 62
QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTTGLSLNITGAKMLQNDIAKKNLESFGLAQ 121
Db 63 LKTLARTDLFADVKIEMLGDLVWKVVENPIINQVVFEGNSLKKDKLQDEVQ---IRPR 119
QY 122 QYFNOATLNOAVAGLKEEYLRGKLNITQITPKVTKLARNVDIDITIDEGSAKITDIEF 181
Db 120 GLFTRAKVQADVQRIELIYRRSGRISATVTPKVELPQKRVLDVFEINGAKSGVLGINF 179
QY 182 EGNQVYSDRKLROMSLTEGGIW-TWLTRSNQFNQKPAQDMKEKVTDFYONNGYDFRI 240
Db 180 LGNAEYSDNLD-RDVIIVTKESRWYKILTSNDNDYDPRIDYEQRLKRYNRNGYDFRVI 238
QY 241 DTDIQTNEKTKQITKITVHEGGRFWGKSTEGDNEVPKAELEKLLTMKPGKWERQ 300
Db 239 SSVAEIAPDKNGFAVYITLIEGPKYKFGKITVETELKLDGNLLAQILPVRTGQLYEDER 298
QY 301 MTAVLGEIQNRMGSAIYSEISVQPLPNAETKTVDFVLHIEPGRIKYVNEIHTGNK 360
Db 299 ISQATDALTTAAAGAAGFAEVDVPRVPRVNRKTKTVDDVVFQVREGPRVYVDRIIDVGNTR 358

Qy 361 RDEVRRELQMSAPYDTSKLORSKERVELLGYFDNVQEDAVPLAGTDPKVDLNMSLTE 420
Db 359 LDYVLRRELEVAEGDAYNRVLVDRSKNNMRRLGFFKEVEIEDAP-GSAPDRTSLRVKVEE 417
Qy 421 RSTGSLDLSAGWQDTCGLVMSAGVSDNLFPGTGKSAALRASRSKTTLNGSLSTDPVFTA 480
Db 418 OPTGEISFSAGYSIDKLVLDVIGITERNFRGRQNLRARASVGSRLRQQIDFGFSEPRFLG 477
Qy 481 DGVS LGYDVYVGKAFDPKRASTSIKOYKTTTGTAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 478 RNLVAGVNLTYFRYD---LSEFAAYDTKSVGGDVRFGRPLTNDSSMSLRYTVRQDEVSU 533
Qy 541 YNKAPHYADFIKKYKTDGTDGTSFKGWLKGTWVWGR--NKYDTSALWPTRGYLTGVNAE 598
Db 534 -----ADSLCASGSVSQILCLQRGAYTTSLIGYGLRIDKKNPDPINPTRGWFADLNQD 585
Qy 599 IALPGSKLQYYSATHNOTWFFPLSKTFTLMLGGEVGIAGGYGRTKEIPFPENFYGGGLGS 658
Db 586 LAGVGGDVKYLKTEADAGWTGFTKDLVFSATGSGFVIEGWG-GDNVRINDRFYRG-T-S 643
Qy 659 VRGYESGTLGPKVYVDEYGEKISYCGNKKANVSALLFP--MPGAKDARTVRLSLFADAGS 716
Db 644 FRGFEIAGIGPR--DISSSFNSMGAKLYALSTTELIVPTPLP---EQYGKALFSDVGT 698
Qy 717 VWDGKYDDNSSSATGGRVONIYGAGNTHKSTFTNLRYSAGGAVTWLSPGLGPMKFRYAY 776
Db 699 A--GLLDDVDVRQSPGVDPNI-----KDNL--GLRASAGISIDWKSPMGIRPDISR 747
Qy 777 PLKKKPEDEIQRQFQLGTTTF 797
Db 748 ILSKEDYDRTETPRFSTSTRF 768

Search completed: July 6, 2005, 15:19:12
Job time : 55.7532 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:22:47 ; Search time 170 Seconds
(without alignments)
1813.224 Million cell updates/sec

Title: US-10-606-618-4
Perfect score: 797
Sequence: 1 MKLKQIASALMLIGISPLAF.....LKKKPEDEIQRFQGLGTF 797

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 2105692 seqs, 386760381 residues

Word size : 0

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : A Genesepc16Dec04:*
1: Genesepc1980s:*
2: Genesepc1990s:*
3: Genesepc2000s:*
4: Genesepc2001s:*
5: Genesepc2002s:*
6: Genesepc2003as:*
7: Genesepc2003bs:*
8: Genesepc2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	797	100.0	797	3	AY84947 Amino aci
2	797	100.0	797	5	ABY79802 Neisseria
3	752	94.4	797	4	AAU03959 Neisseria
4	752	94.4	797	4	AAU03957 Neisseria
5	752	94.4	797	4	AAU04451 Neisseria
6	752	94.4	797	4	AAU04451 Neisseria
7	752	94.4	797	4	AAU04451 Neisseria
8	752	94.4	797	4	AAU04451 Neisseria
9	752	94.4	797	4	AAU04451 Neisseria
10	210	26.3	792	4	AAU03958 Neisseria
11	210	26.3	792	4	AAU03958 Neisseria
12	210	26.3	792	4	AAU03958 Neisseria
13	210	26.3	792	6	ABP80499 N. gonorr
14	210	26.3	792	6	ABP79748 N. gonorr
15	157	19.7	792	5	ABY84946 Amino aci
16	157	19.7	792	5	ABY84946 Amino aci
17	157	19.7	792	5	ABY84946 Amino aci
18	37	4.6	37	4	AAU03997 Neisseria
19	32	4.0	32	4	AAU04410 Neisseria
20	29	3.6	29	4	AAU03987 Neisseria
21	25	3.1	25	4	AAU04412 Neisseria
22	25	3.1	25	4	AAU04000 Neisseria
23	23	2.9	23	4	AAU03971 Neisseria
24	22	2.8	22	4	AAU04401 Neisseria
25	21	2.6	21	4	ABY23787 Neisseria

26	19	2.4	19	4	AAU03988	Neisseria
27	18	2.4	21	4	ABY23785	Neisseria
28	18	2.3	18	4	AAU04428	Neisseria
29	18	2.3	18	4	AAU04434	Neisseria
30	18	2.3	18	4	AAU04425	Neisseria
31	18	2.3	18	4	AAU03990	Neisseria
32	16	2.0	16	4	AAU04427	Neisseria
33	16	2.0	16	4	AAU04435	Neisseria
34	16	2.0	16	4	AAU03992	Neisseria
35	16	2.0	16	4	AAU04430	Neisseria
36	15	1.9	15	4	AAU04442	Neisseria
37	15	1.9	15	4	AAU04404	Neisseria
38	15	1.9	15	4	ABY84743 N-termina	
39	14	1.8	14	4	AAU04438	Neisseria
40	14	1.8	14	4	AAU03980	Neisseria
41	14	1.8	14	4	AAU03984	Neisseria
42	13	1.6	13	4	AAU03985	Neisseria
43	12	1.5	12	4	AAU04423	Neisseria
44	12	1.5	12	4	AAU04424	Neisseria
45	12	1.5	12	4	AAU04416	Neisseria
46	12	1.5	12	4	AAU04418	Neisseria
47	12	1.5	12	4	AAU03986	Neisseria
48	11	1.4	11	4	AAU03981	Neisseria
49	11	1.4	11	4	AAU03999	Neisseria
50	11	1.4	21	4	ABY23789	Neisseria
51	10	1.3	10	4	AAU03993	Neisseria
52	10	1.3	10	4	AAU03982	Neisseria
53	10	1.3	10	4	AAU03975	Neisseria
54	10	1.3	10	4	AAU04413	Neisseria
55	10	1.3	10	4	AAU03974	Neisseria
56	10	1.3	10	4	AAU04411	Neisseria
57	10	1.3	10	4	AAU04450	Neisseria
58	10	1.3	10	4	AAU04405	Neisseria
59	10	1.3	10	4	AAU04439	Neisseria
60	10	1.3	10	4	AAU04403	Neisseria
61	10	1.3	10	4	AAU03965	Neisseria
62	10	1.3	10	4	AAU03965	Neisseria
63	9	1.1	9	4	AAU04448	Neisseria
64	9	1.1	9	4	AAU03961	Neisseria
65	9	1.1	9	4	AAU04414	Neisseria
66	9	1.1	9	4	AAU03994	Neisseria
67	9	1.1	9	4	AAU03967	Neisseria
68	9	1.1	9	4	AAU04420	Neisseria
69	9	1.1	9	4	AAU03995	Neisseria
70	9	1.1	9	4	AAU03991	Neisseria
71	9	1.1	9	4	AAU03998	Neisseria
72	9	1.1	9	4	AAU04447	Neisseria
73	9	1.1	12	4	AAU03964	Neisseria
74	9	1.1	185	3	AGY21459 Arabidops	
75	9	1.1	334	3	AGY21458 Arabidops	
76	9	1.1	362	3	AGY21457 Arabidops	
77	9	1.1	798	6	ABM67563 Phototrab	
78	9	1.1	1035	8	ADJ50326 Oil-assoc	
79	8	1.0	8	4	AAU04436	Neisseria
80	8	1.0	8	4	AAU03996	Neisseria
81	8	1.0	8	4	AAU04422	Neisseria
82	8	1.0	8	4	AAU04445	Neisseria
83	8	1.0	8	4	AAU04402	Neisseria
84	8	1.0	8	4	AAU04426	Neisseria
85	8	1.0	8	4	AAU03970	Neisseria
86	8	1.0	8	4	AAU03973	Neisseria
87	8	1.0	94	7	ABO61646 Klebsiell	
88	8	1.0	95	3	AGY25177 Human sec	
89	8	1.0	97	4	ABY51139 Arabidops	
90	8	1.0	97	6	ABO45396 Novel hum	
91	8	1.0	97	7	ABO26876 Protein a	
92	8	1.0	116	3	AGY57649 Arabidops	
93	8	1.0	117	3	AGY49893 Arabidops	
94	8	1.0	126	3	AGY25176 Arabidops	
95	8	1.0	201	3	AGY57648 Arabidops	
96	8	1.0	202	3	AGY49892 Arabidops	
97	8	1.0	214	3	AGY57647 Arabidops	
98	8	1.0				

99	8	1.0	215	3	AAG49891	Aag49891 Arabidops	172	7	0.9	96	4	AAU64929	Aau64929 Propionib
100	8	1.0	216	5	ADN21670	Adn21670 Bacterial	173	7	0.9	96	6	ABM61448	Abm61448 Propionib
101	8	1.0	217	5	ABG60322	Abg60322 Yeast dyn	174	7	0.9	97	7	ABO69614	AbO69614 Pseudomon
102	8	1.0	266	4	ABG15869	Abg15869 Novel hum	175	7	0.9	101	4	ABM17344	Abm17344 Human ner
103	8	1.0	266	4	ADC32990	Adc32990 Human nov	176	7	0.9	101	4	ABM17344	Abm17344 Human ner
104	8	1.0	289	3	AAG49003	Aag49003 Arabidops	177	7	0.9	102	3	ADM27054	Adm27054 Hyperther
105	8	1.0	299	4	AAG90486	Aag90486 C glutami	178	7	0.9	110	3	AAO06467	Aao06467 Human pol
106	8	1.0	315	8	ADS24860	Ads24860 Bacterial	179	7	0.9	110	4	AAO06467	Aao06467 Human pol
107	8	1.0	335	4	AAB96813	Aab96813 Putative	180	7	0.9	119	5	ABP07824	Abp07824 Human ORF
108	8	1.0	336	8	ADN47487	Adn47487 Thermococ	181	7	0.9	120	4	AAU40749	Aau40749 Propionib
109	8	1.0	349	3	AAG49002	Aag49002 Arabidops	182	7	0.9	120	4	ABM37268	Abm37268 Propionib
110	8	1.0	349	3	AAG49002	Aag49002 Arabidops	182	7	0.9	121	3	ABM37268	Abm37268 Propionib
111	8	1.0	397	3	AAG48988	Aag48988 Arabidops	183	7	0.9	121	3	ABM37268	Abm37268 Propionib
112	8	1.0	402	3	AAG49001	Aag49001 Arabidops	184	7	0.9	122	4	ABM37268	Abm37268 Propionib
113	8	1.0	422	8	ADS23854	Ads23854 Bacterial	185	7	0.9	125	6	ABM69954	Abm69954 Human imm
114	8	1.0	426	3	AAG48987	Aag48987 Arabidops	186	7	0.9	126	4	ABM69954	Abm69954 Human imm
115	8	1.0	426	3	AAG48987	Aag48987 Arabidops	187	7	0.9	126	4	ABM69954	Abm69954 Human imm
116	8	1.0	426	3	AAG48987	Aag48987 Arabidops	187	7	0.9	126	4	ABM69954	Abm69954 Human imm
117	8	1.0	438	3	AAG14941	Aag14941 Arabidops	188	7	0.9	129	7	ADF04752	Adf04752 Bacterial
118	8	1.0	438	3	AAG14940	Aag14940 Arabidops	189	7	0.9	132	4	ABM11237	Abm11237 Human pho
119	8	1.0	445	4	ABG17863	Abg17863 Novel hum	190	7	0.9	132	4	ABM11237	Abm11237 Human pho
120	8	1.0	451	3	AAG06359	Aag06359 Arabidops	191	7	0.9	132	4	ABM11237	Abm11237 Human pho
121	8	1.0	451	3	AAG06359	Aag06359 Arabidops	192	7	0.9	132	4	ABM11237	Abm11237 Human pho
122	8	1.0	461	3	AAG06358	Aag06358 Arabidops	193	7	0.9	132	4	ABM11237	Abm11237 Human pho
123	8	1.0	479	3	AAG06357	Aag06357 Arabidops	194	7	0.9	132	4	ABM11237	Abm11237 Human pho
124	8	1.0	494	8	ADS24095	Ads24095 Bacterial	195	7	0.9	132	4	ABM11237	Abm11237 Human pho
125	8	1.0	583	8	ADS14924	Ads14924 Pseudomon	196	7	0.9	132	4	ABM11237	Abm11237 Human pho
126	8	1.0	648	7	ABO75882	AbO75882 Pseudomon	197	7	0.9	132	4	ABM11237	Abm11237 Human pho
127	8	1.0	745	4	ABG03852	Abg03852 Novel hum	198	7	0.9	132	4	ABM11237	Abm11237 Human pho
128	8	1.0	745	4	ABG09109	Abg09109 Novel hum	199	7	0.9	132	4	ABM11237	Abm11237 Human pho
129	8	1.0	745	4	ABG10367	Abg10367 Novel hum	200	7	0.9	132	4	ABM11237	Abm11237 Human pho
130	8	1.0	745	4	ABG14890	Abg14890 Novel hum	201	7	0.9	132	4	ABM11237	Abm11237 Human pho
131	8	1.0	897	8	ADP98989	Adp98989 C. albica	202	7	0.9	132	4	ABM11237	Abm11237 Human pho
132	8	1.0	1577	6	ABU41145	Abu41145 Protein e	203	7	0.9	132	4	ABM11237	Abm11237 Human pho
133	7	0.9	1589	7	ADF04713	Adf04713 Bacterial	204	7	0.9	132	4	ABM11237	Abm11237 Human pho
134	7	0.9	7	4	AAU04432	Aau04432 Neisseria	205	7	0.9	132	4	ABM11237	Abm11237 Human pho
135	7	0.9	7	4	AAU04441	Aau04441 Neisseria	206	7	0.9	132	4	ABM11237	Abm11237 Human pho
136	7	0.9	7	4	AAU04446	Aau04446 Neisseria	207	7	0.9	132	4	ABM11237	Abm11237 Human pho
137	7	0.9	7	4	AAU03969	Aau03969 Neisseria	208	7	0.9	132	4	ABM11237	Abm11237 Human pho
138	7	0.9	7	4	AAU04437	Aau04437 Neisseria	209	7	0.9	132	4	ABM11237	Abm11237 Human pho
139	7	0.9	7	4	AAU04419	Aau04419 Neisseria	210	7	0.9	132	4	ABM11237	Abm11237 Human pho
140	7	0.9	7	4	AAU04429	Aau04429 Neisseria	211	7	0.9	132	4	ABM11237	Abm11237 Human pho
141	7	0.9	7	4	AAU04443	Aau04443 Neisseria	212	7	0.9	132	4	ABM11237	Abm11237 Human pho
142	7	0.9	23	3	AAU65830	Aau65830 Mismatch	213	7	0.9	132	4	ABM11237	Abm11237 Human pho
143	7	0.9	50	4	AAU20158	Aau20158 Peptide #	214	7	0.9	132	4	ABM11237	Abm11237 Human pho
144	7	0.9	50	4	ABE40395	AbE40395 Peptide #	215	7	0.9	132	4	ABM11237	Abm11237 Human pho
145	7	0.9	50	4	AAU34101	Aau34101 Peptide #	216	7	0.9	132	4	ABM11237	Abm11237 Human pho
146	7	0.9	50	4	ABE24767	AbE24767 Protein #	217	7	0.9	132	4	ABM11237	Abm11237 Human pho
147	7	0.9	50	4	AAU73922	Aau73922 Human bon	218	7	0.9	132	4	ABM11237	Abm11237 Human pho
148	7	0.9	50	4	AAU61203	Aau61203 Human liv	219	7	0.9	132	4	ABM11237	Abm11237 Human pho
149	7	0.9	50	4	ABG55674	Abg55674 Human liv	220	7	0.9	132	4	ABM11237	Abm11237 Human pho
150	7	0.9	50	4	ABG43810	Abg43810 Human pep	221	7	0.9	132	4	ABM11237	Abm11237 Human pho
151	7	0.9	56	8	ADN46996	Adn46996 Thermococ	222	7	0.9	132	4	ABM11237	Abm11237 Human pho
152	7	0.9	58	2	AAW48931	Aaw48931 Schwannom	223	7	0.9	132	4	ABM11237	Abm11237 Human pho
153	7	0.9	60	3	AAU03150	Aau03150 Human sec	224	7	0.9	132	4	ABM11237	Abm11237 Human pho
154	7	0.9	61	4	AAU65753	Aau65753 Propionib	225	7	0.9	132	4	ABM11237	Abm11237 Human pho
155	7	0.9	61	6	ABM62272	Abm62272 Propionib	226	7	0.9	132	4	ABM11237	Abm11237 Human pho
156	7	0.9	69	4	ABM88690	Abm88690 Human imm	227	7	0.9	132	4	ABM11237	Abm11237 Human pho
157	7	0.9	75	7	ADC00302	Adc00302 Enterohae	228	7	0.9	132	4	ABM11237	Abm11237 Human pho
158	7	0.9	76	6	ABU15436	Abu15436 Protein e	229	7	0.9	132	4	ABM11237	Abm11237 Human pho
159	7	0.9	78	4	AAU90288	Aau90288 Human imm	230	7	0.9	132	4	ABM11237	Abm11237 Human pho
160	7	0.9	82	5	ABP33075	Abp33075 Human ORF	231	7	0.9	132	4	ABM11237	Abm11237 Human pho
161	7	0.9	83	4	AAU60561	Aau60561 Propionib	232	7	0.9	132	4	ABM11237	Abm11237 Human pho
162	7	0.9	85	6	ABM57080	Abm57080 Propionib	233	7	0.9	132	4	ABM11237	Abm11237 Human pho
163	7	0.9	85	6	ADN42710	Adn42710 Bacterial	234	7	0.9	132	4	ABM11237	Abm11237 Human pho
164	7	0.9	86	6	ADA34965	Ada34965 Acinetoba	235	7	0.9	132	4	ABM11237	Abm11237 Human pho
165	7	0.9	86	7	ABO63968	AbO63968 Klebsiell	236	7	0.9	132	4	ABM11237	Abm11237 Human pho
166	7	0.9	87	4	AAU17729	Aau17729 Novel hum	237	7	0.9	132	4	ABM11237	Abm11237 Human pho
167	7	0.9	87	7	ADG41109	Adg41109 Human res	238	7	0.9	132	4	ABM11237	Abm11237 Human pho
168	7	0.9	87	7	ADI96883	Adi96883 Human res	239	7	0.9	132	4	ABM11237	Abm11237 Human pho
169	7	0.9	88	3	AAU86404	Aau86404 Human gen	240	7	0.9	132	4	ABM11237	Abm11237 Human pho
170	7	0.9	88	6	ABO53551	AbO53551 Novel hum	241	7	0.9	132	4	ABM11237	Abm11237 Human pho
171	7	0.9	92	7	ADE08224	Ade08224 Novel pro	242	7	0.9	132	4	ABM11237	Abm11237 Human pho
							243	7	0.9	132	4	ABM11237	Abm11237 Human pho
							244	7	0.9	132	4	ABM11237	Abm11237 Human pho
							244	7	0.9	132	4	ABM11237	Abm11237 Human pho

245	7	0.9	294	7	ADC94620	Adc94620 E. faeciu	318	7	0.9	416	6	ABM72077	Abm72077 Staphyloc
246	7	0.9	300	7	ABO63156	Aboc63156 Klebsiell	319	7	0.9	417	4	ABG03334	Abg03334 Novel hum
247	7	0.9	305	8	ADN17987	Adn17987 Bacterial	320	7	0.9	418	5	ABP27080	Abp27080 Streptoco
248	7	0.9	307	3	AGS22488	Agst22488 Arabidops	321	7	0.9	420	4	ABG62035	Abg62035 P. furios
249	7	0.9	310	8	ADS23653	Adst23653 Bacterial	322	7	0.9	420	8	ADM47143	Adm47143 Thermococ
250	7	0.9	314	3	AGG21404	Aggt21404 Arabidops	323	7	0.9	423	4	ABG28086	Abg28086 Novel hum
251	7	0.9	315	4	AGG74783	Aggt74783 Human col	324	7	0.9	423	3	AAU44389	AAu44389 Zea mays
252	7	0.9	315	5	ABB91630	Abb91630 Herbicida	325	7	0.9	426	8	ADN21982	Adn21982 Bacterial
253	7	0.9	318	6	ABM67272	Abm67272 Phototrab	326	7	0.9	429	6	ABU23542	Abu23542 Protein e
254	7	0.9	320	2	AAR33279	Aar33279 43 KD end	327	7	0.9	430	6	ABM68699	Abm68699 Phototrab
255	7	0.9	324	4	AAU38302	Aau38302 Salmonell	328	7	0.9	432	4	ABU96771	Abu96771 Putative
256	7	0.9	324	6	ABU48397	Abu48397 Protein e	329	7	0.9	433	6	ABU21968	Abu21968 Protein e
257	7	0.9	325	4	ABG79630	Abg79630 Corynebac	330	7	0.9	434	7	ABO78489	Abot78489 Pseudomon
258	7	0.9	325	4	AAU91087	Aau91087 C glutami	331	7	0.9	434	8	ADN24740	Adn24740 Bacterial
259	7	0.9	327	5	ABB89542	Abb89542 Human pol	332	7	0.9	436	5	ABU50710	Abu50710 Helicobac
260	7	0.9	327	7	ABO81872	Aboc81872 Pseudomon	333	7	0.9	437	5	AAU47762	AAu47762 RNA bindi
261	7	0.9	328	5	ABU51082	Abu51082 Helicobac	334	7	0.9	441	7	ADH86636	Adh86636 Enterococ
262	7	0.9	329	3	ABAS2512	Abas2512 Helicobac	335	7	0.9	442	5	ABB72317	Abb72317 Rat prote
263	7	0.9	335	5	AAU93075	Aau93075 Arabidops	336	7	0.9	444	4	AAU03821	AAu03821 G protein
264	7	0.9	335	7	ADD30801	Add30801 Plant vie	337	7	0.9	444	4	ABG08390	Abg08390 Novel hum
265	7	0.9	335	8	ADI14831	Adi14831 Plant tra	338	7	0.9	444	8	ADN24258	Adn24258 Bacterial
266	7	0.9	336	8	ADI27927	Adi27927 Murine pr	339	7	0.9	448	4	AAU20358	AAu20358 Human sec
267	7	0.9	337	3	AAU96738	Aau96738 Streptoco	340	7	0.9	448	7	ABR76885	Abt76885 A. gossyp
268	7	0.9	337	5	ABP26971	Abp26971 Streptoco	341	7	0.9	448	8	ADN47683	Adn47683 Thermococ
269	7	0.9	337	5	ABP26970	Abp26970 Streptoco	342	7	0.9	448	8	ADN21452	Adn21452 Bacterial
270	7	0.9	337	5	ABB90355	Abb90355 Human pol	343	7	0.9	456	8	ADP31476	Adp31476 Human sec
271	7	0.9	337	6	ABU46738	Abu46738 Protein e	344	7	0.9	456	8	ADS41854	Ads41854 Bacterial
272	7	0.9	341	4	ABG65050	Abg65050 Drosophil	345	7	0.9	458	5	ABU42209	Abu42209 Protein e
273	7	0.9	341	4	ABG17128	Abg17128 Novel hum	346	7	0.9	459	6	ABU42209	Abu42209 Protein e
274	7	0.9	342	5	ADR19670	Adr19670 Human dru	347	7	0.9	459	6	ABU42209	Abu42209 Protein e
275	7	0.9	349	6	ABU23963	Abu23963 Protein e	348	7	0.9	460	4	AAU41439	AAu41439 Human pol
276	7	0.9	351	7	ABO62898	Aboc62898 Klebsiell	349	7	0.9	464	3	ABU15924	Abu15924 E. coli p
277	7	0.9	351	8	ADN37568	Adn37568 Glycopept	350	7	0.9	464	6	ABU98971	Abu98971 E. coli g
278	7	0.9	351	8	ADN21155	Adn21155 Bacterial	351	7	0.9	464	6	ABU14689	Abu14689 Protein e
279	7	0.9	352	8	ABM83397	Abm83397 Human dia	352	7	0.9	464	7	ADC31497	Adc31497 Human nov
280	7	0.9	353	8	ABM83396	Abm83396 Human dia	353	7	0.9	465	7	ABO80641	Aboc80641 Pseudomon
281	7	0.9	353	8	ABM83395	Abm83395 Human dia	354	7	0.9	466	4	AAU62912	AAu62912 Propionib
282	7	0.9	355	2	AAU74758	Aau74758 Beta-keto	355	7	0.9	466	6	AAU59431	AAu59431 Propionib
283	7	0.9	355	2	AAU31945	Aau31945 Polynhydro	356	7	0.9	469	8	ADS24348	Ads24348 Bacterial
284	7	0.9	355	6	ABM73087	Abm73087 Staphyloc	357	7	0.9	472	3	AAU18420	AAu18420 Amino aci
285	7	0.9	355	6	AAE38417	Aae38417 Arabidops	358	7	0.9	473	6	ADA33992	Ada33992 Acinetoba
286	7	0.9	356	6	ADA34127	Ada34127 Acinetoba	359	7	0.9	478	5	ABR66297	Abt66297 Drosophil
287	7	0.9	356	6	ABU24320	Abu24320 Protein e	360	7	0.9	478	5	ABR38839	Abt38839 A. niger
288	7	0.9	357	7	ABO84393	Aboc84393 Pseudomon	361	7	0.9	482	4	ADM19812	Adm19812 Protein e
289	7	0.9	359	6	ABE36463	Abec36463 Human col	362	7	0.9	485	5	ADJ33852	Adj33852 Protein o
290	7	0.9	359	8	ADP55871	Adp55871 Human PRO	363	7	0.9	490	2	AAU33929	AAu33929 Leukotoxi
291	7	0.9	366	2	AAW69392	Aaw69392 Aspergill	364	7	0.9	490	6	ADA28694	Ada28694 Plasmid p
292	7	0.9	366	8	ADN18365	Adn18365 Bacterial	365	7	0.9	497	4	AAU37751	AAu37751 Streptoco
293	7	0.9	367	7	ADI60171	Adi60171 Secreted	366	7	0.9	497	6	ABU01284	Abu01284 S. pneumo
294	7	0.9	382	2	AAU45261	Aau45261 Human sec	367	7	0.9	497	6	ABU45988	Abu45988 Protein e
295	7	0.9	383	4	AAU91116	Aau91116 C glutami	368	7	0.9	497	8	ADK48573	Adk48573 Streptoco
296	7	0.9	386	4	ABG21113	Abg21113 Novel hum	369	7	0.9	497	8	ADM92139	Adm92139 S pneumon
297	7	0.9	386	8	ADN26073	Adn26073 Bacterial	370	7	0.9	504	8	ADR95097	Adr95097 Novel S.
298	7	0.9	387	7	ADI60400	Adi60400 Secreted	371	7	0.9	514	6	ABJ20237	Abj20237 Human IG
299	7	0.9	387	8	ADP31368	Adp31368 Human sec	372	7	0.9	517	3	AAU32390	AAu32390 Herpesvir
300	7	0.9	390	6	ABU20261	Abu20261 Protein e	373	7	0.9	517	5	AAE23294	AAe23294 Human nec
301	7	0.9	392	8	ADP29346	Adp29346 Human sec	374	7	0.9	518	8	ABG77170	Abg77170 Prostate
302	7	0.9	393	7	ABO68025	Aboc68025 Pseudomon	375	7	0.9	518	8	ADS29669	Ads29669 Bacterial
303	7	0.9	397	2	AAU29659	Aau29659 Homo sapi	376	7	0.9	521	6	ABU35710	Abu35710 Protein e
304	7	0.9	399	4	AAU32410	Aau32410 Novel hum	377	7	0.9	522	6	ABU22090	Abu22090 Protein e
305	7	0.9	399	7	ABO69686	Aboc69686 Pseudomon	378	7	0.9	527	6	ABU19551	Abu19551 Protein e
306	7	0.9	399	8	ADP31313	Adp31313 Human sec	379	7	0.9	528	4	ABR71669	Abt71669 Drosophil
307	7	0.9	405	4	AAU93419	Aau93419 Human pro	380	7	0.9	529	7	ADG61129	Adg61129 Baeyer-Vi
308	7	0.9	405	8	ADN25996	Adn25996 Bacterial	381	7	0.9	531	8	ADP30594	Adp30594 Human sec
309	7	0.9	405	8	ADS42259	Ads42259 Bacterial	382	7	0.9	531	8	ADP31696	Adp31696 Human sec
310	7	0.9	406	4	AAU39653	Aau39653 Human pol	383	7	0.9	544	2	AAW03943	Aaw03943 LKT-GNRH
311	7	0.9	409	6	ABU96684	Abu96684 Human nuc	384	7	0.9	544	2	AAW79570	Aaw79570 LKT-GNRH
312	7	0.9	410	5	ABP29775	Abp29775 Streptoco	385	7	0.9	551	8	ADQ65217	Adq65217 Novel hum
313	7	0.9	410	5	ABP30545	Abp30545 Streptoco	386	7	0.9	559	7	ABO75946	Abot75946 Pseudomon
314	7	0.9	411	8	ADS23906	Adst23906 Bacterial	387	7	0.9	560	4	AAU78929	AAu78929 Human pro
315	7	0.9	413	4	AAU41340	Aau41340 Propionib	388	7	0.9	562	4	ABE64878	Abt64878 Drosophil
316	7	0.9	413	6	ABM37859	Abm37859 Propionib	389	7	0.9	564	6	ABJ37094	Abj37094 Low-affin
317	7	0.9	416	6	ABU42300	Abu42300 Protein e	390	7	0.9	566	6	AAE35922	AAe35922 Human All

391	7	0.9	568	5	ABU51967	Abu51967 Helicobac	464	7	0.9	792	8	ADH12911	Adh12911 Francisel
392	7	0.9	568	5	ABP74083	Abp74083 Candida a	465	7	0.9	797	8	ADS23447	Ads23447 Bacterial
393	7	0.9	572	6	ABJ37095	Abj37095 Low-affin	466	7	0.9	799	3	AAV92061	Aav92061 Human APC
394	7	0.9	572	7	ADC07800	Adc07800 Rice prot	467	7	0.9	809	2	AAV29672	Aav29672 Human cer
395	7	0.9	572	7	ADF74126	Adf74126 Human nov	468	7	0.9	816	8	ADP31581	Adp31581 Human sec
396	7	0.9	573	4	ABB60673	Abb60673 Drosophil	468	7	0.9	818	4	AAV92737	Aav92737 C glutami
397	7	0.9	576	7	ABO74500	Abp74500 Pseudomon	469	7	0.9	821	7	ABO72267	Abp72267 Pseudomon
398	7	0.9	578	8	ADP03592	Adp03592 Infection	470	7	0.9	823	4	ABB71484	Abb71484 Drosophil
399	7	0.9	579	4	ABG24250	Abg24250 Novel hum	471	7	0.9	824	7	ABO72267	Abp72267 Pseudomon
400	7	0.9	580	5	AAG66008	Aag66008 F. necrop	472	7	0.9	827	7	ADF06140	Adf06140 Bacterial
401	7	0.9	580	8	ADO47877	Ado47877 Alpha-her	473	7	0.9	850	4	ABBS2809	Abbs2809 Escherich
402	7	0.9	581	8	ADP03590	Adp03590 Infection	474	7	0.9	861	8	ADP31340	Adp31340 Human sec
403	7	0.9	584	6	ABU19765	Abu19765 Protein e	475	7	0.9	870	8	ADP30646	Adp30646 Human sec
404	7	0.9	587	8	AAU78928	Aau78928 Human pro	476	7	0.9	874	6	ABU33564	Abu33564 Protein e
405	7	0.9	587	5	AAU82982	Aau82982 Human hom	477	7	0.9	892	8	ADP31578	Adp31578 Human sec
406	7	0.9	587	5	AAU10799	Aau10799 Polymorph	478	7	0.9	897	4	ABBE2261	Abbe2261 Drosophil
407	7	0.9	587	5	AAU10796	Aau10796 Reference	479	7	0.9	908	6	ABU08492	Abu08492 Alpha-hel
408	7	0.9	587	5	AAU10797	Aau10797 Polymorph	480	7	0.9	914	6	ABU08604	Abu08604 Neisseria
409	7	0.9	587	5	AAU10798	Aau10798 Polymorph	481	7	0.9	921	2	AAW72033	Aaw72033 HSV-2 str
410	7	0.9	587	8	ADL17020	Adl17020 Human Ran	482	7	0.9	924	2	AAU10889	Aau10889 Leukotoxi
411	7	0.9	587	8	ADQ88017	Adq88017 Human Ran	483	7	0.9	924	2	AAU10889	Aau10889 Leukotoxi
412	7	0.9	587	8	ABM82366	Abm82366 Tumour-as	484	7	0.9	924	2	AAU423380	Aau423380 Recombina
413	7	0.9	589	7	ADB85263	Adb85263 Mouse RNA	485	7	0.9	924	2	AAU423380	Aau423380 Recombina
414	7	0.9	596	8	ADN99873	Adn99873 Novel hum	486	7	0.9	925	5	AAO14246	Aao14246 Human pre
415	7	0.9	596	8	ADN99872	Adn99872 Novel hum	487	7	0.9	926	2	AAU14482	Aau14482 LKT352. 1
416	7	0.9	609	3	AAU73487	Aau73487 Human sec	488	7	0.9	926	2	AAU34545	Aau34545 Leukotoxi
417	7	0.9	614	6	ADA333217	Ada333217 Acinetoba	489	7	0.9	926	2	AAU03945	Aau03945 P. haemol
418	7	0.9	614	8	ADH48376	Adh48376 Human KPP	490	7	0.9	926	2	AAU03945	Aau03945 P. haemol
419	7	0.9	619	8	ADN23202	Adn23202 Bacterial	491	7	0.9	926	2	AAU79568	Aau79568 Leukotoxi
420	7	0.9	620	2	AAU77275	Aau77275 ORC2 subu	492	7	0.9	932	8	ADRO8677	Adro8677 Human pro
421	7	0.9	620	2	AAW22225	Aaw22225 S. cerevi	493	7	0.9	933	7	ABM85855	Abm85855 Human pro
422	7	0.9	620	5	AAU82999	Aau82999 S. cerevi	494	7	0.9	933	8	ADN03759	Adn03759 Antipsori
423	7	0.9	620	6	ABR53643	AbR53643 Protein s	495	7	0.9	934	2	AAW07637	Aaw07637 P. suis 1
424	7	0.9	620	7	ADR64130	Adr64130 Disease t	496	7	0.9	936	2	AAU34547	Aau34547 GnrH-Leuk
425	7	0.9	620	8	ADN18789	Adn18789 Bacterial	497	7	0.9	937	8	ADH13664	Adh13664 Human ENZ
426	7	0.9	621	7	ABO70379	Abp70379 Pseudomon	498	7	0.9	943	2	AAU34546	Aau34546 Somatosta
427	7	0.9	622	5	ABP61455	Abp61455 Human NF-	499	7	0.9	949	4	AAU68553	Aau68553 Human GTP
428	7	0.9	622	6	ABR41026	AbR41026 Human MAP	500	7	0.9	950	4	AAU73355	Aau73355 Human mes
429	7	0.9	623	4	AAU79912	Aau79912 Human pro	501	7	0.9	951	4	AAU34548	Aau34548 Rotavirus
430	7	0.9	623	4	AAU79913	Aau79913 Human pro	502	7	0.9	951	4	AAU73356	Aau73356 Rat meg-1
431	7	0.9	625	8	ADS44452	Ads44452 Bacterial	503	7	0.9	951	4	AAU79261	Aau79261 Human pro
432	7	0.9	627	4	ABG18262	Abg18262 Novel hum	504	7	0.9	953	2	AAU07167	Aau07167 105kD PTX
433	7	0.9	628	4	ABG23677	Abg23677 Novel hum	505	7	0.9	953	2	AAU15159	Aau15159 Leukotoxi
434	7	0.9	632	5	AAO19378	Aao19378 Human pal	506	7	0.9	953	2	AAU43865	Aau43865 Leukotoxi
435	7	0.9	632	5	ABP61456	Abp61456 Human NF-	507	7	0.9	953	2	AAU60072	Aau60072 PtxA prot
436	7	0.9	649	4	ABG61237	Abg61237 Drosophil	508	7	0.9	953	4	AAE04638	Aae04638 Pasteurel
437	7	0.9	663	6	AAU72491	Aau72491 Protein e	509	7	0.9	956	6	ABU08602	Abu08602 Neisseria
438	7	0.9	665	4	AAU78876	Aau78876 Human pro	510	7	0.9	963	4	AAU78880	Aau78880 Human pro
439	7	0.9	666	4	AAU79657	Aau79657 Corynebac	511	7	0.9	963	7	ADB67089	Adb67089 Kinesin h
440	7	0.9	666	4	AAU71885	Aau71885 C. glutam	512	7	0.9	963	7	ADB67091	Adb67091 Kinesin h
441	7	0.9	667	4	ABG16901	Abg16901 Novel hum	513	7	0.9	964	8	ADL99362	Adl99362 Nanostruc
442	7	0.9	667	4	AAU32908	Aau32908 Novel hum	514	7	0.9	964	8	ADL99362	Adl99362 Nanostruc
443	7	0.9	671	2	AAU38505	Aau38505 Streptoco	515	7	0.9	967	4	AAU80245	Aau80245 Human pro
444	7	0.9	671	2	AAU85917	Aau85917 S. pneumo	516	7	0.9	969	6	AAE34448	Aae34448 Human lip
445	7	0.9	671	8	ADK47127	Adk47127 Streptoco	517	7	0.9	977	2	AAU03942	Aau03942 LKT-GnrH
446	7	0.9	673	5	AAE25082	Aae25082 Human kin	518	7	0.9	977	2	AAU79569	Aau79569 LKT-GnrH
447	7	0.9	676	8	ADR95463	Adr95463 Novel S.	519	7	0.9	978	7	ADM05468	Adm05468 Human pro
448	7	0.9	686	6	ABU39853	Abu39853 Protein e	520	7	0.9	983	5	ABU77509	Abu77509 Trameetes
449	7	0.9	692	8	ADN26147	Adn26147 Bacterial	521	7	0.9	983	5	ABU77509	Abu77509 Trameetes
450	7	0.9	695	3	AAU79573	Aau79573 LKT-GnrH	522	7	0.9	998	2	AAU38822	Aau38822 Neisseria
451	7	0.9	695	3	AAU58361	Aau58361 Leukotoxi	523	7	0.9	1004	8	ADO18816	Ado18816 Human lip
452	7	0.9	695	3	AAU58133	Aau58133 Gonadotro	524	7	0.9	1016	4	AAG90609	Aag90609 C glutami
453	7	0.9	699	7	ABO68327	Abp68327 Pseudomon	525	7	0.9	1016	6	ABU41567	Abu41567 Protein e
454	7	0.9	702	5	ABP65679	Abp65679 Bifidobac	526	7	0.9	1017	8	ADP31268	Adp31268 Human sec
455	7	0.9	705	4	AAU79860	Aau79860 Human pro	527	7	0.9	1019	7	ADJ69855	Adj69855 Human hea
456	7	0.9	710	8	ADP30746	Adp30746 Human sec	528	7	0.9	1050	8	ADP31376	Adp31376 Human sec
457	7	0.9	717	8	ABG61609	Abg61609 Drosophil	529	7	0.9	1054	5	ABU79311	Abu79311 Human ova
458	7	0.9	731	6	ADO07924	Ado07924 Fly polyp	530	7	0.9	1069	2	AAU52748	Aau52748 Bovine IF
459	7	0.9	731	6	ABU52070	Abu52070 Helicobac	531	7	0.9	1069	2	AAU13867	Aau13867 Chimeric
460	7	0.9	741	5	ABU42146	Abu42146 Helicobac	532	7	0.9	1069	3	AAU21074	Aau21074 Bovine ga
461	7	0.9	761	5	ABU77431	Abu77431 Human tum	533	7	0.9	1076	5	ABP69070	Abp69070 Human pol
462	7	0.9	792	4	ABG15703	Abg15703 Novel hum	534	7	0.9	1078	4	ABM61597	Abm61597 Drosophil
463	7	0.9	792	7	ABM5854	Abm5854 Mouse pro	535	7	0.9	1088	4	AAU78676	Aau78676 Human pro
										1098	2	AAU22103	Aau22103 Bovine IL

537	7	0.9	1098	2	AAR52747	Aar52747 Bovine IL	610	7	0.9	1628	4	ABG02195	Abg02195 Novel hum
538	7	0.9	1098	2	AAR13866	Aar13866 Chimeric	611	7	0.9	1686	2	AAW70991	Aaw70991 Human cla
539	7	0.9	1098	2	AAR21073	Aar21073 Bovine IL	612	7	0.9	1586	6	ABJ19811	Abj19811 Androgen-
540	7	0.9	1116	8	ADP31692	Adp31692 Human sec	613	7	0.9	1725	8	ADF30654	Adf30654 Human sec
541	7	0.9	1121	5	AAE20419	Aae20419 Human cdc	614	7	0.9	1833	8	ADF30642	Adf30642 Human sec
542	7	0.9	1121	8	ADJ66576	Adj66576 WD-repeat	615	7	0.9	1846	6	ABR39833	Abr39833 Human sca
543	7	0.9	1129	7	ABO79806	AbO79806 Pseudomon	616	7	0.9	1896	6	AAW72095	Aaw72095 HSV-2 str
544	7	0.9	1132	2	AAR77417	Aar77417 Human cel	617	7	0.9	1912	7	ADC32623	Adc32623 Human NOV
545	7	0.9	1132	2	ADD71144	Add71144 Human int	618	7	0.9	1943	6	ABU30826	Abu30826 Protein e
546	7	0.9	1136	6	ABU08605	Abu08605 Neisseria	619	7	0.9	1956	8	ADN00371	Adn00371 Novel hum
547	7	0.9	1139	5	ABG97360	Abg97360 Human CGD	620	7	0.9	1974	2	AAW98391	Aaw98391 H. pylori
548	7	0.9	1156	3	ABJ10104	Abj10104 Feline fo	621	7	0.9	1984	4	ABG01338	Abg01338 Novel hum
549	7	0.9	1161	5	ABG97354	Abg97354 Human CGD	622	7	0.9	2274	4	ABO50674	Abo50674 Mouse APC
550	7	0.9	1178	6	ABU08603	Abu08603 Neisseria	623	7	0.9	2274	8	ADO08047	Ado08047 Mouse pol
551	7	0.9	1187	8	ADJ49198	Adj49198 Oil-associ	624	7	0.9	2303	6	ABR58648	Abr58648 Human can
552	7	0.9	1197	8	ADP31342	Adp31342 Human sec	625	7	0.9	2303	8	ADO08045	Ado08045 Human pol
553	7	0.9	1216	5	AAE22860	Aae22860 Human pho	626	7	0.9	2338	8	ABO58348	Abo58348 Human gen
554	7	0.9	1268	4	ABB61314	Abb61314 Drosophil	627	7	0.9	2349	8	ADP30959	Adp30959 Human sec
555	7	0.9	1269	8	ADP31500	Adp31500 Human sec	628	7	0.9	2382	8	ADP31341	Adp31341 Human sec
556	7	0.9	1296	2	AAW47157	Aaw47157 Nevoid ba	629	7	0.9	2431	2	AAR25138	Aar25138 SFV4 non-
557	7	0.9	1320	5	AAW47603	Aaw47603 Drosophil	630	7	0.9	2732	4	ABR52855	Abr52855 Escherich
558	7	0.9	1334	2	AAR14481	Aar14481 LkA:lacZ	631	7	0.9	2834	5	ABG97576	Abg97576 Haemagglu
559	7	0.9	1334	2	AAW50290	Aaw50290 lktA::lac	632	7	0.9	2834	7	ADH80652	Adh80652 Escherich
560	7	0.9	1336	7	ADJ92014	Adj92014 Semliki f	633	7	0.9	3119	2	AAW72204	Aaw72204 HSV-2 str
561	7	0.9	1390	6	ABP60436	Abp60436 Human and	634	7	0.9	3122	7	ADG75178	Adg75178 Human her
562	7	0.9	1396	8	ADN01130	Adn01130 Human cel	635	7	0.9	3122	7	ADG75129	Adg75129 Human her
563	7	0.9	1403	2	AAR10890	Aar10890 lktA::lac	636	7	0.9	3194	6	ABU31122	Abu31122 Protein e
564	7	0.9	1403	2	AAW79574	Aaw79574 Leukotoxi	637	7	0.9	3339	8	ADP31219	Adp31219 Human sec
565	7	0.9	1419	5	ABU65081	Abu65081 Human NOV	638	7	0.9	3407	8	ADP31060	Adp31060 Human sec
566	7	0.9	1419	8	ADH42427	Adh42427 Novel hum	639	7	0.9	3407	8	ADP31062	Adp31062 Human sec
567	7	0.9	1419	8	ADN61813	Adn61813 Human nov	640	7	0.9	3477	8	ADP30704	Adp30704 Human sec
568	7	0.9	1423	5	ABU65083	Abu65083 Human NOV	641	7	0.9	3579	8	ADP31098	Adp31098 Human sec
569	7	0.9	1423	8	ADH42431	Adh42431 Novel hum	642	7	0.9	4106	8	ABG99872	Abg99872 S. Clinam
570	7	0.9	1423	8	ADN61817	Adn61817 Human nov	643	7	0.9	4752	8	ADP30585	Adp30585 Human sec
571	7	0.9	1433	8	ADO18815	Ado18815 Human lip	644	7	0.9	4752	5	AAO22158	Aao22158 Ramoplani
572	7	0.9	1434	2	AAR94380	Aar94380 Mouse pat	645	7	0.9	4999	5	AAO22158	Aao22158 Ramoplani
573	7	0.9	1434	2	AAW52199	Aaw52199 Mouse pat	646	7	0.9	5304	8	ADP30706	Adp30706 Human sec
574	7	0.9	1434	2	AAW72968	Aaw72968 Mouse pat	647	7	0.9	5304	8	ADP30705	Adp30705 Human sec
575	7	0.9	1434	4	AAB67159	Aab67159 Murine pa	648	7	0.9	8026	6	AAE35489	Aae35489 Streptomy
576	7	0.9	1434	5	AAG79572	Agg79572 Mouse pat	649	7	0.9	8976	8	ADP31425	Adp31425 Human sec
577	7	0.9	1434	7	ABU62271	Abu62271 Mouse pat	650	7	0.9	9195	8	ADP31494	Adp31494 Human sec
578	7	0.9	1434	7	ADH94215	Adh94215 Murine pt	651	7	0.9	10944	8	ADP31311	Adp31311 Human sec
579	7	0.9	1434	7	ADH62722	Adh62722 Mouse pat	652	7	0.9	11328	8	ADP31310	Adp31310 Human sec
580	7	0.9	1434	8	ADE48980	Ade48980 Mouse pat	653	6	0.8	6	4	AAU03972	Aau03972 Neisseria
581	7	0.9	1439	2	AAU7557	Aau7557 Neisseria	654	6	0.8	6	4	AAU03989	Aau03989 Neisseria
582	7	0.9	1447	2	AAR75375	Aar75375 Human pat	655	6	0.8	6	4	AAU04415	Aau04415 Neisseria
583	7	0.9	1447	2	AAW52200	Aaw52200 Human pat	656	6	0.8	6	4	AAU03962	Aau03962 Neisseria
584	7	0.9	1447	2	AAW72969	Aaw72969 Human pat	657	6	0.8	6	4	AAU03968	Aau03968 Neisseria
585	7	0.9	1447	4	AAB67163	Aab67163 Human pat	658	6	0.8	6	4	AAU04431	Aau04431 Neisseria
586	7	0.9	1447	5	AAE19830	Aae19830 Human pat	659	6	0.8	6	4	AAU03983	Aau03983 Neisseria
587	7	0.9	1447	5	ABJ10931	Abj10931 TRC8 rela	660	6	0.8	7	2	AAK44781	Aak44781 Sequence
588	7	0.9	1447	5	AAG79571	Agg79571 Human pat	661	6	0.8	7	2	AAK44782	Aak44782 Sequence
589	7	0.9	1447	7	ABU62275	Abu62275 Human pat	662	6	0.8	7	4	AAE62826	Aae62826 Fibrinoge
590	7	0.9	1447	7	ADH46678	Adh46678 Human Pro	663	6	0.8	7	4	AAE62826	Aae62826 Fibrinoge
591	7	0.9	1447	7	ADH46224	Adh46224 Human ptc	664	6	0.8	7	5	AAO21220	Aao21220 Absorptio
592	7	0.9	1447	7	ADH62731	Adh62731 Human pat	665	6	0.8	8	2	AAK73428	Aak73428 Human TSH
593	7	0.9	1447	8	ADE48989	Ade48989 Human pat	666	6	0.8	8	5	AAO21222	Aao21222 Absorptio
594	7	0.9	1449	2	AAK38824	Aak38824 Neisseria	667	6	0.8	9	2	AAK38824	Aak38824 Selectin
595	7	0.9	1449	6	ABU37787	Abu37787 Protein e	668	6	0.8	9	5	ABB94918	Abb94918 CTL epit
596	7	0.9	1454	3	AAU56621	Aau56621 Neisseria	669	6	0.8	9	5	ABR94587	Abr94587 CTL epit
597	7	0.9	1457	2	AAK38823	Aak38823 Neisseria	670	6	0.8	9	5	ABR95084	Abr95084 CTL epit
598	7	0.9	1457	3	AAK38823	Aak38823 Neisseria	671	6	0.8	9	5	ABR94690	Abr94690 CTL epit
599	7	0.9	1457	3	AAK38823	Aak38823 Neisseria	672	6	0.8	9	5	AAO21237	Aao21237 Absorptio
600	7	0.9	1457	3	AAK38823	Aak38823 Neisseria	673	6	0.8	9	8	ADP25609	Adp25609 Plasmodiu
601	7	0.9	1457	4	AAU27556	Aau27556 Neisseria	674	6	0.8	10	2	AAK38824	Aak38824 Selectin
602	7	0.9	1457	6	ABU08601	Abu08601 Neisseria	675	6	0.8	10	2	AAK38825	Aak38825 Selectin
603	7	0.9	1458	5	ABO9556	Abo9556 Human lip	676	6	0.8	10	2	AAK38833	Aak38833 Selectin
604	7	0.9	1458	5	ABO9555	Abo9555 Human lip	677	6	0.8	10	2	AAK38834	Aak38834 Selectin
605	7	0.9	1458	6	ADP31437	Adp31437 Human sec	678	6	0.8	10	2	AAK50817	Aak50817 Cyclic pe
606	7	0.9	1464	8	ADP31437	Adp31437 Human sec	679	6	0.8	10	4	AAK50817	Aak50817 Cyclic pe
607	7	0.9	1468	2	ABP38825	Abp38825 Neisseria	680	6	0.8	10	4	AAK50817	Aak50817 Cyclic pe
608	7	0.9	1468	6	ABP77279	Abp77279 N. gonorr	681	6	0.8	10	4	AAK50817	Aak50817 Cyclic pe
609	7	0.9	1468	6	ABU37103	Abu37103 Protein e	682	6	0.8	10	5	ABR95044	Abr95044 CTL epit

683	6	0.8	10	5	ABB94737	Abb94737 CTL epit	756	6	0.8	34	2	AAM65997	Aaw65997 Parathyro
684	6	0.8	10	5	ABB94739	Abb94739 CTL epit	757	6	0.8	34	2	AAM91893	Aaw91893 Synthetic
685	6	0.8	10	5	ABB94944	Abb94944 CTL epit	758	6	0.8	34	2	AAW74357	Aaw74357 Modified
686	6	0.8	10	5	ABB94629	Abb94629 CTL epit	759	6	0.8	34	3	AAB38530	Aab38530 Human sec
687	6	0.8	10	8	ADK06129	Adk06129 Hepatitis	760	6	0.8	34	5	AAU73134	Aau73134 Parathyro
688	6	0.8	12	2	AAU721275	Aay21275 Human sem	761	6	0.8	34	5	AAU73100	Aau73100 Parathyro
689	6	0.8	12	6	ABP98955	Abp98955 ErbB2 cel	762	6	0.8	34	5	AAU73101	Aau73101 Parathyro
690	6	0.8	13	2	AAW23015	Aaw23015 R4 recept	763	6	0.8	34	6	ABU42245	Abu42245 Protein e
691	6	0.8	13	6	ABP98589	Abp98589 Beta-barr	764	6	0.8	34	8	ADH35573	Adh35573 Human par
692	6	0.8	14	4	ABBS6739	Abbs6739 Human SNP	765	6	0.8	34	8	ADH35571	Adh35571 Human par
693	6	0.8	15	5	ABP46959	Abp46959 Human BLY	766	6	0.8	34	8	ADQ75415	Adq75415 PTH/PTHrP
694	6	0.8	15	7	ADP32583	Adp32583 Clostridi	767	6	0.8	34	8	ADQ75416	Adq75416 PTH/PTHrP
695	6	0.8	15	7	ADG97786	Adg97786 scFv VHCD	768	6	0.8	34	8	ADQ75449	Adq75449 PTH/PTHrP
696	6	0.8	18	2	AAR40133	Aar40133 Delta'S s	769	6	0.8	35	4	AAO13575	Aao13575 Human pol
697	6	0.8	18	2	AAW36080	Aaw36080 E. coli D	770	6	0.8	36	2	AAR58185	Aar58185 [Lys18]-h
698	6	0.8	18	8	ADL15120	Adl15120 E. coli D	771	6	0.8	36	4	AAW15740	Aaw15740 Peptide #
699	6	0.8	19	2	AAW46341	Aaw46341 Amino aci	772	6	0.8	36	4	AAM15740	Aam15740 Peptide #
700	6	0.8	19	5	ABB07414	Abb07414 Plasmid p	773	6	0.8	36	4	ABB28249	Abb28249 Peptide #
701	6	0.8	19	5	AAO19110	Aao19110 Human cfr	774	6	0.8	36	4	ABB29559	Abb29559 Peptide #
702	6	0.8	20	2	AAW22332	Aaw22332 HIV-1 cli	775	6	0.8	36	4	AAM67923	Aam67923 Human bon
703	6	0.8	20	2	AAW62895	Aaw62895 Peptide s	776	6	0.8	36	4	AAM55539	Aam55539 Human bra
704	6	0.8	21	3	AAW56865	Aay56865 B. catarr	777	6	0.8	36	4	ABG49566	Abg49566 Human liv
705	6	0.8	21	5	ABB07415	Abb07415 Plasmid p	778	6	0.8	36	4	AAM03474	Aam03474 Peptide #
706	6	0.8	21	7	ADC73122	Adc73122 Domain li	779	6	0.8	37	4	AAE00729	Aae00729 Homeodoma
707	6	0.8	22	4	AAB83929	Aab83929 Antigenic	780	6	0.8	38	4	AAW14064	Aaw14064 Peptide #
708	6	0.8	23	6	ADA11828	Ada11828 Human nov	781	6	0.8	38	4	ABB33009	Abb33009 Peptide #
709	6	0.8	24	5	AAU73141	Aau73141 Parathyro	782	6	0.8	38	4	AAM26470	Aam26470 Peptide #
710	6	0.8	24	5	AAU73142	Aau73142 Parathyro	783	6	0.8	38	4	ABB27838	Abb27838 Human pep
711	6	0.8	24	8	ADQ75456	Adq75456 PTH/PTHrP	784	6	0.8	38	4	ABB18482	Abb18482 Protein #
712	6	0.8	24	8	ADQ75457	Adq75457 PTH/PTHrP	785	6	0.8	38	4	AAM66193	Aam66193 Human bon
713	6	0.8	26	4	AAM99735	Aam99735 Human exc	786	6	0.8	38	4	ABG47861	Abg47861 Human liv
714	6	0.8	26	4	AAW42550	Aaw42550 Human kid	787	6	0.8	38	4	ABG47861	Abg47861 Human liv
715	6	0.8	28	2	AAW54400	Aaw54400 MAGE-10 t	788	6	0.8	38	4	AAW01804	Aaw01804 Peptide #
716	6	0.8	28	3	AAW50402	Aay65042 Human 5'	789	6	0.8	38	5	ABG35843	Abg35843 Human pep
717	6	0.8	28	3	AAW99875	Aay99875 Human MAG	790	6	0.8	38	8	ADN46506	Adn46506 Thermococ
718	6	0.8	28	4	AAO13828	Aao13828 Human pol	791	6	0.8	39	3	AAW80174	Aaw80174 MiSP1-der
719	6	0.8	28	5	AAU73105	Aau73105 Parathyro	792	6	0.8	39	3	AAW55704	Aay55704 M. genita
720	6	0.8	28	5	AAU73106	Aau73106 Parathyro	793	6	0.8	39	8	ABO56803	Abo56803 Human nov
721	6	0.8	28	8	ADQ75421	Adq75421 PTH/PTHrP	794	6	0.8	39	8	ABO56803	Abo56803 Human nov
722	6	0.8	28	8	ADQ75420	Adq75420 PTH/PTHrP	795	6	0.8	40	2	AAW85845	Aay85845 S. pneumo
723	6	0.8	29	6	ABJ26817	Abj26817 Endotheli	796	6	0.8	40	5	AAE25415	Aae25415 ZYMV AGII
724	6	0.8	30	5	ABP29400	Abp29400 Streptoco	797	6	0.8	40	8	ADS05943	Ads05943 Staphyloc
725	6	0.8	30	5	AAU73170	Aau73170 Parathyro	798	6	0.8	41	2	AAW85919	Aay85919 S. pneumo
726	6	0.8	30	5	AAU73136	Aau73136 Parathyro	799	6	0.8	41	2	AAW85919	Aay85919 S. pneumo
727	6	0.8	30	5	AAU73137	Aau73137 Parathyro	800	6	0.8	42	4	AAU14818	Aau14818 Novel bon
728	6	0.8	30	8	ADQ75451	Adq75451 PTH/PTHrP	801	6	0.8	42	4	AAE04543	Aae04543 Pacific o
729	6	0.8	30	8	ADQ75485	Adq75485 PTH/PTHrP	802	6	0.8	44	2	AAW42290	Aar42290 Pepstatin
730	6	0.8	30	8	ADQ75452	Adq75452 PTH/PTHrP	803	6	0.8	44	2	AAW87212	Aar87212 Restin de
731	6	0.8	31	2	AAW04222	Aay04222 Human par	804	6	0.8	44	3	AAB16864	Aab16864 Bacteriop
732	6	0.8	31	5	ABB57410	Abb57410 Human sec	805	6	0.8	44	5	ADH32400	Adh32400 Yeast smc
733	6	0.8	31	7	ADI24798	Adi24798 Parathyro	806	6	0.8	44	6	AAM90665	Aam90665 Human imm
734	6	0.8	32	3	AAW58650	Aay58650 Calluna v	807	6	0.8	46	6	ABU00068	Abu00068 Human nov
735	6	0.8	32	3	AAW33972	Aab33972 Human sec	808	6	0.8	46	6	ABU00068	Abu00068 Human nov
736	6	0.8	32	3	AAW44807	Aay44807 Calluna v	809	6	0.8	47	2	AAW80176	Aar80176 MiSP1-der
737	6	0.8	32	4	AAB60746	Aab60746 Human sec	810	6	0.8	47	2	AAW80178	Aar80178 MiSP1-der
738	6	0.8	33	2	AAR60176	Aar60176 MiSP1-der	811	6	0.8	48	2	AAW80172	Aar80172 MiSP1-der
739	6	0.8	33	4	AAW16134	Aam16134 Peptide #	812	6	0.8	48	4	AAO10583	Aao10583 Human pol
740	6	0.8	33	4	AAM28628	Aam28628 Peptide #	813	6	0.8	48	7	ADA49395	Ada49395 Lymphaden
741	6	0.8	33	4	AAM83228	Aam83228 Human imm	814	6	0.8	49	2	AAW80173	Aar80173 MiSP1-der
742	6	0.8	33	4	ABB29945	Abb29945 Peptide #	815	6	0.8	49	3	AAW12570	Aag12570 Zea mays
743	6	0.8	33	4	ABB20544	Abb20544 Protein #	816	6	0.8	49	8	ADL97663	Adl97663 Protein e
744	6	0.8	33	4	AAM68319	Aam68319 Human bon	817	6	0.8	50	2	AAW80179	Aar80179 MiSP1-der
745	6	0.8	33	4	ABGA49983	Abga49983 Human liv	818	6	0.8	50	2	AAW89339	Aaw89339 Salmonell
746	6	0.8	33	4	AAW03864	Aam03864 Peptide #	819	6	0.8	50	5	ABP06117	Abp06117 Human ORF
747	6	0.8	33	5	ABG77069	Abg77069 Prostate	820	6	0.8	50	7	ABW74476	Abw74476 DNA clone
748	6	0.8	33	5	ABG37869	Abg37869 Human pep	821	6	0.8	51	2	AAW80171	Aar80171 MiSP1-der
749	6	0.8	33	8	ABO59958	Abo59958 Human gen	822	6	0.8	51	2	AAW80182	Aar80182 MiSP1-der
750	6	0.8	34	2	AAR45483	Aar45483 Parathyro	823	6	0.8	51	4	ABB42173	Abb42173 Peptide #
751	6	0.8	34	2	AAW80175	Aar80175 MiSP1-der	824	6	0.8	51	4	ABW42863	Abw42863 Peptide #
752	6	0.8	34	2	AAR69009	Aar69009 PTH analo	825	6	0.8	51	4	AAM35980	Aam35980 Peptide #
753	6	0.8	34	2	AAW13300	Aaw13300 Truncated	826	6	0.8	51	4	AAM36677	Aam36677 Peptide #
754	6	0.8	34	2	AAW12179	Aaw12179 Parathyro	827	6	0.8	51	4	ABB26136	Abb26136 Protein #
755	6	0.8	34	2	AAW61677	Aaw61677 Parathyro	828	6	0.8	51	4	AAW75869	Aam75869 Human bon

829	6	0.8	51	4	AAM76570	Aam76570 Human bon	902	6	0.8	60	5	ABJ10575	Abj10575 Galanin-1
830	6	0.8	51	4	AAM63756	Aam63756 Human bra	903	6	0.8	60	6	ABR44366	Abr44366 Rat antib
831	6	0.8	51	4	AAM63058	Aam63058 Human bra	904	6	0.8	60	8	ADW97216	Adw97216 Rat galan
832	6	0.8	51	4	ABG58269	Abg58269 Human liv	905	6	0.8	60	8	ADO80860	Ado80860 Rat galan
833	6	0.8	51	4	ABG57603	Abg57603 Human liv	906	6	0.8	62	2	AAW26187	Aaw26187 Fragment
834	6	0.8	51	4	AAG90451	Aag90451 C glutami	907	6	0.8	62	4	AAU51462	Aau51462 Propionib
835	6	0.8	51	5	ABP02926	Abp02926 Human ORF	908	6	0.8	62	4	ABU15048	Abu15048 Human ner
836	6	0.8	51	5	ABG45818	Abg45818 Human pep	909	6	0.8	62	4	AU20999	Au20999 Human nov
837	6	0.8	52	3	AAB26169	Aab26169 Rat GBX2	910	6	0.8	62	5	ABP09466	Abp09466 Human ORF
838	6	0.8	52	4	AAM87739	Aam87739 Novel hum	911	6	0.8	62	6	ABM47981	Abm47981 Propionib
839	6	0.8	52	4	AAU52328	Aau52328 Propionib	912	6	0.8	63	2	AAW26188	Aaw26188 Fragment
840	6	0.8	52	6	AAM48847	Aam48847 Propionib	913	6	0.8	63	2	AAU60203	Aau60203 Human end
841	6	0.8	52	7	ADB60073	Adb60073 Connectiv	914	6	0.8	63	4	AAU17736	Aau17736 Novel hum
842	6	0.8	52	8	ABO59052	Abos9052 Human gen	915	6	0.8	63	4	AAM70726	Aam70726 Human bon
843	6	0.8	53	7	ADF59117	Adf59117 Human pol	916	6	0.8	63	4	AAU66861	Aau66861 Propionib
844	6	0.8	53	3	ABR34069	Abp34069 Human sec	917	6	0.8	63	4	AUS1025	Aus1025 Propionib
845	6	0.8	54	5	ABP08116	Abp08116 Human ORF	918	6	0.8	63	4	AAG91376	Aag91376 C glutami
846	6	0.8	55	4	AAR80177	Aar80177 MiSP1-der	919	6	0.8	63	6	ABM63380	Abm63380 Propionib
847	6	0.8	55	4	ABB43693	Abb43693 Peptide #	920	6	0.8	63	6	ABM47544	Abm47544 Propionib
848	6	0.8	55	4	AAM82838	Aam82838 Human imm	921	6	0.8	63	7	ADG41116	Adg41116 Human res
849	6	0.8	55	4	AAU40171	Aau40171 Propionib	922	6	0.8	63	7	ADI96890	Adi96890 Human res
850	6	0.8	55	4	AAU52709	Aau52709 Propionib	923	6	0.8	64	4	AAU21216	Aau21216 Human nov
851	6	0.8	55	4	ABG59065	Abg59065 Human liv	924	6	0.8	64	5	ABP11025	Abp11025 Human ORF
852	6	0.8	55	6	ABM36690	Abm36690 Propionib	925	6	0.8	65	3	ABP16790	Abp16790 Bacteriop
853	6	0.8	55	6	ABM49228	Abm49228 Propionib	926	6	0.8	65	3	ABR32555	Abp32555 Eucalyptu
854	6	0.8	55	6	ABU56878	Abu56878 BONT/A Hc	927	6	0.8	65	3	ABG33255	Abg33255 Zea may
855	6	0.8	55	6	ABU56877	Abu56877 BONT/A Hc	928	6	0.8	65	4	ABM40266	Abm40266 Peptide #
856	6	0.8	56	2	AAW77572	Aaw77572 Staphyloc	929	6	0.8	65	4	AAU33947	Aau33947 Peptide #
857	6	0.8	56	3	AAB33881	Aab33881 Human sec	930	6	0.8	65	4	ABB24683	Abb24683 Protein #
858	6	0.8	56	4	AAM19289	Aam19289 Peptide #	931	6	0.8	65	4	AAM73760	Aam73760 Human bon
859	6	0.8	56	4	ABB38566	Abb38566 Peptide #	932	6	0.8	65	4	AUS57533	Aus57533 Propionib
860	6	0.8	56	4	AAM32017	Aam32017 Peptide #	933	6	0.8	65	4	AUS4889	Aus4889 Propionib
861	6	0.8	56	4	ABB23694	Abb23694 Protein #	934	6	0.8	65	4	AAM61056	Aam61056 Human bra
862	6	0.8	56	4	AAW71725	Aaw71725 Human bon	935	6	0.8	65	4	ABG55505	Abg55505 Human liv
863	6	0.8	56	4	AAO10744	Aao10744 Human pol	936	6	0.8	65	5	ABP05332	Abp05332 Human ORF
864	6	0.8	56	4	AAM59190	Aam59190 Human bra	937	6	0.8	65	5	ABG43644	Abg43644 Human pep
865	6	0.8	56	4	ABG53410	Abg53410 Human liv	938	6	0.8	65	5	ABG66811	Abg66811 Human pro
866	6	0.8	56	5	ABP10151	Abp10151 Human ORF	939	6	0.8	65	5	ABM51408	Abm51408 Propionib
867	6	0.8	56	5	ABG41539	Abg41539 Human pep	940	6	0.8	65	6	ABM54052	Abm54052 Propionib
868	6	0.8	57	2	AAU12580	Aau12580 Human 5'	941	6	0.8	65	6	ABM57944	Abm57944 Propionib
869	6	0.8	57	4	AAM13734	Aam13734 Peptide #	942	6	0.8	65	6	ABM51477	Abm51477 Human sec
870	6	0.8	57	4	ABB32669	Abb32669 Peptide #	943	6	0.8	66	3	ABM12794	Abm12794 Clostridi
871	6	0.8	57	4	AAM89897	Aam89897 Human imm	944	6	0.8	66	3	ABM51481	Abm51481 Human sec
872	6	0.8	57	4	ABG47522	Abg47522 Human liv	945	6	0.8	66	3	ABM51477	Abm51477 Human sec
873	6	0.8	58	4	ABM5135	Aab65135 Rat physl	946	6	0.8	66	4	AAO87331	Aao87331 Human imm
874	6	0.8	58	4	AAM89036	Aam89036 Human imm	947	6	0.8	66	4	AAO07490	Aao07490 Human pol
875	6	0.8	58	4	AAU63871	Aau63871 Propionib	948	6	0.8	66	4	AAU31514	Aau31514 Novel hum
876	6	0.8	58	4	ABG22198	Abg22198 Novel hum	949	6	0.8	66	6	AAB36900	Aab36900 Spider (P
877	6	0.8	58	4	ABM60390	Abm60390 Propionib	950	6	0.8	67	4	ABG25158	Abg25158 Novel hum
878	6	0.8	59	2	AAW26186	Aaw26186 Fragment	951	6	0.8	68	4	AAW91587	Aaw91587 Human ORF
879	6	0.8	59	4	ABB69382	Abb69382 Drosophil	952	6	0.8	68	5	ABP08088	Abp08088 Human ORF
880	6	0.8	59	4	ABB28297	Abb28297 Human pep	953	6	0.8	68	7	ABO81828	Abos1828 Pseudomon
881	6	0.8	59	4	AAM66647	Aam66647 Human bon	954	6	0.8	68	7	ABO64949	Abos64949 Klebsiell
882	6	0.8	59	4	AAO12589	Aao12589 Human pol	955	6	0.8	68	8	ADN99417	Adn99417 Novel hum
883	6	0.8	59	4	AUS5699	Aus5699 Propionib	956	6	0.8	68	8	ADP31694	Adp31694 Human sec
884	6	0.8	59	4	AAM54254	Aam54254 Human bra	957	6	0.8	69	2	AAU15052	Aau15052 N-terminu
885	6	0.8	59	6	ABM52218	Abm52218 Propionib	958	6	0.8	69	4	AAU43578	Aau43578 Propionib
886	6	0.8	60	2	AAU05924	Aau05924 Thermophi	959	6	0.8	69	4	AAU56797	Aau56797 Propionib
887	6	0.8	60	2	AAU45146	Aau45146 Rat ligan	960	6	0.8	69	4	AAU21518	Aau21518 Human nov
888	6	0.8	60	4	AAM16802	Aam16802 Peptide #	961	6	0.8	69	5	ABP08792	Abp08792 Human ORF
889	6	0.8	60	4	ABG45132	Abg45132 Rat physl	962	6	0.8	69	5	ABF04965	Abf04965 Human ORF
890	6	0.8	60	4	AAG74452	Aag74452 Human col	963	6	0.8	69	5	ABM53316	Abm53316 Propionib
891	6	0.8	60	4	ABB35785	Abb35785 Peptide #	964	6	0.8	69	6	ABM40097	Abm40097 Propionib
892	6	0.8	60	4	AAM29284	Aam29284 Peptide #	965	6	0.8	69	7	ADC88751	Adc88751 Ribosom
893	6	0.8	60	4	ABB30620	Abb30620 Peptide #	966	6	0.8	69	8	ABO56109	Abos6109 Human gen
894	6	0.8	60	4	ABB21207	Abb21207 Protein.#	967	6	0.8	69	8	ADP30715	Adp30715 Human sec
895	6	0.8	60	4	AAM68973	Aam68973 Human bon	968	6	0.8	70	1	AAU70992	Aau70992 Sequence
896	6	0.8	60	4	AAM56594	Aam56594 Human bra	969	6	0.8	70	2	AAU92243	Aau92243 N-terminu
897	6	0.8	60	4	ABG50636	Abg50636 Human liv	970	6	0.8	70	5	ABP42746	Abp42746 Human ova
898	6	0.8	60	4	AAM04518	Aam04518 Peptide #	971	6	0.8	70	7	ADC88630	Adc88630 Ribosom
899	6	0.8	60	5	ABG38561	Abg38561 Human pep	972	6	0.8	71	4	AAM21309	Aam21309 Peptide #
900	6	0.8	60	5	ABB76804	Abb76804 Rat GALP-	973	6	0.8	71	4	AAM91991	Aam91991 Human dig
901	6	0.8	60	5	AAG68222	Aag68222 Rat galan	974	6	0.8	71	4	ABB43642	Abb43642 Peptide #

975 6 0.8 71 4 AAM37537 Peptide #
976 6 0.8 71 4 AAM38586 Human col
977 6 0.8 71 4 AAM77385 Human bon
978 6 0.8 71 4 AAO10378 Human pol
979 6 0.8 71 4 AAU43958 Propionib
980 6 0.8 71 4 AAM64586 Human bra
981 6 0.8 71 4 ABG59013 Human liv
982 6 0.8 71 5 ABG46399 Human pep
983 6 0.8 71 5 ABG97638 Human col
984 6 0.8 71 6 ABM40477 Propionib
985 6 0.8 71 6 ABU39720 Protein e
986 6 0.8 71 7 ADB32894 Human col
987 6 0.8 71 7 ADC87840 Ribosomal
988 6 0.8 72 2 AAW59265 Human Fan
989 6 0.8 72 3 AAG35300 Zea mays
990 6 0.8 72 4 AAM14285 Peptide #
991 6 0.8 72 4 ABB33232 Peptide #
992 6 0.8 72 4 AAM26695 Peptide #
993 6 0.8 72 4 ABB28058 Human pep
994 6 0.8 72 4 ABB18695 Protein #
995 6 0.8 72 4 AAM66415 Human bon
996 6 0.8 72 4 AAU48612 Propionib
997 6 0.8 72 4 AAM54025 Human bra
998 6 0.8 72 4 ABG48081 Human liv
999 6 0.8 72 4 AAM02014 Peptide #
1000 6 0.8 72 5 AAO22519 Small aci

ALIGNMENTS

RESULT 1
ID AAY84947 standard; protein; 797 AA.
AC AAY84947;
DT 21-AUG-2000 (first entry)
XX Amino acid sequence of outer membrane protein (omp) 85.
DE Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW meningococcal infection; protective immune response; vaccine.
XX Neisseria meningitidis.
XX W0200023595-A1.
XX 27-APR-2000.
XX 22-OCT-1998; 98WO-US022352.
XX 22-OCT-1998; 98WO-US022352.
XX (UTMO-) UNIV MONTANA.
XX Judd RC, Manning SD;
XX WPI; 2000-339694/29.
XX N-PSDB; AAA15156.
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions
XX for gonococcal or meningococcal infections.
XX Claim 41; Page 89-92; 98pp; English.
XX The present sequence represents an outer membrane protein (omp) 85 of
XX Neisseria meningitidis. The omp polypeptides and polynucleotides are
XX useful in compositions for use in the prevention, treatment and diagnosis
XX of non-symptomatic gonococcal infection or meningococcal infection and
XX symptomatic disease. They are also useful for the detection of
XX hybridisation complexes. Antigens and antibodies specific omp proteins

CC also provide diagnostic, therapeutic and prophylactic compositions for
CC the treatment or prevention of the infections described above. The
CC antibodies are useful for inducing a protective immune response in humans
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines
XX
SQ Sequence 797 AA;

Query Match 100.0%; Score 797; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLFVKVGDYVNDTHGSA 60
DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLFVKVGDYVNDTHGSA 60
QY 61 IKSLEYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDALIKONLESFGLAQ 120
DB 61 IKSLEYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDALIKONLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYVLRGKLNIOITPKVTKLARNRVDIDITIDEGSAKITDIE 180
DB 121 SOYFNOATLNQAVAGLKEEYVLRGKLNIOITPKVTKLARNRVDIDITIDEGSAKITDIE 180
QY 181 FEGNQVYSRDKLMRQMSLTGEGITWLTTRSNQFNEQFAQDMKVKTDIFYQNNGYFDFRIL 240
DB 181 FEGNQVYSRDKLMRQMSLTGEGITWLTTRSNQFNEQFAQDMKVKTDIFYQNNGYFDFRIL 240
QY 241 DTDIQNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGWEROQ 300
DB 241 DTDIQNEDKTKQTIKIVHEGGRFRWGKVSIEGDTNEVPKAELEKLLTWKPKGWEROQ 300
QY 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDFVLHIEPRKIYVNEIHTGNKKT 360
DB 301 MTAVLGEIQNRMGSGAGYAYSEISVQPLPNAETKTVDFVLHIEPRKIYVNEIHTGNKKT 360
QY 361 RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFDNVQFADAVPLAGTDPKVDLNNSLTE 420
DB 361 RDEVVRRELQRMESAPYDTSKLQSKERVVELLYGFDNVQFADAVPLAGTDPKVDLNNSLTE 420
QY 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFPTGKSAALRASRSKTTLNGSLSTDPDYFTA 480
DB 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFPTGKSAALRASRSKTTLNGSLSTDPDYFTA 480
QY 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
DB 481 DGVSGLGYDYVYKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
QY 541 YNKAPKHYADFIKKYKTDGTDGSPKGLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
DB 541 YNKAPKHYADFIKKYKTDGTDGSPKGLYKGTGVMGRNKTDSALWPTRGYLTGVNAEIA 600
QY 601 LPGSKLOQYYSATHNQTFWFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
DB 601 LPGSKLOQYYSATHNQTFWFPPLSKTFTMLGGEVGIAGGYGRTKEIIPFFENFYGGGLGSVR 660
QY 661 GYESGTLGPKVYDVEYGEKISYGNKKANYSAEILLFPMPCAKDARTVRLSIFADAGSVWDG 720
DB 661 GYESGTLGPKVYDVEYGEKISYGNKKANYSAEILLFPMPCAKDARTVRLSIFADAGSVWDG 720
QY 721 KYDDNSSSATGGRVQNIYCGANTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
DB 721 KYDDNSSSATGGRVQNIYCGANTHKSTFTNELRYSAGGAVTWLSPLGPMKFRYAYPLKK 780
QY 781 KPEDEIQRFOFQLGTTTF 797
DB 781 KPEDEIQRFOFQLGTTTF 797

RESULT 2
ABB79802

ID ABB79802 standard; protein; 797 AA.
 AC ABB79802;
 XX 15-NOV-2002 (first entry)
 DT
 XX Neisseria meningitidis outer membrane protein Omp85.
 DE
 XX Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
 KW antibacterial.
 XX
 XX Neisseria meningitidis.
 OS
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..797
 FT /label= Mature_protein
 XX
 XX US2002086028-A1.
 PN
 XX
 PD 04-JUL-2002.
 XX
 XX 26-NOV-2001; 2001US-00994192.
 XX
 XX 22-OCT-1998; 98US-00177039.
 PR
 XX (JUDD/) JUDD R C.
 PA (MANN/) MANNING D S.
 XX
 XX JUDD RC, Manning DS;
 PI
 XX
 XX WFI; 2002-642234/69.
 DR
 XX
 XX Novel immunogenic composition for vaccinating against meningococcal or
 PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
 PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
 XX
 XX Claim 13; Fig 5; 30pp; English.
 PS
 XX The present sequence is that of the Neisseria meningitidis strain HH
 CC outer membrane protein 85 (Omp85), as predicted from a gene that was
 CC obtained from a genomic DNA by PCR amplification using primers based on
 CC the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
 CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
 CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
 CC fusion proteins including the Omp85, or nucleic acids encoding them,
 CC which induce a protective immune response in a subject. The immunogenic
 CC compositions may also include an antigen from a heterologous or
 CC homologous pathogen, or a nucleic acid encoding it. They are used in a
 CC claimed method of vaccinating a human or animal against non-symptomatic
 CC meningococcal infection or symptomatic disease. A kit for diagnosing
 CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
 CC The Omp85 polypeptides and polynucleotides are also useful in drug
 CC screening and development
 XX
 SQ Sequence 797 AA;
 Query Match 100.0%; Score 797; DB 5; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLQIASALMLGSGISPLAFADFTIQDIRVEGLQRTPESTVFVYLPVKVGDYNDTHGSA 60
 DB 1 MKLQIASALMLGSGISPLAFADFTIQDIRVEGLQRTPESTVFVYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFPDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFPDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SOYFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDTDEGSAKITDIE 180
 DB 121 SOYFNOATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDTDEGSAKITDIE 180

QY 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTSTNSQNEQKFAQDMKVTDFYQNGYFDFRIL 240
 DB 181 FEGNQVYSDRKLMRQMSLTGGIWTWLTSTNSQNEQKFAQDMKVTDFYQNGYFDFRIL 240
 QY 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVKISIEGDTNEVPKAELEKLLTWKPGWYERQQ 300
 DB 241 DTDIQTNEDKTKQTIKITVHEGGRFRWGVKISIEGDTNEVPKAELEKLLTWKPGWYERQQ 300
 QY 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 DB 301 MTAVLGEIQNRMGSAQYAYSEISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKKT 360
 QY 361 RDEVVRRELROMESAPYDTSKLQSKSERVELLGYFDNVQFQDAVPLAGTDPKVDLNSLITE 420
 DB 361 RDEVVRRELROMESAPYDTSKLQSKSERVELLGYFDNVQFQDAVPLAGTDPKVDLNSLITE 420
 QY 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTCKSAALRASRSKTTTLNGSLSTFDPYFTA 480
 DB 421 RSTGSLDLSAGWVQDTGLVMSAGVSQDNLFGTCKSAALRASRSKTTTLNGSLSTFDPYFTA 480
 QY 481 DGVS LGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 DB 481 DGVS LGYDVYVGKAFDPRKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
 QY 541 YNKAPKHYADFIKKYKTKDTGDSFGWLYKGTGVGGRNKTDLSALWPTRGYLTGVNAEIA 600
 DB 541 YNKAPKHYADFIKKYKTKDTGDSFGWLYKGTGVGGRNKTDLSALWPTRGYLTGVNAEIA 600
 QY 601 LPSGLQYYSATHNOTWTFPLSKTFTLMLGGEVGIAGGYGRTEKIEIPFFENFYGGGLGSVR 660
 DB 601 LPSGLQYYSATHNOTWTFPLSKTFTLMLGGEVGIAGGYGRTEKIEIPFFENFYGGGLGSVR 660
 QY 661 GYBSGTGLPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 DB 661 GYBSGTGLPKVYDEYGEKISYGCNKKANVSALLFPMPGAKDARTVRLSLFADAGSVWDG 720
 QY 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
 DB 721 KTYDDNSSATGGRVQNIYGAGNTHKSTFTNELRYSGAGVATWLSPLGPMKFRYAYPLKK 780
 QY 781 KPEDEIQRFQFQLGTTTF 797
 DB 781 KPEDEIQRFQFQLGTTTF 797
 RESULT 3
 AAU03959
 ID AAU03959 standard; protein; 797 AA.
 XX
 AC AAU03959;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Neisseria gonorrhoeae antigenic protein.
 XX
 XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.
 OS
 XX Neisseria gonorrhoeae.
 XX
 XX Key Location/Qualifiers
 FT Peptide 1..21
 FT /note= "Signal peptide"
 FT Protein 22..797
 FT /note= "Mature N. gonorrhoeae antigen"
 XX
 XX W0200138350-A2.
 PN
 XX 31-MAY-2001.
 PD
 XX 28-NOV-2000; 2000WO-IB001851.
 PF
 XX

PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 PA (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR N-PSDB; AAS07279.
 XX
 PT Novel 85 kDa antigen from *Neisseria meningitidis* and *Neisseria*
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing *Neisseria* bacteria infection.
 XX
 PS Claim 1; Page 37-39; 92pp; English.
 XX
 CC The sequence represents a *Neisseria gonorrhoeae* 85 kDa antigenic protein.
 CC *N. gonorrhoeae* is closely related to *N. meningitidis*, which colonises the
 CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
 CC of meningitis. This antigenic protein is useful in the manufacture of a
 CC medicament for treating or preventing infection due to *Neisseria*
 CC bacteria, such as meningitis and septicaemia. It is also useful as a
 CC diagnostic reagent for detecting the presence of *Neisseria* bacteria or
 CC antibodies raised against *Neisseria*, and as a reagent for raising the
 CC antibodies. The *Neisseria* nucleotide sequences can be expressed in a
 CC variety of different expression systems, for example, mammalian cells,
 CC baculoviruses, plants, bacteria and yeast
 CC
 SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTSPSTVFNLPVKVGTVDYNDTHGSAIIKSLYATGFFDVRVETAD 80
 Db 21 ADFTIQDIRVEGLQRTSPSTVFNLPVKVGTVDYNDTHGSAIIKSLYATGFFDVRVETAD 80
 Qy 81 GQLLTWIERPTTIGSLNITGAKMLQNDIAIKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140
 Db 81 GQLLTWIERPTTIGSLNITGAKMLQNDIAIKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140
 Qy 141 LGRGKLNIIQTPKVKTLARNRVDIIDIIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
 Db 141 LGRGKLNIIQTPKVKTLARNRVDIIDIIDEGKSAKITDIEFEGNQVYSDRKLQRMSLTE 200
 Qy 201 GGIWTLTRSNQFNEQFAQDMKVTFYQNGVYDFRILDTDIQTNEDTKTKITKIVH 260
 Db 201 GGIWTLTRSNQFNEQFAQDMKVTFYQNGVYDFRILDTDIQTNEDTKTKITKIVH 260
 Qy 261 EGGFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQTAVLGEIQNRMSAGVAYS 320
 Db 261 EGGFRGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQTAVLGEIQNRMSAGVAYS 320
 Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
 Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
 Qy 381 KLQSKERVLLGFFDNDVQFQDAVPLAGTPDKVDLNMSLTRSTGSLDLSAGVQDTGLVM 440
 Db 381 KLQSKERVLLGFFDNDVQFQDAVPLAGTPDKVDLNMSLTRSTGSLDLSAGVQDTGLVM 440
 Qy 441 SAGVQNLPLFCTGKSAALRASRTKTLNGSLISFTDYPFTADGVSGLVDYVKGKAFDPDKAS 500
 Db 441 SAGVQNLPLFCTGKSAALRASRTKTLNGSLISFTDYPFTADGVSGLVDYVKGKAFDPDKAS 500
 Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHYADFIKKYKGTG 560
 Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPKHYADFIKKYKGTG 560
 Qy 561 TDGSFKGLYKGTVGWRNKTDTSALWTRGVLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620

Db 561 TDGSFKGLYKGTVGWRNKTDTSALWTRGVLTVGNVNAEIALPGSKLOYYSATHNQWTFPP 620
 Qy 621 LSKTFTMLGGEVGIAGGYGRTKKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
 Db 621 LSKTFTMLGGEVGIAGGYGRTKKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
 Qy 681 YGKNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
 Db 681 YGKNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
 Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
 Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
 RESULT 4
 AAU03957
 ID AAU03957 standard; protein; 797 AA.
 AC AAU03957;
 XX 23-OCT-2001 (first entry)
 XX *Neisseria meningitidis* serogroup B antigenic protein.
 XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX *Neisseria meningitidis*.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein 22..797 /note= "Signal peptide"
 FT Binding-site 715..722 /note= "Mature N. meningitidis serogroup B antigen"
 FT /note= "ATP/GTP-binding site motif A (P-loop)"
 XX WO200138350-A2.
 XX 31-MAY-2001.
 XX 28-NOV-2000; 2000WO-IB001851.
 XX 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 XX
 XX (CHIR-) CHIRON SPA.
 XX (STAT-) STATENS INST FOLKEHELSE.
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR N-PSDB; AAS07277.
 XX
 PT Novel 85 kDa antigen from *Neisseria meningitidis* and *Neisseria*
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing *Neisseria* bacteria infection.
 XX
 PS Claim 1; Fig 1; 92pp; English.
 XX
 CC The sequence represents a *Neisseria meningitidis* serogroup B 85 kDa
 CC antigenic protein. *Neisseria meningitidis* colonises the pharynx, causing
 CC meningitis and, occasionally, septicaemia in the absence of meningitis.
 CC This antigenic protein is useful in the manufacture of a medicament for
 CC treating or preventing infection due to *Neisseria* bacteria, such as
 CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
 CC detecting the presence of *Neisseria* bacteria or antibodies raised against
 CC *Neisseria*, and as a reagent for raising the antibodies. The *Neisseria*
 CC nucleotide sequences can be expressed in a variety of different
 CC expression systems, for example, mammalian cells, baculoviruses, plants,
 CC bacteria and yeast
 CC

SQ	Sequence 797 AA;	
	Query Match 94.4%; Score 752; DB 4; Length 797;	
	Best Local Similarity 100.0%; Pred. No. 0;	
	Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Qy	21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80	
Db	21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80	
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140	
Db	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140	
Qy	141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNQVYSRKLQRMQSLTE 200	
Db	141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNQVYSRKLQRMQSLTE 200	
Qy	201 GGIWTLWLTSSNQFNEQFAQDMKVTDYFQNGYFDFRILDDIQTNEDEKTKQTIKITHV 260	
Db	201 GGIWTLWLTSSNQFNEQFAQDMKVTDYFQNGYFDFRILDDIQTNEDEKTKQTIKITHV 260	
Qy	261 EGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQTAVLGEIQNRMGSAGYAYS 320	
Db	261 EGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQTAVLGEIQNRMGSAGYAYS 320	
Qy	321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNTRDEVVRRELQMESAPYDTS 380	
Db	321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNTRDEVVRRELQMESAPYDTS 380	
Qy	381 KLQRSKERVVELLYGDFNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440	
Db	381 KLQRSKERVVELLYGDFNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440	
Qy	441 SAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSGLGYDVYKGAFFPRKAS 500	
Db	441 SAGVSQDNLFCTGKSAALRASRSKTTLLNGSLSFDPYFTADGVSGLGYDVYKGAFFPRKAS 500	
Qy	501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560	
Db	501 TSISKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG 560	
Qy	561 TDGSFKGWLKYGTVGWRGNKTDLSALWPTGRVLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Db	561 TDGSFKGWLKYGTVGWRGNKTDLSALWPTGRVLTGVNAEIALPGSKLOYYSATNQWTFPP 620	
Qy	621 LSKTFTLMLGGEVGIAGGYGRTEIIPFFENFYGGGLGVSRYESGTLGPKVYDYEYGEKIS 680	
Db	621 LSKTFTLMLGGEVGIAGGYGRTEIIPFFENFYGGGLGVSRYESGTLGPKVYDYEYGEKIS 680	
Qy	681 YGNKKNANVAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSSATGGRVQNIYG 740	
Db	681 YGNKKNANVAELLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSSATGGRVQNIYG 740	
Qy	741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772	
Db	741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772	
RESULT 5		
AAU04451		
ID	AAU04451 standard; protein; 797 AA.	
XX		
AC	AAU04451;	
XX		
DT	23-OCT-2001 (first entry)	
XX		
DE	Neisseria meningitidis serogroup A antigenic protein #2.	
XX		
KW	Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;	
KW	bacterial infection; baculovirus; yeast.	
OS	Neisseria meningitidis.	

XX	Key	Location/Qualifiers	
PH	Peptide	1..21 "Signal peptide"	
FT	Protein	22..797	
XX		/note= "Mature N. meningitidis serogroup A antigen"	
XX	WO200138350-A2.		
XX	31-MAY-2001.		
XX	28-NOV-2000; 2000WO-IB001851.		
XX	29-NOV-1999; 99GB-00028197.		
PR	09-MAR-2000; 2000GB-00005698.		
XX	(CHIR-) CHIRON SPA.		
PA	(STAT-) STATENS INST FOLKEHELSE.		
XX	Giuliani MM, Pizza M, Rappuoli R, Holst J;		
XX	WPI; 2001-381289/40.		
XX	Novel 85 kDa antigen from Neisseria meningitidis and Neisseria		
PT	gonorrhoeae, useful in the manufacture of a medicament for treating and		
PT	preventing Neisserial bacteria infection.		
XX	Claim 1; Page 39-40; 92pp; English.		
XX	The sequence represents a Neisseria meningitidis serogroup A 85 kDa		
CC	antigenic protein. Neisseria meningitidis colonises the pharynx, causing		
CC	meningitis and, occasionally, septicaemia in the absence of meningitis.		
CC	This antigenic protein is useful in the manufacture of a medicament for		
CC	treating or preventing infection due to Neisseria bacteria, such as		
CC	meningitis and septicaemia. It is also useful as a diagnostic reagent for		
CC	detecting the presence of Neisseria bacteria or antibodies raised against		
CC	Neisseria, and as a reagent for raising the antibodies. The Neisserial		
CC	nucleotide sequences can be expressed in a variety of different		
CC	expression systems, for example, mammalian cells, baculoviruses, plants,		
CC	bacteria and yeast. Note: There are two versions of this sequence		
CC	displayed in the specification (see AAU03958)		
XX	Sequence 797 AA;		
SQ	Query Match 94.4%; Score 752; DB 4; Length 797;		
	Best Local Similarity 100.0%; Pred. No. 0;		
	Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Qy	21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80		
Db	21 ADFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD 80		
Qy	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140		
Db	81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140		
Qy	141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNQVYSRKLQRMQSLTE 200		
Db	141 LGRGKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNQVYSRKLQRMQSLTE 200		
Qy	201 GGIWTLWLTSSNQFNEQFAQDMKVTDYFQNGYFDFRILDDIQTNEDEKTKQTIKITHV 260		
Db	201 GGIWTLWLTSSNQFNEQFAQDMKVTDYFQNGYFDFRILDDIQTNEDEKTKQTIKITHV 260		
Qy	261 EGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQTAVLGEIQNRMGSAGYAYS 320		
Db	261 EGRFRWGKVSIEGDTNEVPKAELEKLLTMKPKWYERQQTAVLGEIQNRMGSAGYAYS 320		
Qy	321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNTRDEVVRRELQMESAPYDTS 380		
Db	321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKNTRDEVVRRELQMESAPYDTS 380		
Qy	381 KLQRSKERVVELLYGDFNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440		

Db 381 KQSRKERVLLGYFDNVQFVDAVFLAGTDPDKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKAFDPRKAS 500
Db 441 SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKWLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSFKWLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
Qy 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVTVLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVTVLSPGPMKF 772

RESULT 6
AAB23788
ID AAB23788 standard; protein; 797 AA.
AC AAB23788;
XX
DT 12-JAN-2001 (first entry)
DE Neisseria meningitidis serogroup A amino acid sequence.
XX
KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
OS Neisseria meningitidis.
XX
FN WO2000050075-A2.
XX
PD 31-AUG-2000.
XX
PF 09-FEB-2000; 2000WO-IB000176.
XX
XX 26-FEB-1999; 99US-0121792P.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX
XX WPI; 2001-015529/02.
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
XX Claim 22; Page 33; 39pp; English.
XX
CC The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response

CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup A amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
SQ Sequence 797 AA;
Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 21 ADFTIQDIRVEGIQRTPESTVFNYPVKVGDYTNDSHSAIKSLYATGFFDVRVETAD 80
Db 21 ADFTIQDIRVEGIQRTPESTVFNYPVKVGDYTNDSHSAIKSLYATGFFDVRVETAD 80
Qy 81 GQLLLVIERPTTIGSNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNQAVAGLKEEY 140
Db 81 GQLLLVIERPTTIGSNITGAKMLQNDAIKKNLESFGLAQSOYFNQATLNQAVAGLKEEY 140
Qy 141 LGRGKLNIOITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNOYVSDRKLQRQSLTE 200
Db 141 LGRGKLNIOITPKVTKLARNRVDIDITIDEGSAKITDIEFEGNOYVSDRKLQRQSLTE 200
Qy 201 GGIWTWLTNRNQFNQEQFAQDMKVTDYFQNNGYFDFRILDTDIQTNEDKTKQTIKTVH 260
Db 201 GGIWTWLTNRNQFNQEQFAQDMKVTDYFQNNGYFDFRILDTDIQTNEDKTKQTIKTVH 260
Qy 261 EGRFRWGVKSVIEGDTNEVPKAELEKLTMKKPGKWTYERQMTAVLGEIQNRMGSAAYAS 320
Db 261 EGRFRWGVKSVIEGDTNEVPKAELEKLTMKKPGKWTYERQMTAVLGEIQNRMGSAAYAS 320
Qy 321 EISVQPLPNAETKTVDVFLHIIEPRKIYNEIHTGNNTKTRDEVVRRELQMESAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIIEPRKIYNEIHTGNNTKTRDEVVRRELQMESAPYDTS 380
Qy 381 KLQSRKERVLLGYFDNVQFVDAVFLAGTDPDKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Db 381 KLQSRKERVLLGYFDNVQFVDAVFLAGTDPDKVDLNNLSLTERSTGSLDLSAGWQDTGLVM 440
Qy 441 SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKAFDPRKAS 500
Db 441 SAGVSQDNLFGTGSAAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDVYKAFDPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYKGTG 560
Qy 561 TDGSFKWLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Db 561 TDGSFKWLYKGTGWRGNKTDLSALWTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
Qy 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
Db 621 LSKTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESTGLGPKVYDEYGEKIS 680
Qy 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNNKANVSAELLFPMPGAKDARTVRLSLFADAGSVMDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSGAGVTVLSPGPMKF 772
Db 741 AGNTHKSTFTNELRYSGAGVTVLSPGPMKF 772

RESULT 7
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX
AC AAB23784;
XX
DT 12-JAN-2001 (first entry)

XX Neisseria meningitidis serogroup B amino acid sequence.

XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;

KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;

KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;

KW immune response.

XX Neisseria meningitidis.

XX WO2000050075-A2.

XX 31-AUG-2000.

XX 09-FEB-2000; 2000WO-IB000176.

XX 26-FEB-1999; 99US-0121792P.

XX (CHIR-) CHIRON SPA.

XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;

XX WPI; 2001-015529/02.

XX Immunogenic composition useful for stimulating an immune response in a

PT mammal against Neisseria infection, comprises Neisseria antigen and an

PT adjuvant composition comprising an oligonucleotide with a CG motif.

XX Claim 22; Page 32; 39pp; English.

XX The present invention describes an immunogenic composition (I) comprising

CC a Neisseria antigen and an adjuvant composition comprising an

CC oligonucleotide comprising at least 1 CG motif. Also described is an

CC adjuvant composition (II) comprising an oligonucleotide which comprises

CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the

CC oligonucleotide preferably comprises at least one phosphorothioate bond.

CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of

CC the present invention. (I) is useful for stimulating an immune response

CC in a mammal, preferably a human, against Neisseria infection, preferably

CC Neisseria meningitidis infection and in the manufacture of a medicament

CC for inducing a protective immune response in a mammal. The present

CC sequence represents the claimed Neisseria meningitidis serogroup B amino

CC acid sequence disclosed in GB-9928197.4, which is given in the present

CC invention

XX Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTI0IRVEGLQRTPEFTVFNLPVKVGTNDTHGSAIIKSLYATGFFDDVRVETAD 80

Db 21 ADFTI0IRVEGLQRTPEFTVFNLPVKVGTNDTHGSAIIKSLYATGFFDDVRVETAD 80

Qy 81 GQLLTIVERTTGSLLNITGAKMLQNDIAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140

Db 81 GQLLTIVERTTGSLLNITGAKMLQNDIAIKNLESFGLAQSYFNQATLNQAVAGLKEEY 140

Qy 141 LGRGKLNQITPKVTKLARNVDITDITDEGSAKITDIEFEGNQVYSDRKLQMSLTE 200

Db 141 LGRGKLNQITPKVTKLARNVDITDITDEGSAKITDIEFEGNQVYSDRKLQMSLTE 200

Qy 201 GGIWTLTRSNQFNQEQFAQDMKVDFYQNGGYDFDRILDTDITQNEKTKQITKIVH 260

Db 201 GGIWTLTRSNQFNQEQFAQDMKVDFYQNGGYDFDRILDTDITQNEKTKQITKIVH 260

Qy 261 EGGFRNGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQMTAVLGBIQNRMGSAGVAYS 320

Db 261 EGGFRNGKVSIEGDTNEVPKAELEKLLTWKPGKWERQQMTAVLGBIQNRMGSAGVAYS 320

Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380

Db 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380

Qy 381 KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLGAGWQDTGLVM 440

Db 381 KLQRSKERVLLGYFDNVQFQDAVPLAGTDPKVDLNNLSLTERSTGSLDLGAGWQDTGLVM 440

Qy 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSTFDYFTADGVSIGYDVYVKAFDPRKAS 500

Db 441 SAGVSQDNLFQGTGSAALRASRSKTTLNGSLSTFDYFTADGVSIGYDVYVKAFDPRKAS 500

Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTDG 560

Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHADFIKKYKTDG 560

Qy 561 TDGSPFKGWLKGTGVRNKTDSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Db 561 TDGSPFKGWLKGTGVRNKTDSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620

Qy 621 LSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSRGYESGTLPKPYDEYGEKIS 680

Db 621 LSKTFTMLGGEVGIAGGYGRTEKEIPFFENFYGGGLGSRGYESGTLPKPYDEYGEKIS 680

Qy 681 YGNNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740

Db 681 YGNNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIY 740

Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 8

AAB84746

ID AAB84746 standard; protein; 797 AA.

XX AAB84746;

XX 17-SEP-2001 (first entry)

XX Amino acid sequence of a Neisseria serogroup A protein.

XX Serogroup A protein; outer membrane protein; Neisserial infection;

XX Neisseria meningitidis.

XX Key Location/Qualifiers

FT Peptide 1..21

FT Protein /note= "signal peptide"

FT /note= "mature protein"

XX WO200152885-A1.

XX 26-JUL-2001.

XX 17-JAN-2001; 2001WO-IB000166.

XX 17-JAN-2000; 2000GB-00001067.

XX 09-MAR-2000; 2000GB-00005699.

XX (CHIR-) CHIRON SPA.

XX Pizza M, Rappuoli R, Giuliani M;

XX WPI; 2001-451895/48.

XX N-PSDB; AA42130.

XX Composition for treating or preventing infection to, detecting, or for

PT raising antibodies against Neisserial bacteria, comprises an N.

PT meningitidis serogroup B outer membrane preparation and an immunogenic

PT component.

XX

PS Disclosure; Page 71-74; 83pp; English.

XX The present sequence represents a Neisseria serogroup A protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
CC bacteria; or of antibodies raised against Neisseria bacteria; and/or a
CC reagent which can raise antibodies against Neisseria bacteria. It may
CC also be used as a vaccine
XX

SQ Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTFVNFYLPVKVGTVDNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||||
Qy 21 ADFTIQDIRVEGLQRTPESTFVNFYLPVKVGTVDNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140
Db |||||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140
Db |||||||
Qy 141 LGRGKLNQITPKVTKLARNVDIDITDEGKSAKITDIEFEGNQVYSDRKLNRQMSLTE 200
Db |||||||
Qy 141 LGRGKLNQITPKVTKLARNVDIDITDEGKSAKITDIEFEGNQVYSDRKLNRQMSLTE 200
Db |||||||
Qy 201 GGIWTLTRSNQFNEQFAQDMEKVTDFYQNNGVDFDRIIDTDIOTNEDKTQTIKTIHV 260
Db |||||||
Qy 201 GGIWTLTRSNQFNEQFAQDMEKVTDFYQNNGVDFDRIIDTDIOTNEDKTQTIKTIHV 260
Db |||||||
Qy 261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGBIQRNMGSAVAYS 320
Db |||||||
Qy 261 EGGFRMGKVSIEGDTNEVPKAELEKLLTMKPGKWERQQTAVLGBIQRNMGSAVAYS 320
Db |||||||
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIIYVNEIHTGNKTRDDEVRRRLQMESAPYDTS 380
Db |||||||
Qy 321 EISVQPLPNAETKTVDVFLHIEPGRKIIYVNEIHTGNKTRDDEVRRRLQMESAPYDTS 380
Db |||||||
Qy 381 KLOBSKERVLLGYFDNVQFADVPAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db |||||||
Qy 381 KLOBSKERVLLGYFDNVQFADVPAGTDPKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
Db |||||||
Qy 441 SAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFPTDYPFTADGVSIGYDVYVGKAFDPRKAS 500
Db |||||||
Qy 441 SAGVSQDNLFGTGSAALRASRSKTTLLNGSLSFPTDYPFTADGVSIGYDVYVGKAFDPRKAS 500
Db |||||||
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYAFIKKYKGTG 560
Db |||||||
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYAFIKKYKGTG 560
Db |||||||
Qy 561 TDGSFKGLYKGTGWRNKTDLSALWPTRGVLTGVNAEIALPGSKLOYYSATHNQTFPP 620
Db |||||||
Qy 561 TDGSFKGLYKGTGWRNKTDLSALWPTRGVLTGVNAEIALPGSKLOYYSATHNQTFPP 620
Db |||||||
Qy 621 LSKTFTLMLGGEVGIAGYGRKTEIPEFFENFYGGGLSGVRGYSGLTGPVKVYDEYGEKIS 680
Db |||||||
Qy 621 LSKTFTLMLGGEVGIAGYGRKTEIPEFFENFYGGGLSGVRGYSGLTGPVKVYDEYGEKIS 680
Db |||||||
Qy 681 YGNKKNANVAEALLFPMGAKADARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
Db |||||||
Qy 681 YGNKKNANVAEALLFPMGAKADARTVRLSLFADAGSVWDGKTYDDNSSSSATGGRVQNIY 740
Db |||||||
Qy 741 AGNTHKSTFTNEURYSGAGVATWLSPLGPMKF 772
Db |||||||
Qy 741 AGNTHKSTFTNEURYSGAGVATWLSPLGPMKF 772
Db |||||||

RESULT 9
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX
XX AAB84744;
AC
XX 17-SBP-2001 (first entry)
DT
XX
DE Amino acid sequence of a Neisseria serogroup B protein.
XX
XX Serogroup B protein; outer membrane protein; Neisseria infection;
KW vaccine.
XX
XX Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX
XX WO200152885-A1.
PN
XX 26-JUL-2001.
PD
XX 17-JAN-2001; 2001WO-IB000166.
PF
XX 17-JAN-2000; 2000GB-00001067.
PR
XX 09-MAR-2000; 2000GB-00005699.
XX
XX (CHIR-) CHIRON SPA.
PA
XX
XX Pizza M, Rappuoli R, Giuliani M;
PI
XX WPI; 2001-451895/48.
DR
XX N-PSDB; AAH42128.
XX
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisseria bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX
XX Disclosure; Page 59-61; 83pp; English.
XX
XX The present sequence represents a Neisseria serogroup B protein. The
CC protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
CC bacteria; or of antibodies raised against Neisseria bacteria; and/or a
CC reagent which can raise antibodies against Neisseria bacteria. It may
CC also be used as a vaccine
XX
XX Sequence 797 AA;

Query Match 94.4%; Score 752; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADFTIQDIRVEGLQRTPESTFVNFYLPVKVGTVDNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||||
Qy 21 ADFTIQDIRVEGLQRTPESTFVNFYLPVKVGTVDNDTHGSAIIKSLYATGFFDVRVETAD 80
Db |||||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140
Db |||||||
Qy 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNQAVAGLKEEY 140
Db |||||||

141 LGRGKLNIOITPKVTKLARNRVDIDITIDEKSAKITDIEPEGNOVYSDRKLMEQMSLTE 200
 141 LGRGKLNIOITPKVTKLARNRVDIDITIDEKSAKITDIEPEGNOVYSDRKLMEQMSLTE 200
 201 GGIWTLTRSNQFNEQKFAQMEKVTDFYQNNGYDFRILDTDIQTNEDEKTKQIKITVH 260
 201 GGIWTLTRSNQFNEQKFAQMEKVTDFYQNNGYDFRILDTDIQTNEDEKTKQIKITVH 260
 261 EGGFRGKVSIEGDTNEVPKAELEKLLTMKPGKQWYERQQTAVLGEIQNRMGAGVAYS 320
 261 EGGFRGKVSIEGDTNEVPKAELEKLLTMKPGKQWYERQQTAVLGEIQNRMGAGVAYS 320
 321 EISVQPLPNAETKTVDVFLHIEPGRKLYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380
 321 EISVQPLPNAETKTVDVFLHIEPGRKLYVNEIHITGNKTRDEVVRRELQMESAPYDTS 380
 381 KLQSKERVVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
 381 KLQSKERVVLLGYFDNVQFPAVLGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM 440
 441 SAGVSONLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSGLGYDVYKAPDPRKAS 500
 441 SAGVSONLFGTGSAALRASRSKTTTLNGSLSFDPYFTADGVSGLGYDVYKAPDPRKAS 500
 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNEGLVAEHLTVNTYKAPKHVADFIKKYKGTG 560
 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNEGLVAEHLTVNTYKAPKHVADFIKKYKGTG 560
 561 TDGSPKGLYKGTGWRGNKTDLSALWPTGRGLTVGNVNAEIALPGSKLOYYSATHNOTWFFP 620
 561 TDGSPKGLYKGTGWRGNKTDLSALWPTGRGLTVGNVNAEIALPGSKLOYYSATHNOTWFFP 620
 621 LSKTFTLMGGEVGIAGGYRTKEIPFFENFYGGGLSVRGYESGTLPKPYDEYGEKIS 680
 621 LSKTFTLMGGEVGIAGGYRTKEIPFFENFYGGGLSVRGYESGTLPKPYDEYGEKIS 680
 681 YGNKKANVAEALLFPMPGAKDARTVLSLFPADAGSVWDGKTYDDNSSSATGGRVQNIY 740
 681 YGNKKANVAEALLFPMPGAKDARTVLSLFPADAGSVWDGKTYDDNSSSATGGRVQNIY 740
 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 10
 AAU03958
 ID AAU03958 standard; protein; 792 AA.
 AC AAU03958;
 XX
 XX 23-OCT-2001 (first entry)
 DE Neisseria meningitidis serogroup A antigenic protein #1.
 XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX Neisseria meningitidis.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT Protein /note= "Signal peptide"
 FT Protein 22..792
 XX /note= "Mature N. meningitidis serogroup A antigen"
 PN WO200138350-A2.
 XX
 XX 31-MAY-2001.
 XX
 XX 28-NOV-2000; 2000WO-IB001851.
 XX

29-NOV-1999; 99GB-00028197.
 09-MAR-2000; 2000GB-00005698.
 (CHIR-) CHIRON SPA.
 (STAT-) STATENS INST FOLKEHELSE.
 Giuliani MM, Pizza M, Rappuoli R, Holst J;
 WPI; 2001-381289/40.
 N-PSDB; AAS07278.
 Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.
 Claim 1; Page 66-68; 92pp; English.
 The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for treating or preventing infection due to Neisseria bacteria, such as meningitis and septicaemia. It is also useful as a diagnostic reagent for detecting the presence of Neisseria bacteria or antibodies raised against Neisseria, and as a reagent for raising the antibodies. The Neisserial nucleotide sequences can be expressed in a variety of different expression systems, for example, mammalian cells, baculoviruses, plants, bacteria and yeast. Note: There are two versions of this sequence displayed in the specification (see AAU04451)
 Query Match 26.3%; Score 210; DB 4; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 1 MKLKQITASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGDYNDTHGSA 60
 1 MKLKQITASALMLGISPLAFADFTIQDIRVEGLQRTPESTVFNLPVKVGDYNDTHGSA 60
 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120
 121 SQYFNQATLNQAVAGLUKEEYLGKGLNIQITPKVTKLARNRVDITIDEKSAKITDIE 180
 121 SQYFNQATLNQAVAGLUKEEYLGKGLNIQITPKVTKLARNRVDITIDEKSAKITDIE 180
 181 FEGNQVYSDRKLQMSLTGGIWTWLTSS 210
 181 FEGNQVYSDRKLQMSLTGGIWTWLTSS 210

RESULT 11
 AAB23786
 ID AAB23786 standard; protein; 792 AA.
 AC AAB23786;
 XX
 XX 11-SEP-2003 (revised)
 DT 12-JAN-2001 (first entry)
 DE Neisseria gonorrhoeae amino acid sequence.
 XX
 XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
 KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
 KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
 KW immune response.
 XX
 OS Neisseria gonorrhoeae.
 XX
 XX WO200050075-A2.
 XX

PD 31-AUG-2000.
 XX
 PF 09-FEB-2000; 2000WO-IB000176.
 XX
 PR 26-FEB-1999; 99US-0121792P.
 XX
 FA (CHIR-) CHIRON SPA.
 XX
 PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;
 XX WPI; 2001-015529/02.
 DR
 XX Immunogenic composition useful for stimulating an immune response in a
 PT mammal against Neisseria infection, comprises Neisseria antigen and an
 PT adjuvant composition comprising an oligonucleotide with a CG motif.
 XX
 PS Claim 22; Page 32; 39pp; English.
 XX
 CC The present invention describes an immunogenic composition (I) comprising
 CC a Neisseria antigen and an adjuvant composition comprising an
 CC oligonucleotide comprising at least 1 CG motif. Also described is an
 CC adjuvant composition (II) comprising an oligonucleotide which comprises
 CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
 CC oligonucleotide preferably comprises at least one phosphorothioate bond.
 CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
 CC the present invention. (I) is useful for stimulating an immune response
 CC in a mammal, preferably a human, against Neisseria infection, preferably
 CC Neisseria meningitidis infection and in the manufacture of a medicament
 CC for inducing a protective immune response in a mammal. The present
 CC sequence represents the claimed Neisseria gonorrhoeae amino acid sequence
 CC disclosed in GB-9928197.4, which is given in the present invention.
 CC (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 4; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRS 210
 DB 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRS 210
 RESULT 12
 AAB84745
 ID AAB84745 standard; protein; 792 AA.
 XX
 AC AAB84745;
 AC
 XX 11-SEP-2003 (revised)
 DT 17-SEP-2001 (first entry)
 XX
 DE Amino acid sequence of a Neisseria gonorrhoeae protein.
 XX
 KW Serogroup B protein; outer membrane protein; Neisseria infection;
 XX vaccine.
 OS Neisseria gonorrhoeae.
 XX
 FH Key Location/Qualifiers

FT Peptide 1. .21
 FT /note= "signal peptide"
 FT Protein 22. .792
 FT /note= "mature protein"
 XX
 DN WO200152885-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 17-JAN-2001; 2001WO-IB000166.
 XX
 PR 17-JAN-2000; 2000GB-00001067.
 PR 09-MAR-2000; 2000GB-00005699.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Pizza M, Rappuoli R, Giuliani M;
 XX WPI; 2001-451895/48.
 DR N-PSDB; AAH42129.
 XX
 CC Composition for treating or preventing infection to, detecting, or for
 CC raising antibodies against Neisseria bacteria, comprises an N.
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component.
 XX
 PS Disclosure; Page 65-67; 83pp; English.
 XX
 CC The present sequence represents a Neisseria gonorrhoeae protein. The
 CC protein is used to produce the compositions of the invention. The
 CC specification describes a composition, comprising a Neisseria
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component. The immunogenic component is protein disclosed in WO99/57280,
 CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
 CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
 CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
 CC medicament for treating or preventing infection due to Neisseria
 CC bacteria; a diagnostic reagent for detecting the presence of Neisseria
 CC bacteria or of antibodies raised against Neisseria bacteria; and/or a
 CC reagent which can raise antibodies against Neisseria bacteria. It may
 CC also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS
 CC field)
 XX
 SQ Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 4; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRS 210
 DB 181 FEGNQVYSRDKLMRQMSLTGGIWTWLTTRS 210
 RESULT 13
 AAB80499
 ID AAB80499 standard; protein; 792 AA.
 XX
 AC AAB80499;
 XX
 DT 07-MAR-2003 (first entry)

XX N. gonorrhoeae amino acid sequence SEQ ID 7528.
 XX Antibacterial; infection; vaccine; gene therapy.
 XX Neisseria gonorrhoeae.
 XX WO200279243-A2.
 XX 10-OCT-2002.
 XX 12-FEB-2002; 2002WO-IB002069.
 XX 12-FEB-2001; 2001GB-00003424.
 XX (CHIR-) CHIRON SPA.
 XX Fontana MR, Pizza M, Massignani V, Monaci E;
 XX WPI; 2003-058415/05.
 XX N-PSDB; ABZ41469.
 XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 XX medicament for treating or preventing N. gonorrhoeae infection.
 XX Disclosure; Page 736; 815pp; English.
 XX The present invention relates to proteins from Neisseria gonorrhoeae.
 XX Also disclosed are the nucleic acid molecules encoding the proteins and
 XX antibodies that specifically bind to the proteins. The composition
 XX comprising the protein, nucleic acid or antibody is useful for the
 XX manufacture of a medicament for treating or preventing N. gonorrhoeae
 XX infection, this may be in the form of a vaccine or gene therapy.
 XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
 XX molecules of the invention
 XX Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 6; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 DB 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRKLQMSLTGGIWTWLTSS 210
 DB 181 FEGNOVYSDRKLQMSLTGGIWTWLTSS 210
 RESULT 14
 ID ABP79748 standard; protein; 792 AA.
 AC ABP79748;
 XX 07-MAR-2003 (first entry)
 DE N. gonorrhoeae amino acid sequence SEQ ID 6026.
 XX Antibacterial; infection; vaccine; gene therapy.
 XX Neisseria gonorrhoeae.

PN WO200279243-A2.
 XX 10-OCT-2002.
 XX 12-FEB-2002; 2002WO-IB002069.
 XX 12-FEB-2001; 2001GB-00003424.
 XX (CHIR-) CHIRON SPA.
 XX Fontana MR, Pizza M, Massignani V, Monaci E;
 XX WPI; 2003-058415/05.
 XX N-PSDB; ABZ40718.
 XX New protein from Neisseria gonorrhoeae, useful for the manufacture of a
 XX medicament for treating or preventing N. gonorrhoeae infection.
 XX Disclosure; Page 628; 815pp; English.
 XX The present invention relates to proteins from Neisseria gonorrhoeae.
 XX Also disclosed are the nucleic acid molecules encoding the proteins and
 XX antibodies that specifically bind to the proteins. The composition
 XX comprising the protein, nucleic acid or antibody is useful for the
 XX manufacture of a medicament for treating or preventing N. gonorrhoeae
 XX infection, this may be in the form of a vaccine or gene therapy.
 XX Sequences given in records ABP76736-ABP81046 represent nucleic acid
 XX molecules of the invention
 XX Sequence 792 AA;
 Query Match 26.3%; Score 210; DB 6; Length 792;
 Best Local Similarity 100.0%; Pred. No. 3.3e-201;
 Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 DB 1 MCLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
 QY 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 DB 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
 QY 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 DB 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITDIE 180
 QY 181 FEGNOVYSDRKLQMSLTGGIWTWLTSS 210
 DB 181 FEGNOVYSDRKLQMSLTGGIWTWLTSS 210
 RESULT 15
 ID AAY84946 standard; protein; 792 AA.
 AC AAY84946;
 XX 12-SEP-2003 (revised)
 DT 21-AUG-2000 (first entry)
 XX Amino acid sequence of outer membrane protein (omp) 85.
 DE Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
 XX meningococcal infection; protective immune response; vaccine.
 XX Neisseria gonorrhoeae.
 XX Key Location/Qualifiers
 XX Peptide 1..21
 XX /note= "signal peptide"
 XX WO200023595-A1.

```
XX 27-APR-2000.
XX
XX 22-OCT-1998; 98WO-US022352.
XX
XX 22-OCT-1998; 98WO-US022352.
XX
XX (UYMO-) UNIV MONTANA.
XX
XX Judd RC, Manning SD;
XX
XX WPI; 2000-339694/29.
XX
XX N-PSDB; AAA15155.
XX
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions
XX for gonococcal or meningococcal infections.
XX
XX Claim 1; Fig 2; 98pp; English.
XX
XX The present sequence represents an outer membrane protein (omp) 85 of
XX Neisseria gonorrhoeae. The omp polypeptides and polynucleotides are
XX useful in compositions for use in the prevention, treatment and diagnosis
XX of non-symptomatic gonococcal infection or meningococcal infection and
XX symptomatic disease. They are also useful for the detection of
XX hybridisation complexes. Antigens and antibodies specific omp proteins
XX also provide diagnostic, therapeutic and prophylactic compositions for
XX the treatment or prevention of the infections described above. The
XX antibodies are useful for inducing a protective immune response in humans
XX or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
XX species. The proteins, antibodies and polynucleotide sequences of the
XX present invention may also be used in the screening and development of
XX chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to
XX standardise OS field)
XX
XX SQ Sequence 792 AA;

Query Match 19.7%; Score 157; DB 3; Length 792;
Best Local Similarity 100.0%; Pred. No. 5.4e-148;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Db |||||
Qy 332 TKTVDFVLHIEPGRKIYVNEIHTGNKTRDEVVRRELROMESAPYDTSKLQSKERVEL 391
Db |||||
Qy 392 LGYFDNVQFDAPVPLAGTPDKVDLNMSLTERSTGSLDLSAGWVQDTGLVMSAGVSQDNLFG 451
Db |||||
Qy 452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488
Db |||||
Qy 452 TGKSAALRASRSKTTLNGSLSFDTDPYFTADGVSLGYD 488
Db |||||

Search completed: July 6, 2005, 15:47:37
Job time : 210 secs
```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:44:30 ; Search time 162 Seconds

(without alignments)

1898.018 Million cell updates/sec

Title: US-10-606-618-4

Perfect score: 797

Sequence: 1 MKLKQIASALMLGISPLAF.....LKKKPEIDIQRFQQLGTF 757

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 1722976 seqs, 385795295 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubpa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubpa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/2/pubpa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/2/pubpa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/2/pubpa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/2/pubpa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/2/pubpa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/2/pubpa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/2/pubpa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/2/pubpa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/2/pubpa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/2/pubpa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/2/pubpa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/2/pubpa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/2/pubpa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/2/pubpa/US10E_PUBCOMB.pep.*
18: /cgn2_6/ptodata/2/pubpa/US10_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubpa/US11A_PUBCOMB.pep.*
20: /cgn2_6/ptodata/2/pubpa/US11_NEW_PUB.pep.*
21: /cgn2_6/ptodata/2/pubpa/US60_NEW_PUB.pep.*
22: /cgn2_6/ptodata/2/pubpa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	797	100.0	797	9	US-09-994-192-4
2	797	100.0	797	17	US-10-606-618-4
3	752	94.4	797	14	US-10-181-660-3
4	752	94.4	797	14	US-10-181-660-11
5	752	94.4	797	15	US-10-320-800-6
6	752	94.4	797	16	US-10-181-600-3
7	752	94.4	797	16	US-10-181-600-11
8	751	94.2	776	14	US-10-181-660-5
9	751	94.2	776	14	US-10-181-660-13
10	751	94.2	776	16	US-10-181-600-5
11	751	94.2	776	16	US-10-181-600-13

12	210	26.3	792	14	US-10-181-660-7	Sequence 7, Appli
13	210	26.3	792	16	US-10-181-600-7	Sequence 7, Appli
14	189	23.7	771	14	US-10-181-660-9	Sequence 9, Appli
15	189	23.7	771	14	US-10-181-660-9	Sequence 9, Appli
16	157	19.7	792	9	US-09-994-192-2	Sequence 2, Appli
17	157	19.7	792	16	US-10-467-534-92	Sequence 92, Appli
18	157	19.7	792	17	US-10-606-618-2	Sequence 2, Appli
19	21	2.6	21	14	US-10-181-660-8	Sequence 8, Appli
20	21	2.6	21	16	US-10-181-600-8	Sequence 8, Appli
21	19	2.4	21	14	US-10-181-660-4	Sequence 4, Appli
22	19	2.4	21	16	US-10-181-600-4	Sequence 4, Appli
23	15	1.9	15	14	US-10-181-660-1	Sequence 1, Appli
24	15	1.9	15	16	US-10-181-600-1	Sequence 1, Appli
25	11	1.4	21	14	US-10-181-660-12	Sequence 12, Appli
26	11	1.4	21	16	US-10-181-600-12	Sequence 12, Appli
27	9	1.1	177	15	US-10-425-114-63291	Sequence 13891, A
28	9	1.1	177	15	US-10-425-114-63291	Sequence 13891, A
29	9	1.1	381	16	US-10-424-599-149837	Sequence 149837, A
30	9	1.1	381	16	US-10-437-963-154779	Sequence 154779, A
31	30	1.1	408	15	US-10-425-114-72370	Sequence 72370, A
32	30	1.1	408	16	US-10-425-115-266878	Sequence 266878, A
33	9	1.1	443	15	US-10-424-599-147939	Sequence 147939, A
34	33	1.1	1035	15	US-10-389-566-2330	Sequence 2330, Ap
35	8	1.0	97	10	US-09-933-767-1092	Sequence 1092, Ap
36	8	1.0	97	14	US-10-004-860-1092	Sequence 1092, Ap
37	8	1.0	104	16	US-10-023-282-1092	Sequence 1092, Ap
38	8	1.0	154	15	US-10-424-599-217994	Sequence 217994, A
39	8	1.0	216	15	US-10-369-493-4323	Sequence 4323, Ap
40	8	1.0	250	15	US-10-425-114-51162	Sequence 51162, A
41	8	1.0	299	9	US-09-738-626-4240	Sequence 4240, Ap
42	8	1.0	315	15	US-10-369-493-13893	Sequence 13893, A
43	8	1.0	367	16	US-10-437-963-146233	Sequence 146233, A
44	8	1.0	422	15	US-10-369-493-12887	Sequence 12887, A
45	8	1.0	494	15	US-10-369-493-13128	Sequence 13128, A
46	8	1.0	583	15	US-10-389-647-479	Sequence 479, App
47	8	1.0	785	16	US-10-437-963-201769	Sequence 201769, A
48	8	1.0	882	16	US-10-437-963-118138	Sequence 118138, A
49	8	1.0	897	17	US-10-741-843-7164	Sequence 7164, Ap
50	8	1.0	1577	15	US-10-282-122A-69069	Sequence 69069, A
51	8	1.0	2903	17	US-10-732-923-13991	Sequence 13991, A
52	7	0.9	23	17	US-10-776-224-147	Sequence 147, App
53	7	0.9	32	16	US-10-425-115-275165	Sequence 275165, A
54	7	0.9	37	16	US-10-425-115-352701	Sequence 352701, A
55	7	0.9	50	9	US-09-864-761-4065	Sequence 4065, A
56	7	0.9	52	16	US-10-425-115-215004	Sequence 215004, A
57	7	0.9	55	16	US-10-767-701-50935	Sequence 50935, A
58	7	0.9	56	16	US-10-425-115-341846	Sequence 341846, A
59	7	0.9	58	13	US-10-117-604-10	Sequence 10, Appl
60	7	0.9	62	16	US-10-425-115-196424	Sequence 196424, A
61	7	0.9	64	15	US-10-424-599-144303	Sequence 144303, A
62	7	0.9	64	15	US-10-424-599-203518	Sequence 203518, A
63	7	0.9	64	16	US-10-767-701-53260	Sequence 53260, A
64	7	0.9	66	15	US-10-424-599-248374	Sequence 248374, A
65	7	0.9	68	15	US-10-424-599-190349	Sequence 190349, A
66	7	0.9	69	16	US-10-425-115-359285	Sequence 359285, A
67	7	0.9	71	15	US-10-424-599-249223	Sequence 249223, A
68	7	0.9	76	15	US-10-282-122A-43360	Sequence 43360, A
69	7	0.9	76	16	US-10-425-115-246828	Sequence 246828, A
70	7	0.9	78	15	US-10-424-599-189046	Sequence 189046, A
71	7	0.9	79	16	US-10-437-963-104699	Sequence 104699, A
72	7	0.9	80	16	US-10-437-963-156781	Sequence 156781, A
73	7	0.9	82	11	US-09-864-408A-4096	Sequence 4096, Ap
74	7	0.9	83	15	US-10-424-599-188471	Sequence 188471, A
75	7	0.9	84	16	US-10-425-115-219581	Sequence 219581, A
76	7	0.9	85	15	US-10-369-493-21140	Sequence 21140, A
77	7	0.9	87	9	US-09-764-860-347	Sequence 347, App
78	7	0.9	87	14	US-10-074-095-347	Sequence 347, App
79	7	0.9	87	15	US-10-212-872-347	Sequence 347, App
80	7	0.9	88	14	US-10-012-542-325	Sequence 325, App
81	7	0.9	88	14	US-10-115-123-325	Sequence 325, App
82	7	0.9	88	16	US-10-425-115-364770	Sequence 364770, A
83	7	0.9	90	15	US-10-424-599-174289	Sequence 174289, A
84	7	0.9	92	16	US-10-437-963-188438	Sequence 188438, A

85	7	0.9	93	15	US-10-424-599-146654	Sequence 146654,	158	7	0.9	308	14	US-10-156-761-14268	Sequence 14268, A
86	7	0.9	96	16	US-10-437-963-123593	Sequence 123593,	159	7	0.9	308	17	US-10-732-923-10057	Sequence 10057, A
87	7	0.9	101	16	US-10-425-115-258624	Sequence 258624,	160	7	0.9	310	15	US-10-369-493-12686	Sequence 12686, A
88	7	0.9	102	15	US-10-424-599-259323	Sequence 259323,	161	7	0.9	315	14	US-10-106-698-5557	Sequence 5557, Ap
89	7	0.9	105	15	US-10-424-599-227387	Sequence 227387,	162	7	0.9	324	9	US-09-815-242-13895	Sequence 13895, A
90	7	0.9	106	16	US-10-425-115-338480	Sequence 338480,	163	7	0.9	324	15	US-10-282-122A-76321	Sequence 76321, A
91	7	0.9	107	16	US-10-425-115-354503	Sequence 354503,	164	7	0.9	325	9	US-09-738-626-4781	Sequence 4781, Ap
92	7	0.9	110	14	US-10-291-851-93	Sequence 93, Appl	165	7	0.9	325	16	US-10-781-014-776	Sequence 776, App
93	7	0.9	113	16	US-10-425-115-258019	Sequence 258019,	166	7	0.9	327	15	US-10-264-237-1918	Sequence 1918, Ap
94	7	0.9	122	15	US-10-424-599-166965	Sequence 166965,	167	7	0.9	329	14	US-10-012-819-60	Sequence 60, Appl
95	7	0.9	122	15	US-10-424-599-256379	Sequence 256379,	168	7	0.9	335	10	US-09-934-455-226	Sequence 226, App
96	7	0.9	122	16	US-10-425-115-347287	Sequence 347287,	169	7	0.9	335	15	US-10-225-066A-834	Sequence 834, App
97	7	0.9	122	16	US-10-739-930-8036	Sequence 8036, Ap	170	7	0.9	335	15	US-10-374-780A-294	Sequence 294, App
98	7	0.9	123	16	US-10-425-115-235907	Sequence 235907,	171	7	0.9	336	14	US-10-146-733-20	Sequence 20, Appl
99	7	0.9	123	16	US-10-425-115-314619	Sequence 314619,	172	7	0.9	337	15	US-10-264-237-2731	Sequence 2731, Ap
100	7	0.9	125	16	US-10-767-701-32380	Sequence 32380, A	173	7	0.9	337	15	US-10-282-122A-74662	Sequence 74662, A
101	7	0.9	129	16	US-10-437-963-104429	Sequence 104429,	174	7	0.9	340	16	US-10-767-701-41329	Sequence 41329, A
102	7	0.9	132	15	US-10-276-774-1607	Sequence 1607, Ap	175	7	0.9	342	15	US-10-381-898-9	Sequence 9, Appli
103	7	0.9	133	16	US-10-425-115-239682	Sequence 239682,	176	7	0.9	349	15	US-10-282-122A-51887	Sequence 51887, A
104	7	0.9	145	16	US-10-425-115-366479	Sequence 366479,	177	7	0.9	351	15	US-10-369-493-3808	Sequence 3808, Ap
105	7	0.9	150	15	US-10-282-122A-54511	Sequence 54511, A	178	7	0.9	353	16	US-10-425-115-271431	Sequence 271431,
106	7	0.9	150	16	US-10-767-701-54531	Sequence 54531, A	179	7	0.9	355	15	US-10-357-521-4	Sequence 4, Appli
107	7	0.9	150	16	US-10-425-115-187306	Sequence 187306,	180	7	0.9	355	17	US-10-915-029-8	Sequence 8, Appli
108	7	0.9	150	16	US-10-425-115-331739	Sequence 331739,	181	7	0.9	356	15	US-10-282-122A-52244	Sequence 52244, A
109	7	0.9	151	16	US-10-424-599-171238	Sequence 171238,	182	7	0.9	359	14	US-10-225-486-54	Sequence 54, Appl
110	7	0.9	154	16	US-10-425-115-337169	Sequence 337169,	183	7	0.9	366	15	US-10-369-493-1018	Sequence 1018, Ap
111	7	0.9	157	15	US-10-424-599-257335	Sequence 257335,	184	7	0.9	381	15	US-10-633-680-49	Sequence 49, Appl
112	7	0.9	169	16	US-10-437-963-125771	Sequence 125771,	185	7	0.9	382	10	US-09-798-889-49	Sequence 49, Appl
113	7	0.9	171	17	US-10-472-928-2480	Sequence 2480, Ap	186	7	0.9	383	9	US-09-738-626-4870	Sequence 4870, Ap
114	7	0.9	176	15	US-10-425-114-49034	Sequence 49034, A	187	7	0.9	384	17	US-10-732-923-2861	Sequence 2861, Ap
115	7	0.9	176	17	US-10-732-923-5057	Sequence 5057, Ap	188	7	0.9	386	15	US-10-369-493-8726	Sequence 8726, Ap
116	7	0.9	177	15	US-10-633-680-76	Sequence 76, Appl	189	7	0.9	390	15	US-10-282-122A-48185	Sequence 48185, A
117	7	0.9	177	15	US-10-632-983-55	Sequence 55, Appl	190	7	0.9	391	16	US-10-437-963-189621	Sequence 189621,
118	7	0.9	178	10	US-09-798-889-76	Sequence 76, Appl	191	7	0.9	398	15	US-10-425-114-71531	Sequence 71531, A
119	7	0.9	182	16	US-10-767-701-52318	Sequence 52318, A	192	7	0.9	401	15	US-10-424-599-269452	Sequence 269452,
120	7	0.9	186	16	US-10-739-930-8997	Sequence 8997, Ap	193	7	0.9	405	15	US-10-369-493-8649	Sequence 8649, Ap
121	7	0.9	191	16	US-10-437-963-133805	Sequence 133805,	194	7	0.9	405	15	US-10-369-493-20689	Sequence 20689, A
122	7	0.9	194	15	US-10-424-599-173855	Sequence 173855,	195	7	0.9	405	16	US-10-425-115-192417	Sequence 192417,
123	7	0.9	197	15	US-10-425-114-42546	Sequence 42546, A	196	7	0.9	411	15	US-10-369-493-12939	Sequence 12939, A
124	7	0.9	199	15	US-10-424-599-19625	Sequence 19625,	197	7	0.9	416	15	US-10-282-122A-70224	Sequence 70224, A
125	7	0.9	199	16	US-10-767-701-46512	Sequence 46512, A	198	7	0.9	425	14	US-10-117-015-8	Sequence 8, Appli
126	7	0.9	200	16	US-10-425-115-279847	Sequence 279847,	199	7	0.9	425	17	US-10-946-424-8	Sequence 8, Appli
127	7	0.9	213	14	US-10-029-386-34063	Sequence 34063, A	200	7	0.9	426	15	US-10-369-493-4635	Sequence 4635, Ap
128	7	0.9	213	16	US-10-425-115-185030	Sequence 185030,	201	7	0.9	426	16	US-10-425-115-368617	Sequence 368617,
129	7	0.9	217	15	US-10-425-114-39820	Sequence 39820, A	202	7	0.9	428	17	US-10-732-923-10735	Sequence 10735, A
130	7	0.9	220	16	US-10-437-963-187087	Sequence 187087,	203	7	0.9	429	15	US-10-282-122A-51466	Sequence 51466, A
131	7	0.9	221	15	US-10-369-493-8397	Sequence 8397, Ap	204	7	0.9	432	16	US-10-437-963-182668	Sequence 182668
132	7	0.9	221	16	US-10-425-115-337161	Sequence 337161,	205	7	0.9	433	15	US-10-282-122A-49892	Sequence 49892, A
133	7	0.9	228	15	US-10-369-493-20929	Sequence 20929, A	206	7	0.9	434	15	US-10-369-493-7393	Sequence 7393, Ap
134	7	0.9	228	15	US-10-424-599-171239	Sequence 171239,	207	7	0.9	442	10	US-09-866-050A-641	Sequence 641, App
135	7	0.9	234	10	US-09-882-227-24	Sequence 24, Appl	208	7	0.9	444	15	US-10-369-493-6911	Sequence 6911, Ap
136	7	0.9	234	16	US-10-335-977-8510	Sequence 8510, Ap	209	7	0.9	448	15	US-10-369-493-4105	Sequence 4105, Ap
137	7	0.9	234	16	US-10-425-115-185029	Sequence 185029,	210	7	0.9	456	15	US-10-369-493-20284	Sequence 20284, A
138	7	0.9	245	16	US-10-425-115-351748	Sequence 351748,	211	7	0.9	458	10	US-09-972-268-21	Sequence 21, Appl
139	7	0.9	254	15	US-10-395-607-127	Sequence 127, App	212	7	0.9	458	15	US-10-299-636-99	Sequence 99, Appl
140	7	0.9	254	16	US-10-799-870-127	Sequence 127, App	213	7	0.9	459	15	US-10-282-122A-70133	Sequence 70133, A
141	7	0.9	255	17	US-10-472-928-4076	Sequence 4076, Ap	214	7	0.9	464	9	US-09-912-020-281	Sequence 281, App
142	7	0.9	260	16	US-10-425-115-249662	Sequence 249662,	215	7	0.9	464	14	US-10-287-274-441	Sequence 441, App
143	7	0.9	262	15	US-10-424-599-232524	Sequence 232524,	216	7	0.9	464	15	US-10-282-122A-42613	Sequence 42613, A
144	7	0.9	263	15	US-10-424-599-189044	Sequence 189044,	217	7	0.9	464	16	US-10-771-241-281	Sequence 281, App
145	7	0.9	272	16	US-10-437-963-201475	Sequence 201475,	218	7	0.9	465	17	US-10-904-588-18	Sequence 18, Appl
146	7	0.9	273	16	US-10-437-963-127798	Sequence 127798,	219	7	0.9	469	15	US-10-369-493-13381	Sequence 13381, A
147	7	0.9	274	16	US-10-437-963-116008	Sequence 116008,	220	7	0.9	472	9	US-09-870-162A-3	Sequence 3, Appli
148	7	0.9	280	15	US-10-282-122A-74821	Sequence 74821, A	221	7	0.9	478	17	US-10-469-204-141	Sequence 141, App
149	7	0.9	282	15	US-10-094-749-2096	Sequence 2096, Ap	222	7	0.9	488	16	US-10-437-963-180174	Sequence 180174,
150	7	0.9	285	15	US-10-282-122A-72956	Sequence 72956, A	223	7	0.9	490	14	US-10-074-152-26	Sequence 26, Appl
151	7	0.9	288	15	US-10-369-493-22433	Sequence 22433, A	224	7	0.9	497	9	US-09-815-242-13344	Sequence 13344, A
152	7	0.9	290	15	US-10-776-774-1357	Sequence 1357, Ap	225	7	0.9	497	15	US-10-282-122A-73912	Sequence 73912, A
153	7	0.9	292	15	US-10-282-122A-57001	Sequence 57001, A	226	7	0.9	497	17	US-10-472-928-1718	Sequence 1718, Ap
154	7	0.9	293	15	US-10-369-493-13324	Sequence 13324, A	227	7	0.9	504	18	US-10-617-320-3732	Sequence 3732, Ap
155	7	0.9	301	14	US-10-156-761-13367	Sequence 13367, A	228	7	0.9	510	17	US-10-732-923-13923	Sequence 13923, A
156	7	0.9	305	15	US-10-369-493-640	Sequence 640, App	229	7	0.9	514	14	US-10-161-572-60	Sequence 60, Appl
157	7	0.9	307	15	US-10-424-599-224191	Sequence 224191,	230	7	0.9	517	10	US-09-972-268-20	Sequence 20, Appl

231	7	0.9	518	9	US-09-919-172-20	Sequence 20, Appl	304	7	0.9	953	10	US-09-884-696-3	Sequence 3, Appl
232	7	0.9	518	15	US-10-369-493-18702	Sequence 18702, A	305	7	0.9	953	16	US-10-148-884-5	Sequence 5, Appl
233	7	0.9	518	16	US-10-752-986-20	Sequence 20, Appl	306	7	0.9	959	16	US-10-428-115-37013	Sequence 337013, A
234	7	0.9	521	15	US-10-282-122A-63634	Sequence 63634, A	307	7	0.9	963	14	US-10-080-608A-20	Sequence 20, Appl
235	7	0.9	522	15	US-10-282-122A-50014	Sequence 50014, A	308	7	0.9	963	14	US-10-080-608A-22	Sequence 22, Appl
236	7	0.9	527	15	US-10-282-122A-47475	Sequence 47475, A	309	7	0.9	963	15	US-10-370-685-109	Sequence 109, App
237	7	0.9	527	9	US-09-954-314-22	Sequence 22, Appl	310	7	0.9	963	15	US-10-370-685-111	Sequence 111, App
238	7	0.9	529	14	US-10-230-562-22	Sequence 22, Appl	311	7	0.9	969	16	US-10-478-245-9	Sequence 9, Appl
239	7	0.9	529	14	US-10-230-026-16	Sequence 16, Appl	312	7	0.9	978	15	US-10-108-260A-4153	Sequence 4153, Ap
240	7	0.9	529	16	US-10-739-930-9550	Sequence 9550, Ap	313	7	0.9	992	16	US-10-425-115-194052	Sequence 194052, A
241	7	0.9	529	16	US-10-486-307-16	Sequence 16, Appl	314	7	0.9	1016	9	US-09-738-626-4363	Sequence 64363, Ap
242	7	0.9	539	15	US-10-424-599-227399	Sequence 227399, A	315	7	0.9	1016	15	US-10-282-122A-69491	Sequence 69491, A
243	7	0.9	564	16	US-10-739-930-9713	Sequence 9713, Ap	316	7	0.9	1019	16	US-10-408-765A-1661	Sequence 1661, Ap
244	7	0.9	564	17	US-10-481-113-28	Sequence 28, Appl	317	7	0.9	1031	16	US-10-437-963-169433	Sequence 169433, A
245	7	0.9	568	14	US-10-032-585-7920	Sequence 7920, Ap	318	7	0.9	1054	15	US-10-001-885-108	Sequence 108, App
246	7	0.9	572	16	US-10-437-963-173191	Sequence 173191, A	319	7	0.9	1120	15	US-10-335-977-5265	Sequence 5265, Ap
247	7	0.9	572	17	US-10-481-113-104	Sequence 104, App	320	7	0.9	1120	16	US-10-437-963-152821	Sequence 152821, A
248	7	0.9	578	16	US-10-425-115-249810	Sequence 249810, A	321	7	0.9	1121	8	US-08-915-048A-2	Sequence 2, Appl
249	7	0.9	580	15	US-10-647-057-4	Sequence 4, Appl	322	7	0.9	1174	14	US-10-184-644-353	Sequence 353, App
250	7	0.9	581	16	US-10-767-701-46924	Sequence 46924, A	323	7	0.9	1174	14	US-10-184-634-333	Sequence 353, App
251	7	0.9	584	15	US-10-282-122A-47689	Sequence 47689, A	324	7	0.9	1187	15	US-10-389-566-1202	Sequence 1202, Ap
252	7	0.9	587	10	US-09-893-519A-42	Sequence 42, Appl	325	7	0.9	1248	16	US-10-437-963-188299	Sequence 188299, A
253	7	0.9	589	14	US-10-205-194-144	Sequence 144, App	326	7	0.9	1264	14	US-10-123-155-1	Sequence 1, Appl
254	7	0.9	589	16	US-10-437-963-127286	Sequence 127286, A	327	7	0.9	1264	14	US-10-146-731-1	Sequence 1, Appl
255	7	0.9	590	17	US-10-831-070-10	Sequence 10, Appl	328	7	0.9	1264	14	US-10-140-472-1	Sequence 1, Appl
256	7	0.9	604	9	US-09-862-027-17	Sequence 17, Appl	329	7	0.9	1264	14	US-10-141-761-1	Sequence 1, Appl
257	7	0.9	604	17	US-10-989-228-17	Sequence 17, Appl	330	7	0.9	1264	14	US-10-142-885-1	Sequence 1, Appl
258	7	0.9	619	15	US-10-369-493-5855	Sequence 5855, Ap	331	7	0.9	1264	14	US-10-158-790-1	Sequence 1, Appl
259	7	0.9	620	10	US-09-893-519A-59	Sequence 59, Appl	332	7	0.9	1264	15	US-10-137-871-1	Sequence 1, Appl
260	7	0.9	620	15	US-10-369-493-1442	Sequence 1442, Ap	333	7	0.9	1264	15	US-10-140-923-1	Sequence 1, Appl
261	7	0.9	622	14	US-10-197-668A-22	Sequence 22, Appl	334	7	0.9	1264	15	US-10-141-756-1	Sequence 1, Appl
262	7	0.9	622	14	US-10-024-298A-63	Sequence 63, Appl	335	7	0.9	1264	15	US-10-141-759-1	Sequence 1, Appl
263	7	0.9	622	14	US-10-042-211A-63	Sequence 63, Appl	336	7	0.9	1264	15	US-10-140-805-1	Sequence 1, Appl
264	7	0.9	622	15	US-10-617-217A-63	Sequence 63, Appl	337	7	0.9	1264	15	US-10-140-864-1	Sequence 1, Appl
265	7	0.9	622	16	US-10-024-298A-63	Sequence 63, Appl	338	7	0.9	1264	15	US-10-142-426-1	Sequence 1, Appl
266	7	0.9	625	15	US-10-369-493-22882	Sequence 22882, A	339	7	0.9	1296	14	US-10-302-279-60	Sequence 60, Appl
267	7	0.9	628	14	US-10-156-761-10990	Sequence 10990, A	340	7	0.9	1297	14	US-10-184-644-599	Sequence 599, App
268	7	0.9	632	14	US-10-024-298A-65	Sequence 65, Appl	341	7	0.9	1297	14	US-10-184-634-599	Sequence 599, App
269	7	0.9	632	14	US-10-042-211A-65	Sequence 65, Appl	342	7	0.9	1297	14	US-10-123-155-435	Sequence 435, App
270	7	0.9	632	15	US-10-617-217A-65	Sequence 65, Appl	343	7	0.9	1297	14	US-10-146-731-435	Sequence 435, App
271	7	0.9	632	16	US-10-024-298A-65	Sequence 65, Appl	344	7	0.9	1297	14	US-10-140-472-435	Sequence 435, App
272	7	0.9	640	16	US-10-425-115-317987	Sequence 317987, A	345	7	0.9	1297	14	US-10-141-761-435	Sequence 435, App
273	7	0.9	663	15	US-10-282-122A-52415	Sequence 52415, A	346	7	0.9	1297	14	US-10-142-885-435	Sequence 435, App
274	7	0.9	666	10	US-09-746-660A-46	Sequence 46, Appl	347	7	0.9	1297	14	US-10-158-790-435	Sequence 435, App
275	7	0.9	667	16	US-10-767-701-46248	Sequence 46248, A	348	7	0.9	1297	15	US-10-137-871-435	Sequence 435, App
276	7	0.9	673	15	US-10-433-794-2	Sequence 2, Appl	349	7	0.9	1297	15	US-10-140-923-435	Sequence 435, App
277	7	0.9	676	18	US-10-617-320-4098	Sequence 4098, Ap	350	7	0.9	1297	15	US-10-141-756-435	Sequence 435, App
278	7	0.9	684	16	US-10-437-963-111247	Sequence 111247, A	351	7	0.9	1297	15	US-10-141-759-435	Sequence 435, App
279	7	0.9	686	15	US-10-282-122A-67777	Sequence 67777, A	352	7	0.9	1297	15	US-10-140-805-435	Sequence 435, App
280	7	0.9	692	15	US-10-369-493-8800	Sequence 8800, Ap	353	7	0.9	1297	15	US-10-140-864-435	Sequence 435, App
281	7	0.9	695	10	US-09-305-924-13	Sequence 13, Appl	354	7	0.9	1297	15	US-10-142-426-435	Sequence 435, App
282	7	0.9	699	14	US-10-156-761-12338	Sequence 12338, A	355	7	0.9	1320	14	US-10-161-051-167	Sequence 167, App
283	7	0.9	705	15	US-10-425-114-46512	Sequence 46512, A	356	7	0.9	1334	14	US-10-184-644-339	Sequence 339, App
284	7	0.9	711	15	US-10-425-114-54901	Sequence 54901, A	357	7	0.9	1334	14	US-10-184-634-339	Sequence 339, App
285	7	0.9	711	16	US-10-425-115-317988	Sequence 317988, A	358	7	0.9	1336	14	US-10-224-999A-3482	Sequence 110486, A
286	7	0.9	717	15	US-10-267-502-250	Sequence 250, App	359	7	0.9	1355	16	US-10-437-963-110486	Sequence 110486, A
287	7	0.9	732	14	US-10-184-634-577	Sequence 577, App	360	7	0.9	1376	14	US-10-123-155-161	Sequence 161, App
288	7	0.9	732	14	US-10-184-634-577	Sequence 577, App	361	7	0.9	1376	14	US-10-146-731-161	Sequence 161, App
289	7	0.9	741	15	US-10-282-122A-70070	Sequence 70070, A	362	7	0.9	1376	14	US-10-140-472-161	Sequence 161, App
290	7	0.9	755	16	US-10-437-963-171603	Sequence 171603, A	363	7	0.9	1376	14	US-10-141-761-161	Sequence 161, App
291	7	0.9	761	16	US-10-416-330-35	Sequence 35, Appl	364	7	0.9	1376	14	US-10-142-885-161	Sequence 161, App
292	7	0.9	786	17	US-10-874-049-3	Sequence 3, Appl	365	7	0.9	1376	14	US-10-158-790-161	Sequence 161, App
293	7	0.9	789	17	US-10-874-049-5	Sequence 5, Appl	366	7	0.9	1376	15	US-10-137-871-161	Sequence 161, App
294	7	0.9	792	13	US-10-087-192-1977	Sequence 1977, Ap	367	7	0.9	1376	15	US-10-140-923-161	Sequence 161, App
295	7	0.9	797	15	US-10-369-493-12480	Sequence 12480, A	368	7	0.9	1376	15	US-10-141-756-161	Sequence 161, App
296	7	0.9	818	9	US-09-738-626-6491	Sequence 6491, Ap	369	7	0.9	1376	15	US-10-141-759-161	Sequence 161, App
297	7	0.9	822	16	US-10-437-963-104983	Sequence 104983, A	370	7	0.9	1376	15	US-10-140-805-161	Sequence 161, App
298	7	0.9	850	14	US-10-238-075-1021	Sequence 1021, Ap	371	7	0.9	1376	15	US-10-140-864-161	Sequence 161, App
299	7	0.9	874	15	US-10-282-122A-61488	Sequence 61488, A	372	7	0.9	1376	15	US-10-142-426-161	Sequence 161, App
300	7	0.9	902	14	US-10-184-644-303	Sequence 303, App	373	7	0.9	1390	14	US-10-137-418A-2	Sequence 2, Appl
301	7	0.9	902	14	US-10-184-634-303	Sequence 303, App	374	7	0.9	1419	14	US-10-123-155-517	Sequence 517, App
302	7	0.9	902	14	US-10-063-685-93	Sequence 93, Appl	375	7	0.9	1419	14	US-10-146-731-517	Sequence 517, App
303	7	0.9	933	13	US-10-087-192-1980	Sequence 1980, Ap	376	7	0.9	1419	14	US-10-140-472-517	Sequence 517, App

377 7 0.9 1419 14 US-10-141-761-517 Sequence 517, App
 378 7 0.9 1419 14 US-10-142-885-517 Sequence 517, App
 379 7 0.9 1419 14 US-10-158-790-517 Sequence 517, App
 380 7 0.9 1419 15 US-10-137-871-517 Sequence 517, App
 381 7 0.9 1419 15 US-10-140-923-517 Sequence 517, App
 382 7 0.9 1419 15 US-10-141-756-517 Sequence 517, App
 383 7 0.9 1419 15 US-10-141-756-517 Sequence 517, App
 384 7 0.9 1419 15 US-10-140-805-517 Sequence 517, App
 385 7 0.9 1419 15 US-10-140-864-517 Sequence 517, App
 386 7 0.9 1419 15 US-10-092-900A-82 Sequence 82, Appl
 387 7 0.9 1419 15 US-10-142-426-517 Sequence 517, App
 388 7 0.9 1423 15 US-10-092-900A-86 Sequence 86, Appl
 389 7 0.9 1434 8 US-08-954-701A-10 Sequence 10, Appl
 390 7 0.9 1434 10 US-09-754-032-10 Sequence 10, Appl
 391 7 0.9 1434 14 US-10-421-446-10 Sequence 10, Appl
 392 7 0.9 1439 16 US-10-220-481-73 Sequence 73, Appl
 393 7 0.9 1447 8 US-08-954-701A-19 Sequence 19, Appl
 394 7 0.9 1447 9 US-08-898-533-5 Sequence 5, Appl
 395 7 0.9 1447 10 US-09-754-032-19 Sequence 19, Appl
 396 7 0.9 1447 14 US-10-421-446-19 Sequence 19, Appl
 397 7 0.9 1449 15 US-10-282-122A-65711 Sequence 65711, A
 398 7 0.9 1454 16 US-10-742-345-2 Sequence 2, Appl
 399 7 0.9 1457 16 US-10-220-481-71 Sequence 71, Appl
 400 7 0.9 1457 16 US-10-742-345-4 Sequence 4, Appl
 401 7 0.9 1458 13 US-10-054-691-2 Sequence 2, Appl
 402 7 0.9 1458 16 US-10-478-245-1 Sequence 1, Appl
 403 7 0.9 1468 15 US-10-282-122A-65027 Sequence 65027, A
 404 7 0.9 1471 14 US-10-123-155-281 Sequence 281, App
 405 7 0.9 1471 14 US-10-146-731-281 Sequence 281, App
 406 7 0.9 1471 14 US-10-140-472-281 Sequence 281, App
 407 7 0.9 1471 14 US-10-141-761-281 Sequence 281, App
 408 7 0.9 1471 14 US-10-142-885-281 Sequence 281, App
 409 7 0.9 1471 14 US-10-158-790-281 Sequence 281, App
 410 7 0.9 1471 15 US-10-137-871-281 Sequence 281, App
 411 7 0.9 1471 15 US-10-140-923-281 Sequence 281, App
 412 7 0.9 1471 15 US-10-141-756-281 Sequence 281, App
 413 7 0.9 1471 15 US-10-141-759-281 Sequence 281, App
 414 7 0.9 1471 15 US-10-140-805-281 Sequence 281, App
 415 7 0.9 1471 15 US-10-140-864-281 Sequence 281, App
 416 7 0.9 1471 15 US-10-142-426-281 Sequence 281, App
 417 7 0.9 1484 14 US-10-123-155-447 Sequence 447, App
 418 7 0.9 1484 14 US-10-146-731-447 Sequence 447, App
 419 7 0.9 1484 14 US-10-140-472-447 Sequence 447, App
 420 7 0.9 1484 14 US-10-141-761-447 Sequence 447, App
 421 7 0.9 1484 14 US-10-142-885-447 Sequence 447, App
 422 7 0.9 1484 14 US-10-158-790-447 Sequence 447, App
 423 7 0.9 1484 15 US-10-137-871-447 Sequence 447, App
 424 7 0.9 1484 15 US-10-140-923-447 Sequence 447, App
 425 7 0.9 1484 15 US-10-141-756-447 Sequence 447, App
 426 7 0.9 1484 15 US-10-140-805-447 Sequence 447, App
 427 7 0.9 1484 15 US-10-140-864-447 Sequence 447, App
 428 7 0.9 1484 15 US-10-142-426-447 Sequence 447, App
 429 7 0.9 1515 14 US-10-184-644-399 Sequence 399, App
 430 7 0.9 1515 14 US-10-184-634-399 Sequence 399, App
 431 7 0.9 1515 14 US-10-063-685-157 Sequence 157, App
 432 7 0.9 1536 14 US-10-184-644-461 Sequence 461, App
 433 7 0.9 1536 14 US-10-184-634-461 Sequence 461, App
 434 7 0.9 1576 15 US-10-335-977-5266 Sequence 5266, App
 435 7 0.9 1584 17 US-10-732-923-12885 Sequence 12885, A
 436 7 0.9 1624 14 US-10-123-155-181 Sequence 181, App
 437 7 0.9 1624 14 US-10-146-731-181 Sequence 181, App
 438 7 0.9 1624 14 US-10-140-472-181 Sequence 181, App
 439 7 0.9 1624 14 US-10-141-761-181 Sequence 181, App
 440 7 0.9 1624 14 US-10-142-885-181 Sequence 181, App
 441 7 0.9 1624 14 US-10-158-790-181 Sequence 181, App
 442 7 0.9 1624 15 US-10-137-871-181 Sequence 181, App
 443 7 0.9 1624 15 US-10-140-923-181 Sequence 181, App
 444 7 0.9 1624 15 US-10-141-756-181 Sequence 181, App
 445 7 0.9 1624 15 US-10-141-759-181 Sequence 181, App
 446 7 0.9 1624 15 US-10-140-805-181 Sequence 181, App
 447 7 0.9 1624 15 US-10-140-864-181 Sequence 181, App
 448 7 0.9 1624 15 US-10-142-426-181 Sequence 181, App
 449 7 0.9 1624 15 US-10-142-426-181 Sequence 181, App

14 1665 14 US-10-184-644-285 Sequence 285, App
 14 1665 14 US-10-184-634-285 Sequence 285, App
 14 1665 14 US-10-063-685-85 Sequence 85, App
 13 1686 13 US-10-092-219-2 Sequence 2, Appl
 14 1730 14 US-10-123-155-7 Sequence 7, Appl
 14 1730 14 US-10-146-731-7 Sequence 7, Appl
 14 1730 14 US-10-140-472-7 Sequence 7, Appl
 14 1730 14 US-10-141-761-7 Sequence 7, Appl
 14 1730 14 US-10-142-885-7 Sequence 7, Appl
 14 1730 14 US-10-158-790-7 Sequence 7, Appl
 15 1730 15 US-10-137-871-7 Sequence 7, Appl
 15 1730 15 US-10-140-923-7 Sequence 7, Appl
 15 1730 15 US-10-141-756-7 Sequence 7, Appl
 15 1730 15 US-10-141-759-7 Sequence 7, Appl
 15 1730 15 US-10-140-805-7 Sequence 7, Appl
 15 1730 15 US-10-140-864-7 Sequence 7, Appl
 15 1730 15 US-10-142-426-7 Sequence 7, Appl
 14 1771 14 US-10-184-644-17 Sequence 17, Appl
 14 1771 14 US-10-184-634-17 Sequence 17, Appl
 15 1775 15 US-10-335-977-5267 Sequence 5267, App
 14 1808 14 US-10-123-155-47 Sequence 47, Appl
 14 1808 14 US-10-146-731-47 Sequence 47, Appl
 14 1808 14 US-10-140-472-47 Sequence 47, Appl
 14 1808 14 US-10-141-761-47 Sequence 47, Appl
 14 1808 14 US-10-142-885-47 Sequence 47, Appl
 14 1808 14 US-10-158-790-47 Sequence 47, Appl
 15 1808 15 US-10-137-871-47 Sequence 47, Appl
 15 1808 15 US-10-140-923-47 Sequence 47, Appl
 15 1808 15 US-10-141-756-47 Sequence 47, Appl
 15 1808 15 US-10-141-759-47 Sequence 47, Appl
 15 1808 15 US-10-140-805-47 Sequence 47, Appl
 15 1808 15 US-10-140-864-47 Sequence 47, Appl
 14 1849 14 US-10-184-644-133 Sequence 133, App
 14 1849 14 US-10-184-634-133 Sequence 133, App
 14 1849 14 US-10-063-685-21 Sequence 21, Appl
 14 1883 14 US-10-123-155-501 Sequence 501, App
 14 1883 14 US-10-146-731-501 Sequence 501, App
 14 1883 14 US-10-140-472-501 Sequence 501, App
 14 1883 14 US-10-141-761-501 Sequence 501, App
 14 1883 14 US-10-142-885-501 Sequence 501, App
 14 1883 14 US-10-158-790-501 Sequence 501, App
 15 1883 15 US-10-137-871-501 Sequence 501, App
 15 1883 15 US-10-140-923-501 Sequence 501, App
 15 1883 15 US-10-141-756-501 Sequence 501, App
 15 1883 15 US-10-141-759-501 Sequence 501, App
 15 1883 15 US-10-140-805-501 Sequence 501, App
 15 1883 15 US-10-140-864-501 Sequence 501, App
 15 1883 15 US-10-142-426-501 Sequence 501, App
 15 1912 15 US-10-188-186-48 Sequence 48, Appl
 9 1943 9 US-10-282-132A-58750 Sequence 58750, A
 7 0.9 1974 9 US-09-895-913A-12 Sequence 12, Appl
 14 1975 14 US-10-123-155-105 Sequence 105, App
 14 1975 14 US-10-146-731-105 Sequence 105, App
 14 1975 14 US-10-140-472-105 Sequence 105, App
 14 1975 14 US-10-141-761-105 Sequence 105, App
 14 1975 14 US-10-142-885-105 Sequence 105, App
 14 1975 14 US-10-158-790-105 Sequence 105, App
 15 1975 15 US-10-137-871-105 Sequence 105, App
 15 1975 15 US-10-140-923-105 Sequence 105, App
 15 1975 15 US-10-141-756-105 Sequence 105, App
 15 1975 15 US-10-141-759-105 Sequence 105, App
 15 1975 15 US-10-140-805-105 Sequence 105, App
 15 1975 15 US-10-140-864-105 Sequence 105, App
 15 1975 15 US-10-142-426-105 Sequence 105, App
 14 2037 14 US-10-184-644-591 Sequence 591, App
 14 2037 14 US-10-184-634-591 Sequence 591, App
 17 2055 17 US-10-481-582-3 Sequence 3, Appl
 14 2103 14 US-10-184-644-319 Sequence 319, App
 14 2103 14 US-10-184-634-319 Sequence 319, App
 14 2103 14 US-10-063-685-105 Sequence 105, App
 14 2134 14 US-10-123-155-179 Sequence 179, App
 14 2134 14 US-10-146-731-179 Sequence 179, App

523	7	0.9	2134	14	US-10-140-472-179	Sequence 179, App	596	7	0.9	2615	14	US-10-184-644-523	Sequence 523, App
524	7	0.9	2134	14	US-10-141-761-179	Sequence 179, App	597	7	0.9	2615	14	US-10-184-634-523	Sequence 523, App
525	7	0.9	2134	14	US-10-142-885-179	Sequence 179, App	598	7	0.9	2732	14	US-10-238-075-1119	Sequence 1119, App
526	7	0.9	2134	14	US-10-158-790-179	Sequence 179, App	599	7	0.9	2819	14	US-10-184-644-109	Sequence 109, App
527	7	0.9	2134	15	US-10-137-871-179	Sequence 179, App	600	7	0.9	2819	14	US-10-184-634-109	Sequence 109, App
528	7	0.9	2134	15	US-10-140-923-179	Sequence 179, App	601	7	0.9	2834	14	US-10-085-959-252	Sequence 252, App
529	7	0.9	2134	15	US-10-141-756-179	Sequence 179, App	602	7	0.9	2916	14	US-10-123-155-69	Sequence 69, App
530	7	0.9	2134	15	US-10-141-759-179	Sequence 179, App	603	7	0.9	2916	14	US-10-123-155-69	Sequence 69, App
531	7	0.9	2134	15	US-10-140-805-179	Sequence 179, App	604	7	0.9	2916	14	US-10-146-731-69	Sequence 69, App
532	7	0.9	2134	15	US-10-140-864-179	Sequence 179, App	605	7	0.9	2916	14	US-10-140-472-69	Sequence 69, App
533	7	0.9	2134	15	US-10-142-426-179	Sequence 179, App	606	7	0.9	2916	14	US-10-141-761-69	Sequence 69, App
534	7	0.9	2237	14	US-10-123-155-45	Sequence 45, App	607	7	0.9	2916	14	US-10-142-885-69	Sequence 69, App
535	7	0.9	2237	14	US-10-146-731-45	Sequence 45, App	608	7	0.9	2916	15	US-10-158-790-69	Sequence 69, App
536	7	0.9	2237	14	US-10-140-472-45	Sequence 45, App	609	7	0.9	2916	15	US-10-137-871-69	Sequence 69, App
537	7	0.9	2237	14	US-10-141-761-45	Sequence 45, App	610	7	0.9	2916	15	US-10-140-923-69	Sequence 69, App
538	7	0.9	2237	14	US-10-142-885-45	Sequence 45, App	611	7	0.9	2916	15	US-10-141-756-69	Sequence 69, App
539	7	0.9	2237	14	US-10-158-790-45	Sequence 45, App	612	7	0.9	2916	15	US-10-141-759-69	Sequence 69, App
540	7	0.9	2237	15	US-10-137-871-45	Sequence 45, App	613	7	0.9	2916	15	US-10-140-805-69	Sequence 69, App
541	7	0.9	2237	15	US-10-140-923-45	Sequence 45, App	614	7	0.9	2916	15	US-10-140-864-69	Sequence 69, App
542	7	0.9	2237	15	US-10-141-756-45	Sequence 45, App	615	7	0.9	2956	14	US-10-142-426-69	Sequence 69, App
543	7	0.9	2237	15	US-10-141-759-45	Sequence 45, App	616	7	0.9	2956	14	US-10-184-634-73	Sequence 73, App
544	7	0.9	2237	15	US-10-140-805-45	Sequence 45, App	617	7	0.9	3033	14	US-10-184-634-73	Sequence 73, App
545	7	0.9	2237	15	US-10-140-864-45	Sequence 45, App	618	7	0.9	3033	14	US-10-184-644-1	Sequence 1, App
546	7	0.9	2237	15	US-10-142-426-45	Sequence 45, App	619	7	0.9	3038	14	US-10-184-644-261	Sequence 261, App
547	7	0.9	2274	15	US-10-267-502-373	Sequence 373, App	620	7	0.9	3038	14	US-10-184-634-261	Sequence 261, App
548	7	0.9	2274	17	US-10-805-684-140	Sequence 140, App	621	7	0.9	3089	14	US-10-184-644-61	Sequence 61, App
549	7	0.9	2275	14	US-10-184-644-401	Sequence 401, App	622	7	0.9	3089	14	US-10-184-634-61	Sequence 61, App
550	7	0.9	2275	14	US-10-184-634-401	Sequence 401, App	623	7	0.9	3122	14	US-10-200-562-201	Sequence 201, App
551	7	0.9	2303	15	US-10-267-502-371	Sequence 371, App	624	7	0.9	3122	14	US-10-237-551-201	Sequence 201, App
552	7	0.9	2303	17	US-10-852-335A-109	Sequence 109, App	625	7	0.9	3122	14	US-10-237-551-250	Sequence 250, App
553	7	0.9	2338	14	US-10-029-386-31982	Sequence 31982, A	626	7	0.9	3122	18	US-10-945-050-201	Sequence 201, App
554	7	0.9	2387	14	US-10-123-155-527	Sequence 527, App	627	7	0.9	3122	18	US-10-945-050-250	Sequence 250, App
555	7	0.9	2387	14	US-10-146-731-527	Sequence 527, App	628	7	0.9	3150	14	US-10-184-644-81	Sequence 81, App
556	7	0.9	2387	14	US-10-140-472-527	Sequence 527, App	629	7	0.9	3150	14	US-10-184-634-81	Sequence 81, App
557	7	0.9	2387	14	US-10-141-761-527	Sequence 527, App	630	7	0.9	3192	14	US-10-123-155-75	Sequence 75, App
558	7	0.9	2387	14	US-10-142-885-527	Sequence 527, App	631	7	0.9	3192	14	US-10-146-731-75	Sequence 75, App
559	7	0.9	2387	14	US-10-158-790-527	Sequence 527, App	632	7	0.9	3192	14	US-10-140-472-75	Sequence 75, App
560	7	0.9	2387	15	US-10-137-871-527	Sequence 527, App	633	7	0.9	3192	14	US-10-141-761-75	Sequence 75, App
561	7	0.9	2387	15	US-10-140-923-527	Sequence 527, App	634	7	0.9	3192	14	US-10-142-885-75	Sequence 75, App
562	7	0.9	2387	15	US-10-141-756-527	Sequence 527, App	635	7	0.9	3192	14	US-10-158-790-75	Sequence 75, App
563	7	0.9	2387	15	US-10-141-759-527	Sequence 527, App	636	7	0.9	3192	15	US-10-137-871-75	Sequence 75, App
564	7	0.9	2387	15	US-10-140-805-527	Sequence 527, App	637	7	0.9	3192	15	US-10-140-923-75	Sequence 75, App
565	7	0.9	2387	15	US-10-140-864-527	Sequence 527, App	638	7	0.9	3192	15	US-10-141-756-75	Sequence 75, App
566	7	0.9	2387	15	US-10-142-426-527	Sequence 527, App	639	7	0.9	3192	15	US-10-141-759-75	Sequence 75, App
567	7	0.9	2397	14	US-10-184-644-29	Sequence 29, App	640	7	0.9	3192	15	US-10-140-805-75	Sequence 75, App
568	7	0.9	2397	14	US-10-184-644-323	Sequence 323, App	641	7	0.9	3192	15	US-10-140-864-75	Sequence 75, App
569	7	0.9	2397	14	US-10-184-634-29	Sequence 29, App	642	7	0.9	3192	15	US-10-142-426-75	Sequence 75, App
570	7	0.9	2397	14	US-10-184-634-323	Sequence 323, App	643	7	0.9	3194	15	US-10-282-122A-59046	Sequence 59046, A
571	7	0.9	2397	14	US-10-063-685-107	Sequence 107, App	644	7	0.9	3233	14	US-10-123-155-81	Sequence 81, App
572	7	0.9	2431	9	US-09-901-106-2	Sequence 2, App	645	7	0.9	3233	14	US-10-146-731-81	Sequence 81, App
573	7	0.9	2457	14	US-10-184-644-569	Sequence 569, App	646	7	0.9	3233	14	US-10-140-472-81	Sequence 81, App
574	7	0.9	2457	14	US-10-184-634-569	Sequence 569, App	647	7	0.9	3233	14	US-10-141-761-81	Sequence 81, App
575	7	0.9	2478	14	US-10-184-644-107	Sequence 107, App	648	7	0.9	3233	14	US-10-142-885-81	Sequence 81, App
576	7	0.9	2478	14	US-10-184-634-107	Sequence 107, App	649	7	0.9	3233	14	US-10-158-790-81	Sequence 81, App
577	7	0.9	2497	17	US-10-481-582-4	Sequence 4, App	650	7	0.9	3233	15	US-10-137-871-81	Sequence 81, App
578	7	0.9	2558	14	US-10-184-644-103	Sequence 103, App	651	7	0.9	3233	15	US-10-140-923-81	Sequence 81, App
579	7	0.9	2558	14	US-10-184-634-103	Sequence 103, App	652	7	0.9	3233	15	US-10-141-756-81	Sequence 81, App
580	7	0.9	2594	14	US-10-123-155-245	Sequence 245, App	653	7	0.9	3233	15	US-10-141-759-81	Sequence 81, App
581	7	0.9	2594	14	US-10-146-731-245	Sequence 245, App	654	7	0.9	3233	15	US-10-140-805-81	Sequence 81, App
582	7	0.9	2594	14	US-10-140-472-245	Sequence 245, App	655	7	0.9	3233	15	US-10-140-864-81	Sequence 81, App
583	7	0.9	2594	14	US-10-141-761-245	Sequence 245, App	656	7	0.9	3233	15	US-10-142-426-81	Sequence 81, App
584	7	0.9	2594	14	US-10-142-885-245	Sequence 245, App	657	7	0.9	3240	14	US-10-184-644-415	Sequence 415, App
585	7	0.9	2594	14	US-10-158-790-245	Sequence 245, App	658	7	0.9	3240	14	US-10-184-634-415	Sequence 415, App
586	7	0.9	2594	15	US-10-137-871-245	Sequence 245, App	659	7	0.9	3233	14	US-10-123-155-167	Sequence 167, App
587	7	0.9	2594	15	US-10-140-923-245	Sequence 245, App	660	7	0.9	3233	14	US-10-146-731-167	Sequence 167, App
588	7	0.9	2594	15	US-10-141-756-245	Sequence 245, App	661	7	0.9	3233	14	US-10-140-472-167	Sequence 167, App
589	7	0.9	2594	15	US-10-141-759-245	Sequence 245, App	662	7	0.9	3233	14	US-10-141-761-167	Sequence 167, App
590	7	0.9	2594	15	US-10-140-805-245	Sequence 245, App	663	7	0.9	3233	14	US-10-142-885-167	Sequence 167, App
591	7	0.9	2594	15	US-10-140-864-245	Sequence 245, App	664	7	0.9	3233	14	US-10-158-790-167	Sequence 167, App
592	7	0.9	2594	15	US-10-142-426-245	Sequence 245, App	665	7	0.9	3233	15	US-10-137-871-167	Sequence 167, App
593	7	0.9	2598	14	US-10-063-685-151	Sequence 151, App	666	7	0.9	3233	15	US-10-140-923-167	Sequence 167, App
594	7	0.9	2609	14	US-10-184-644-407	Sequence 407, App	667	7	0.9	3233	15	US-10-141-756-167	Sequence 167, App
595	7	0.9	2609	14	US-10-184-634-407	Sequence 407, App	668	7	0.9	3233	15	US-10-141-759-167	Sequence 167, App

669	7	0.9	3323	15	US-10-140-805-167	Sequence 167, App	742	13	15	US-10-411-869A-53	Sequence 53, Appl
670	7	0.9	3323	15	US-10-140-864-167	Sequence 167, App	743	14	14	US-10-312-691-6	Sequence 6, Appl
671	7	0.9	3323	15	US-10-142-426-167	Sequence 167, App	744	14	16	US-10-813-638-1304	Sequence 1304, Ap
672	7	0.9	3401	14	US-10-184-644-411	Sequence 411, App	745	15	10	US-09-880-748-2970	Sequence 2970, Ap
673	7	0.9	3401	14	US-10-184-634-411	Sequence 411, App	746	15	15	US-10-293-418-2970	Sequence 2970, Ap
674	7	0.9	3552	14	US-10-123-155-339	Sequence 339, App	747	15	15	US-10-412-964-68	Sequence 68, Appl
675	7	0.9	3552	14	US-10-146-731-339	Sequence 339, App	748	18	15	US-10-187-496A-20	Sequence 20, Appl
676	7	0.9	3552	14	US-10-140-472-339	Sequence 339, App	749	18	9	US-09-932-923-1	Sequence 1, Appl
677	7	0.9	3552	14	US-10-141-761-339	Sequence 339, App	750	16	16	US-10-297-969-6	Sequence 6, Appl
678	7	0.9	3552	14	US-10-142-885-339	Sequence 339, App	751	21	15	US-10-449-735-3	Sequence 3, Appl
679	7	0.9	3552	14	US-10-158-790-339	Sequence 339, App	752	23	14	US-10-097-065-356	Sequence 356, App
680	7	0.9	3552	15	US-10-137-871-339	Sequence 339, App	753	23	15	US-10-372-876-356	Sequence 356, App
681	7	0.9	3552	15	US-10-140-923-339	Sequence 339, App	754	24	10	US-09-843-221A-129	Sequence 129, App
682	7	0.9	3552	15	US-10-141-756-339	Sequence 339, App	755	24	10	US-09-843-221A-130	Sequence 130, App
683	7	0.9	3552	15	US-10-141-759-339	Sequence 339, App	756	24	12	US-09-999-608-129	Sequence 129, App
684	7	0.9	3552	15	US-10-140-805-339	Sequence 339, App	757	24	12	US-09-999-608-130	Sequence 130, App
685	7	0.9	3552	15	US-10-140-864-339	Sequence 339, App	758	24	16	US-10-425-115-338692	Sequence 338692,
686	7	0.9	3552	15	US-10-142-426-339	Sequence 339, App	759	24	16	US-10-839-037-129	Sequence 129, App
687	7	0.9	3871	14	US-10-184-644-347	Sequence 347, App	760	24	16	US-10-839-037-130	Sequence 130, App
688	7	0.9	3871	14	US-10-184-634-347	Sequence 347, App	761	25	9	US-09-911-888-35	Sequence 35, Appl
689	7	0.9	4040	14	US-10-123-155-425	Sequence 425, App	762	25	9	US-09-911-927-35	Sequence 35, Appl
690	7	0.9	4040	14	US-10-146-731-425	Sequence 425, App	763	26	15	US-10-243-355-472	Sequence 472, App
691	7	0.9	4040	14	US-10-140-472-425	Sequence 425, App	764	28	10	US-09-843-221A-53	Sequence 93, Appl
692	7	0.9	4040	14	US-10-141-761-425	Sequence 425, App	765	28	10	US-09-843-221A-94	Sequence 94, Appl
693	7	0.9	4040	14	US-10-142-885-425	Sequence 425, App	766	28	12	US-09-999-608-93	Sequence 93, Appl
694	7	0.9	4040	14	US-10-158-790-425	Sequence 425, App	767	28	12	US-09-999-608-94	Sequence 94, Appl
695	7	0.9	4040	15	US-10-137-871-425	Sequence 425, App	768	28	14	US-10-261-208-4	Sequence 4, Appl
696	7	0.9	4040	15	US-10-140-923-425	Sequence 425, App	769	28	15	US-10-424-599-156146	Sequence 156146,
697	7	0.9	4040	15	US-10-141-756-425	Sequence 425, App	770	28	16	US-10-839-037-93	Sequence 93, Appl
698	7	0.9	4040	15	US-10-141-759-425	Sequence 425, App	771	28	16	US-10-839-037-94	Sequence 94, Appl
699	7	0.9	4040	15	US-10-140-805-425	Sequence 425, App	772	28	17	US-10-926-683-1203	Sequence 1203, Ap
700	7	0.9	4060	15	US-10-140-864-425	Sequence 425, App	773	30	10	US-09-843-221A-124	Sequence 124, App
701	7	0.9	4060	15	US-10-142-426-425	Sequence 425, App	774	30	10	US-09-843-221A-125	Sequence 125, App
702	7	0.9	4060	14	US-10-123-155-197	Sequence 197, App	775	30	10	US-09-843-221A-158	Sequence 158, App
703	7	0.9	4060	14	US-10-146-731-197	Sequence 197, App	776	30	12	US-09-999-608-124	Sequence 124, App
704	7	0.9	4060	14	US-10-140-472-197	Sequence 197, App	777	30	12	US-09-999-608-125	Sequence 125, App
705	7	0.9	4060	14	US-10-141-761-197	Sequence 197, App	778	30	12	US-09-999-608-158	Sequence 158, App
706	7	0.9	4060	14	US-10-142-885-197	Sequence 197, App	779	30	16	US-10-437-963-138633	Sequence 138633,
707	7	0.9	4060	14	US-10-158-790-197	Sequence 197, App	780	30	16	US-10-839-037-124	Sequence 124, App
708	7	0.9	4060	15	US-10-137-871-197	Sequence 197, App	781	30	16	US-10-839-037-125	Sequence 125, App
709	7	0.9	4060	15	US-10-140-923-197	Sequence 197, App	782	30	16	US-10-839-037-158	Sequence 158, App
710	7	0.9	4060	15	US-10-141-756-197	Sequence 197, App	783	31	13	US-10-097-079-50	Sequence 50, Appl
711	7	0.9	4060	15	US-10-141-759-197	Sequence 197, App	784	33	9	US-09-864-761-35842	Sequence 35842, A
712	7	0.9	4060	15	US-10-140-805-197	Sequence 197, App	785	33	14	US-10-000-256A-175	Sequence 175, App
713	7	0.9	4060	15	US-10-140-864-197	Sequence 197, App	786	33	14	US-10-029-386-33592	Sequence 33592, A
714	7	0.9	4060	15	US-10-142-426-197	Sequence 197, App	787	33	15	US-10-424-599-205494	Sequence 205494,
715	7	0.9	4106	11	US-09-980-217-23	Sequence 23, Appl	788	34	10	US-09-843-221A-88	Sequence 88, Appl
716	7	0.9	4106	17	US-10-732-923-20549	Sequence 20549, A	789	34	10	US-09-843-221A-89	Sequence 89, Appl
717	7	0.9	4640	14	US-10-184-644-75	Sequence 75, Appl	790	34	10	US-09-843-221A-122	Sequence 122, App
718	7	0.9	4640	14	US-10-184-634-75	Sequence 75, Appl	791	34	10	US-09-935-384-755	Sequence 755, App
719	7	0.9	4679	9	US-09-804-898-2	Sequence 2, Appl	792	34	10	US-09-935-384-756	Sequence 756, App
720	7	0.9	4999	9	US-09-976-059-14	Sequence 14, Appl	793	34	12	US-09-999-608-88	Sequence 88, Appl
721	7	0.9	8026	14	US-10-132-134-12	Sequence 12, Appl	794	34	12	US-09-999-608-89	Sequence 89, Appl
722	7	0.9	18636	14	US-10-073-912-17	Sequence 17, Appl	795	34	12	US-09-999-608-122	Sequence 122, App
723	7	0.9	35346	17	US-10-874-049-2	Sequence 2, Appl	796	34	15	US-10-425-115-265306	Sequence 265306,
724	7	0.9	35823	17	US-10-874-049-1	Sequence 1, Appl	797	34	16	US-10-425-115-265306	Sequence 265306,
725	7	0.9	36946	18	US-10-840-512-155	Sequence 155, App	798	34	16	US-10-839-037-88	Sequence 88, Appl
726	6	0.8	9	10	US-09-935-384-116	Sequence 116, App	799	34	16	US-10-839-037-89	Sequence 89, Appl
727	6	0.8	9	10	US-09-935-384-219	Sequence 219, App	800	34	16	US-10-839-037-122	Sequence 122, App
728	6	0.8	9	10	US-09-935-384-447	Sequence 447, App	801	35	16	US-10-425-115-356970	Sequence 356970,
729	6	0.8	9	10	US-09-935-384-613	Sequence 613, App	802	35	16	US-09-864-761-35450	Sequence 35450, A
730	6	0.8	10	10	US-09-572-404B-512	Sequence 512, App	803	36	16	US-10-437-963-134795	Sequence 134795,
731	6	0.8	10	10	US-09-935-384-158	Sequence 158, App	804	36	16	US-10-437-963-195293	Sequence 195293,
732	6	0.8	10	10	US-09-935-384-266	Sequence 266, App	805	36	16	US-10-425-115-227274	Sequence 227274,
733	6	0.8	10	10	US-09-935-384-268	Sequence 268, App	806	36	16	US-10-425-115-263124	Sequence 263124,
734	6	0.8	10	10	US-09-935-384-473	Sequence 473, App	807	38	9	US-09-864-761-33780	Sequence 33780, A
735	6	0.8	10	10	US-09-935-384-573	Sequence 573, App	808	39	14	US-10-029-386-30437	Sequence 30437, A
736	6	0.8	10	14	US-10-319-340-4	Sequence 4, Appl	809	39	16	US-10-425-115-367446	Sequence 367446,
737	6	0.8	10	14	US-10-319-340-5	Sequence 5, Appl	810	40	15	US-10-424-599-158157	Sequence 158157,
738	6	0.8	10	14	US-10-319-340-6	Sequence 6, Appl	811	41	15	US-10-424-599-159947	Sequence 159947,
739	6	0.8	10	14	US-10-319-340-19	Sequence 19, Appl	812	41	15	US-10-424-599-170123	Sequence 170123,
740	6	0.8	10	16	US-10-297-969-2	Sequence 2, Appl	813	41	15	US-10-424-599-238198	Sequence 238198,
741	6	0.8	12	16	US-10-700-330-137	Sequence 137, App	814	42	15	US-10-424-599-269505	Sequence 269505,

815	6	0.8	42	15	US-10-424-599-270459	Sequence 270459	888	6	0.8	58	16	US-10-425-115-316296	Sequence 316296
816	6	0.8	42	16	US-10-425-115-273437	Sequence 273437	889	6	0.8	59	9	US-09-864-761-42686	Sequence 42686, A
817	6	0.8	43	15	US-10-424-599-254844	Sequence 254844	890	6	0.8	59	15	US-10-424-599-187445	Sequence 187445
818	6	0.8	43	16	US-10-424-599-254844	Sequence 254844, A	891	6	0.8	59	16	US-10-437-963-196161	Sequence 196161
819	6	0.8	43	16	US-10-425-115-284961	Sequence 284961	892	6	0.8	59	16	US-10-767-701-33262	Sequence 33262, A
820	6	0.8	44	9	US-09-925-299-1094	Sequence 1094, Ap	893	6	0.8	59	16	US-10-425-115-198279	Sequence 198279
821	6	0.8	44	10	US-09-925-299-1094	Sequence 1094, Ap	894	6	0.8	59	16	US-10-425-115-230151	Sequence 230151
822	6	0.8	44	14	US-10-083-357-858	Sequence 858, App	895	6	0.8	59	16	US-10-425-115-268417	Sequence 268417
823	6	0.8	44	14	US-10-097-111-462	Sequence 462, App	896	6	0.8	59	16	US-10-425-115-326057	Sequence 326057
824	6	0.8	44	15	US-10-424-599-181073	Sequence 181073	897	6	0.8	60	9	US-09-864-761-36505	Sequence 36505, A
825	6	0.8	44	15	US-10-424-599-208117	Sequence 208117	898	6	0.8	60	10	US-09-935-384-773	Sequence 773, App
826	6	0.8	44	15	US-10-424-599-222849	Sequence 222849	899	6	0.8	60	10	US-09-935-384-774	Sequence 774, App
827	6	0.8	45	15	US-10-424-599-200405	Sequence 200405	900	6	0.8	60	14	US-10-106-698-5226	Sequence 5226, Ap
828	6	0.8	45	16	US-10-425-115-215060	Sequence 215060	901	6	0.8	60	15	US-10-424-599-217289	Sequence 217289
829	6	0.8	46	15	US-10-424-599-192929	Sequence 192929	902	6	0.8	60	15	US-10-424-599-255017	Sequence 255017
830	6	0.8	46	15	US-10-424-599-250018	Sequence 250018	903	6	0.8	60	15	US-10-424-599-275730	Sequence 275730
831	6	0.8	46	15	US-10-424-599-284367	Sequence 284367	904	6	0.8	60	15	US-10-424-599-278739	Sequence 278739
832	6	0.8	47	15	US-10-424-599-164462	Sequence 164462	905	6	0.8	60	15	US-10-466-205-33	Sequence 33, Appl
833	6	0.8	47	15	US-10-424-599-175289	Sequence 175289	906	6	0.8	60	15	US-10-240-801A-15	Sequence 15, Appl
834	6	0.8	49	15	US-10-424-599-214676	Sequence 214676	907	6	0.8	60	15	US-10-437-963-145637	Sequence 145637
835	6	0.8	49	15	US-10-424-599-247006	Sequence 247006	908	6	0.8	60	16	US-10-437-963-145637	Sequence 1, Appl
836	6	0.8	49	16	US-10-425-115-201029	Sequence 201029	909	6	0.8	60	16	US-10-425-115-249337	Sequence 249337
837	6	0.8	49	16	US-10-425-115-212882	Sequence 212882	910	6	0.8	60	16	US-10-425-115-258455	Sequence 258455
838	6	0.8	49	16	US-10-425-115-343792	Sequence 343792	911	6	0.8	60	16	US-10-425-115-282677	Sequence 282677
839	6	0.8	50	15	US-10-424-599-142892	Sequence 142892	912	6	0.8	60	16	US-10-425-115-288275	Sequence 288275
840	6	0.8	50	16	US-10-437-963-143258	Sequence 143258	913	6	0.8	60	16	US-10-425-115-340928	Sequence 340928
841	6	0.8	50	16	US-10-437-963-144934	Sequence 144934	914	6	0.8	61	15	US-10-424-599-216350	Sequence 216350
842	6	0.8	50	16	US-10-425-115-246059	Sequence 246059	915	6	0.8	61	16	US-10-425-115-225088	Sequence 225088
843	6	0.8	50	16	US-10-425-115-258548	Sequence 258548	916	6	0.8	61	16	US-10-425-115-273735	Sequence 273735
844	6	0.8	50	16	US-10-425-115-289140	Sequence 289140	917	6	0.8	61	16	US-10-425-115-351161	Sequence 351161
845	6	0.8	50	16	US-10-425-115-345542	Sequence 345542	918	6	0.8	62	15	US-10-424-599-178215	Sequence 178215
846	6	0.8	51	9	US-09-864-761-41434	Sequence 41434, A	919	6	0.8	62	15	US-10-424-599-244018	Sequence 244018
847	6	0.8	51	9	US-09-864-761-45353	Sequence 45353, A	920	6	0.8	62	15	US-10-424-599-246325	Sequence 246325
848	6	0.8	51	9	US-09-738-626-4205	Sequence 4205, Ap	921	6	0.8	62	16	US-10-425-115-226730	Sequence 226730
849	6	0.8	51	15	US-10-424-599-188733	Sequence 188733	922	6	0.8	62	16	US-10-425-115-251725	Sequence 251725
850	6	0.8	51	15	US-10-424-599-192988	Sequence 192988	923	6	0.8	62	16	US-10-425-115-280551	Sequence 280551
851	6	0.8	51	16	US-10-425-115-229574	Sequence 229574	924	6	0.8	63	9	US-09-864-761-48451	Sequence 48451, A
852	6	0.8	51	16	US-10-425-115-281091	Sequence 281091	925	6	0.8	63	9	US-09-764-860-354	Sequence 354, App
853	6	0.8	52	9	US-09-764-847-804	Sequence 804, App	926	6	0.8	63	9	US-09-738-626-5130	Sequence 5130, App
854	6	0.8	52	14	US-10-092-154-804	Sequence 804, App	927	6	0.8	63	14	US-10-074-095-354	Sequence 354, App
855	6	0.8	52	14	US-10-092-386-32686	Sequence 32686, A	928	6	0.8	63	15	US-10-212-872-354	Sequence 354, App
856	6	0.8	52	15	US-10-424-599-210770	Sequence 210770	929	6	0.8	63	15	US-10-424-599-198003	Sequence 198003
857	6	0.8	52	15	US-10-424-599-241749	Sequence 241749	930	6	0.8	63	15	US-10-424-599-232260	Sequence 232260
858	6	0.8	52	16	US-10-437-963-135363	Sequence 135363	931	6	0.8	63	15	US-10-424-599-239634	Sequence 239634
859	6	0.8	52	16	US-10-437-963-183149	Sequence 183149	932	6	0.8	63	16	US-10-425-115-185582	Sequence 185582
860	6	0.8	52	16	US-10-767-701-59635	Sequence 59635, A	933	6	0.8	63	16	US-10-425-115-207449	Sequence 207449
861	6	0.8	53	15	US-10-424-599-233874	Sequence 233874	934	6	0.8	63	16	US-10-425-115-265999	Sequence 265999
862	6	0.8	53	16	US-10-425-115-209875	Sequence 209875	935	6	0.8	63	16	US-10-425-115-293345	Sequence 293345
863	6	0.8	53	16	US-10-425-115-273363	Sequence 273363	936	6	0.8	64	15	US-10-349-607-130	Sequence 130, App
864	6	0.8	54	15	US-10-424-599-192315	Sequence 192315	937	6	0.8	64	15	US-10-424-599-154815	Sequence 154815
865	6	0.8	54	15	US-10-424-599-236359	Sequence 236359	938	6	0.8	64	16	US-10-425-115-234850	Sequence 234850
866	6	0.8	54	16	US-10-425-115-211925	Sequence 211925	939	6	0.8	64	16	US-10-425-115-255147	Sequence 255147
867	6	0.8	54	16	US-10-425-115-261837	Sequence 261837	940	6	0.8	64	16	US-10-425-115-312105	Sequence 312105
868	6	0.8	54	16	US-10-425-115-308996	Sequence 308996	941	6	0.8	65	9	US-09-864-761-39981	Sequence 39981, A
869	6	0.8	54	16	US-10-425-115-333948	Sequence 333948	942	6	0.8	65	13	US-10-001-870-119	Sequence 119, App
870	6	0.8	54	17	US-10-808-187-1904	Sequence 1904, Ap	943	6	0.8	65	14	US-10-097-111-388	Sequence 388, App
871	6	0.8	55	9	US-09-864-761-47472	Sequence 47472, A	944	6	0.8	65	16	US-10-425-115-279901	Sequence 279901
872	6	0.8	55	15	US-10-424-599-150228	Sequence 150228	945	6	0.8	65	16	US-10-856-498-604	Sequence 604, App
873	6	0.8	55	16	US-10-425-115-281675	Sequence 281675	946	6	0.8	66	15	US-10-424-599-193996	Sequence 193996
874	6	0.8	55	9	US-09-864-761-38992	Sequence 38992, A	947	6	0.8	66	15	US-10-424-599-198991	Sequence 198991
875	6	0.8	56	9	US-09-939-980-332	Sequence 332, App	948	6	0.8	66	15	US-10-424-599-223134	Sequence 223134
876	6	0.8	56	15	US-10-424-599-181170	Sequence 181170	949	6	0.8	66	16	US-10-425-115-336417	Sequence 336417
877	6	0.8	56	15	US-10-424-599-196379	Sequence 196379	950	6	0.8	67	14	US-10-156-761-8250	Sequence 8250, Ap
878	6	0.8	56	15	US-10-424-599-211496	Sequence 211496	951	6	0.8	67	15	US-10-424-599-160950	Sequence 160950
879	6	0.8	56	16	US-10-425-115-193599	Sequence 193599	952	6	0.8	67	15	US-10-424-599-261870	Sequence 261870
880	6	0.8	57	9	US-09-864-761-46468	Sequence 46468, A	953	6	0.8	67	15	US-10-424-599-266764	Sequence 266764
881	6	0.8	57	15	US-10-424-599-155487	Sequence 155487	954	6	0.8	67	16	US-10-425-115-313696	Sequence 313696
882	6	0.8	57	15	US-10-424-599-173228	Sequence 173228	955	6	0.8	68	15	US-10-424-599-205787	Sequence 205787
883	6	0.8	57	15	US-10-424-599-249260	Sequence 249260	956	6	0.8	68	16	US-10-425-115-189961	Sequence 189961
884	6	0.8	57	16	US-10-437-963-104783	Sequence 104783	957	6	0.8	68	16	US-10-425-115-213549	Sequence 213549
885	6	0.8	57	16	US-10-437-963-145277	Sequence 145277	958	6	0.8	68	16	US-10-425-115-215610	Sequence 215610
886	6	0.8	57	16	US-10-425-115-315915	Sequence 315915	959	6	0.8	69	14	US-10-029-386-29743	Sequence 29743, A
887	6	0.8	58	16	US-10-425-115-218982	Sequence 218982	960	6	0.8	69	15	US-10-424-599-153521	Sequence 153521


```
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-606-618-4

Query Match      100.0%; Score 797; DB 17; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 797; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSA 60

Qy 61 IIKSLYATGPFDDVRVETADQGLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGPFDDVRVETADQGLLTWIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNOAVAGLEEVLRGKLMQITPKVTYKLARNRVDITIDEGSKAKITDIE 180
Db 121 SQYFNQATLNOAVAGLEEVLRGKLMQITPKVTYKLARNRVDITIDEGSKAKITDIE 180

Qy 181 PEGNQVSDRKLQMSLTEGGIWTWLTNSQNEQKFAQDMKVTDYQNNGYDFDPRIL 240
Db 181 PEGNQVSDRKLQMSLTEGGIWTWLTNSQNEQKFAQDMKVTDYQNNGYDFDPRIL 240

Qy 241 DTDIQTNEKTKQTIKITVHEGFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300
Db 241 DTDIQTNEKTKQTIKITVHEGFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQ 300

Qy 301 MTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKT 360
Db 301 MTAVLGEIQNRMSAGVAYSEISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKT 360

Qy 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNSL 420
Db 361 RDEVVRRELQMSAPYDTSKLQSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNSL 420

Qy 421 RSTGSLDSAGVQDTGLVMSAGVSDQNLFGTGKSAALRASRKTTLNGSLSFDPYFTA 480
Db 421 RSTGSLDSAGVQDTGLVMSAGVSDQNLFGTGKSAALRASRKTTLNGSLSFDPYFTA 480

Qy 481 DGVSGLGVYVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540
Db 481 DGVSGLGVYVYKAPDPKASTSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNT 540

Qy 541 YNKAPHYADFIIKYKGTGDTGDSFGWLYKGTGWRNKTDTSALWPTRGYLTGVNAEIA 600
Db 541 YNKAPHYADFIIKYKGTGDTGDSFGWLYKGTGWRNKTDTSALWPTRGYLTGVNAEIA 600

Qy 601 LPSGKLYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVR 660
Db 601 LPSGKLYYSATHNQWTFPLSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVR 660

Qy 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720
Db 661 GYESGTLGPKVYDEYGEKISYGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDG 720

Qy 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFFAYVPLKK 780
Db 721 KTYDDNSSATGGRVQNIYAGNTHKSTFTNELRYSAGGAVTWLSPLGPMKFFAYVPLKK 780

Qy 781 KPEDEIQRFQGLGTTFF 797
Db 781 KPEDEIQRFQGLGTTFF 797
```

RESULT 3

```
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
```

```
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match      94.4%; Score 752; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ADPTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGPFDDVRVETAD 80
Db 21 ADPTIQDIRVEGLQRTPESTVFNYLPVKVGDYVNDTHGSAIIKSLYATGPFDDVRVETAD 80

Qy 81 GQLLLVIERPTIGSNITGAKMLONDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140
Db 81 GQLLLVIERPTIGSNITGAKMLONDAIKKNLESFGLAQSOYFNQATLNOAVAGLKEEY 140

Qy 141 LGRGKLNQITPKVTYKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSL 200
Db 141 LGRGKLNQITPKVTYKLARNRVDITIDEGSKAKITDIEFEGNQVYSDRKLQMSL 200

Qy 201 GGIWTLTNRNQNPKFAQDMKVTDYQNNGYDFDRIIDTDIQTNEKTKQTIKITVH 260
Db 201 GGIWTLTNRNQNPKFAQDMKVTDYQNNGYDFDRIIDTDIQTNEKTKQTIKITVH 260

Qy 261 EGRFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQMTAVLGEIQNRMSAGVAYS 320
Db 261 EGRFRNGKVSIEGDTNEVPKAELEKLLTMKPKWYERQMTAVLGEIQNRMSAGVAYS 320

Qy 321 EISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKTRDEVVRRELQMSAPYDTS 380
Db 321 EISVQPLPNAETKTVDVFLHIEPRKIYVNEIHTGNKTRDEVVRRELQMSAPYDTS 380

Qy 381 KLQSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNSLTERSTGSLDLSAGWYQDTGLVM 440
Db 381 KLQSKERVVELLGYFDNVQFQDAVPLAGTDPKVDLNSLTERSTGSLDLSAGWYQDTGLVM 440

Qy 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDPYFTADGVSLGYDYVYKAFDPRKAS 500
Db 441 SAGVSQDNLFGTGKSAALRASRKTTLNGSLSFDPYFTADGVSLGYDYVYKAFDPRKAS 500

Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIIKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKNKAPHYADFIIKYKGTG 560

Qy 561 TDGSPKGLYKGTGWRNKTDTSALWPTRGYLTGVNAEIALPGSKLYYSATHNQWTFPP 620
Db 561 TDGSPKGLYKGTGWRNKTDTSALWPTRGYLTGVNAEIALPGSKLYYSATHNQWTFPP 620

Qy 621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLSVRGYESGTLGPKVYDEYGEKIS 680

Qy 681 YGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIY 740
Db 681 YGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIY 740

Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
```

RESULT 4

US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match 94.4%; Score 752; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	21	ADFTIQDIRVEGLQRTSPSTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Db	21	ADFTIQDIRVEGLQRTSPSTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
Qy	141	LGRKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNOVYSDRKLWRQMSLTE	200
Db	141	LGRKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNOVYSDRKLWRQMSLTE	200
Qy	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQTNEKTKQTIKITH	260
Db	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQTNEKTKQTIKITH	260
Qy	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Db	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Qy	381	KLQSKERVVELLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Db	381	KLQSKERVVELLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Qy	441	SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDVYVYKAFDPRKAS	500
Db	441	SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDVYVYKAFDPRKAS	500
Qy	501	TSIIQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Db	501	TSIIQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Qy	561	TGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNOTWFFP	620
Db	561	TGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNOTWFFP	620
Qy	621	LSKFTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS	680
Db	621	LSKFTFTMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS	680
Qy	681	YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG	740
Db	681	YGGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG	740

Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772

RESULT 5

US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

Query Match 94.4%; Score 752; DB 15; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	21	ADFTIQDIRVEGLQRTSPSTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Db	21	ADFTIQDIRVEGLQRTSPSTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETAD	80
Qy	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
Db	81	GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSOYFNOATLNOAVAGLKEEY	140
Qy	141	LGRKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNOVYSDRKLWRQMSLTE	200
Db	141	LGRKLNIOITPKVTKLARNVDIDITIDEGSKAKITDIEFEGNOVYSDRKLWRQMSLTE	200
Qy	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQTNEKTKQTIKITH	260
Db	201	GGIWTWLTNRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIQTNEKTKQTIKITH	260
Qy	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Db	261	EGGRFRWGKVSIEGDTNEVPKAELEKLLTMKPGKWERQOMTAVLGEIQNRMGSAAYAYS	320
Qy	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Db	321	EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRBELRQMSAPYDTS	380
Qy	381	KLQSKERVVELLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Db	381	KLQSKERVVELLGYFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGWQDTGLVM	440
Qy	441	SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDVYVYKAFDPRKAS	500
Db	441	SAGVSQDNLFQTKGSAALRASRSKTTLNGSLSFPTDPYFTADGVSGLGYDVYVYKAFDPRKAS	500
Qy	501	TSIIQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Db	501	TSIIQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYKAPKHYADFIKKYKGTG	560
Qy	561	TGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNOTWFFP	620
Db	561	TGSGFKGWLKYGTVGWRNKTDLSALWPTRGYLTVGNVNAEIALPGSKLOYYSATHNOTWFFP	620

```
QY 621 LSKFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
DB 621 LSKFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGNNKKANVSALLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
DB 681 YGNNKKANVSALLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 6
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3

Query Match 94.4%; Score 752; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGYDYNTHGSAIIKSLYATGFFDDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGYDYNTHGSAIIKSLYATGFFDDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
QY 141 LGRGKLNIOITPKVTKLARNRVDITITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200
DB 141 LGRGKLNIOITPKVTKLARNRVDITITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200
QY 201 GGIWTLTRSNQFNEQKPAQDMKVDFYQNNGYDFRILDTDIQTNEDEKTKQITKIVH 260
DB 201 GGIWTLTRSNQFNEQKPAQDMKVDFYQNNGYDFRILDTDIQTNEDEKTKQITKIVH 260
QY 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMSGAGYAYS 320
DB 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMSGAGYAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
QY 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
DB 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
QY 441 SAGVSONLFGTGSAALRASRSTTLNGSLSFDPYFTADGVSGLVDYVYKGAFPDRKAS 500
DB 441 SAGVSONLFGTGSAALRASRSTTLNGSLSFDPYFTADGVSGLVDYVYKGAFPDRKAS 500
QY 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYGTGD 560
DB 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYGTGD 560
```

```
DB 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHYADFIKKYGTGD 560
QY 561 TDSGFKWLYKGYVWGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
DB 561 TDSGFKWLYKGYVWGRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQWTFPP 620
QY 621 LSKFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
DB 621 LSKFTTLMGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
QY 681 YGNNKKANVSALLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
DB 681 YGNNKKANVSALLFPMPGAKDARTVRLSLPADAGSVWDGKTYDDNSSATGGRVQNIYG 740
QY 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772
DB 741 AGNTHKSTFTNELRYSGAGVATWLSPLGPMKF 772

RESULT 7
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match 94.4%; Score 752; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 752; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGYDYNTHGSAIIKSLYATGFFDDVRVETAD 80
DB 21 ADFTIQDIRVEGLQRTPESTVFVNYLPVKVGYDYNTHGSAIIKSLYATGFFDDVRVETAD 80
QY 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
DB 81 GQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEY 140
QY 141 LGRGKLNIOITPKVTKLARNRVDITITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200
DB 141 LGRGKLNIOITPKVTKLARNRVDITITDEGSAKITDIEFEGNOVYSDRKLQMSLTE 200
QY 201 GGIWTLTRSNQFNEQKPAQDMKVDFYQNNGYDFRILDTDIQTNEDEKTKQITKIVH 260
DB 201 GGIWTLTRSNQFNEQKPAQDMKVDFYQNNGYDFRILDTDIQTNEDEKTKQITKIVH 260
QY 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMSGAGYAYS 320
DB 261 EGGFRPWGKVSIEGDTNEVPKAELEKLLTWKPGKYERQOMTAVLGEIQNRMSGAGYAYS 320
QY 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
DB 321 EISVQPLPNAETKTVDVFLHIEPGRKIYVNEIHTGNKTRDEVVRRELQMESAPYDTS 380
QY 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
DB 381 KLQSKERVVELLYGFDNVQFQDAVPLAGTPDKVDLNMSLTERSTGSLDLSAGVQDITGLVM 440
```

```
Qy 441 SAGVSDNLFGTGKSAALRASRSKTTTLNGSLSFPTDPTADGVSGLGYDVYKGFADPRKAS 500
Db 441 SAGVSDNLFGTGKSAALRASRSKTTTLNGSLSFPTDPTADGVSGLGYDVYKGFADPRKAS 500
Qy 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHAYADFIKKYKGTG 560
Db 501 TSIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHAYADFIKKYKGTG 560
Qy 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 620
Db 561 TDGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 620
Qy 621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Db 621 LSKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 680
Qy 681 YGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Db 681 YGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 740
Qy 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 741 AGNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772

RESULT 8
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 94.2%; Score 751; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEYL 120
Qy 142 GRGKLNQITPQVTKLARNRVDIDITDEGKSAKITDIEFEGNQVSDRKLQRMQMSLITEG 201
Db 121 GRGKLNQITPQVTKLARNRVDIDITDEGKSAKITDIEFEGNQVSDRKLQRMQMSLITEG 180
Qy 202 GIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTKQTIKITVHE 261
Db 181 GIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTKQTIKITVHE 240
Qy 262 GGRFRWGVKSTEGTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRWMSAGYAYSE 321
Db 241 GGRFRWGVKSTEGTNEVPKAELEKLLTMKPGKMYERQOMTAVLGEIQNRWMSAGYAYSE 300
Qy 322 ISVOPLNAETKTVDVFLHIEPGRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 381
Db 322 ISVOPLNAETKTVDVFLHIEPGRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 381
```

```
Db 301 ISVOPLNAETKTVDVFLHIEPGRKIIYVNEIHIITGNKTRDEVVRRELQMESAPYDTSK 360
Qy 382 LQRSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVODTGLVMS 441
Db 361 LQRSKERVLLGYFDNVQFADVPLAGTDPKVDLNMSLTERSTGSLDLSAGWVODTGLVMS 420
Qy 442 AGVSDNLFGTGKSAALRASRSKTTTLNGSLSFPTDPTADGVSGLGYDVYKGFADPRKAS 501
Db 421 AGVSDNLFGTGKSAALRASRSKTTTLNGSLSFPTDPTADGVSGLGYDVYKGFADPRKAS 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHAYADFIKKYKGTG 561
Db 481 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHAYADFIKKYKGTG 540
Qy 562 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 621
Db 541 DGSFKGWLKYGTVGWRNKTDLSALWPTRGYLTGVNAEIALPGSKLOYYSATHNQTWFFP 600
Qy 622 SKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 681
Db 601 SKTFTLMLGGEVGIAGGYGRTKEIPFFENFYGGGLGSRVGYESGTLGPKVYDEYGEKIS 660
Qy 682 GGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 741
Db 661 GGNKKANVSAELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSSATGGRVQNIYG 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPGLPMKF 751

RESULT 9
US-10-181-660-13
; Sequence 13, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-13

Query Match 94.2%; Score 751; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 751; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFVNLVVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNOAVAGLKEEYL 120
Qy 142 GRGKLNQITPQVTKLARNRVDIDITDEGKSAKITDIEFEGNQVSDRKLQRMQMSLITEG 201
Db 121 GRGKLNQITPQVTKLARNRVDIDITDEGKSAKITDIEFEGNQVSDRKLQRMQMSLITEG 180
Qy 202 GIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTKQTIKITVHE 261
Db 181 GIWTLWTRSNQFNEQKFAQDMKVTDFYQNNGYDFRILDTDIOTNEDKTKQTIKITVHE 240
```



```
Qy 82 QLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQSQYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIEPEGNOQVSDRKLQMSLTEG 201
Db 121 GRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIEPEGNOQVSDRKLQMSLTEG 180
Qy 202 GIWTWLTFRSQFNOQKFAQDMEKVTDFYQNNGYDFRILDTDIOTNEDKTKQIKITVHE 261
Db 181 GIWTWLTFRSQFNOQKFAQDMEKVTDFYQNNGYDFRILDTDIOTNEDKTKQIKITVHE 240
Qy 262 GGRFRWGKVSIEGTNEVPKAELEKLLTMKPGKYERQOMTAVLGEIQNRMSGAGYAYSE 321
Db 241 GGRFRWGKVSIEGTNEVPKAELEKLLTMKPGKYERQOMTAVLGEIQNRMSGAGYAYSE 300
Qy 322 ISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKTDRDEVVRRRLQWESAPYDTSK 381
Db 301 ISVQPLPNAETKTDFVLHIEPGRKIYVNEIHTGNKKTDRDEVVRRRLQWESAPYDTSK 360
Qy 382 LQSKSERVELLYGPDNQFOAIVPAGTDPDKVDLNNSLTERSTGSLDLSAGWVDOTGLVMS 441
Db 361 LQSKSERVELLYGPDNQFOAIVPAGTDPDKVDLNNSLTERSTGSLDLSAGWVDOTGLVMS 420
Qy 442 AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDYVYGKAFDPRKAST 501
Db 421 AGVSQDNLFGTGKSAALRASRSKTTLNGSLSFDPYFTADGVSGLGYDYVYGKAFDPRKAST 480
Qy 502 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADPIKKYGTGDT 561
Db 481 SIKQYKTTTAGAGIRMSVPVTEYDRVNFGLVAEHLTVNTYNKAPKHVADPIKKYGTGDT 540
Qy 562 DGSFKGWLKXGTGCGRNKNTDSALWPRGYLTGVNAEIALPGSKLOYYSAATHNQTWFFPL 621
Db 541 DGSFKGWLKXGTGCGRNKNTDSALWPRGYLTGVNAEIALPGSKLOYYSAATHNQTWFFPL 600
Qy 622 SKTFTMLGGEVGIAGGYRTEKEIPFFENFYGGSLGVRGYESGTLGPKVYDEYGEKISY 681
Db 601 SKTFTMLGGEVGIAGGYRTEKEIPFFENFYGGSLGVRGYESGTLGPKVYDEYGEKISY 660
Qy 682 GGNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYGA 741
Db 661 GGNKKANVSARELLFPMPGAKDARTVRLSLFADAGSVWDGKTYDDNSSATGGRVQNIYGA 720
Qy 742 GNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 772
Db 721 GNTHKSTFTNELRYSAGGAVTWLSPLGPMKF 751

RESULT 12
US-10-181-660-7
; Sequence 7, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-7

Query Match 26.3%; Score 210; DB 14; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Qy 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210
Db 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210

RESULT 13
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match 26.3%; Score 210; DB 16; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Qy 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210
Db 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210

RESULT 14
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
```

```
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Qy 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210
Db 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210

RESULT 13
US-10-181-600-7
; Sequence 7, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 7
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-7

Query Match 26.3%; Score 210; DB 16; Length 792;
Best Local Similarity 100.0%; Pred. No. 1.9e-199;
Matches 210; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Db 61 IIKSLYATGCFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDIAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Db 121 SOYFNOATLNQAVAGLKEEYLGRGKLNITQIPKVKTLARNVDIDITIDEGSKAKITDIE 180
Qy 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210
Db 181 FEGNOVYSRDKLRQMSLTEGGIWTWLTFRS 210

RESULT 14
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; PRIOR FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
```

; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-9

Query Match 23.7%; Score 189; DB 14; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-178;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNVDIDITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 201
Db 121 GRGKLNIIQITPKVTKLARNVDIDITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 180
Qy 202 GIWTLTRS 210
Db 181 GIWTLTRS 189

RESULT 15
US-10-181-600-9
; Sequence 9, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-9

Query Match 23.7%; Score 189; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 1.5e-178;
Matches 189; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 22 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db 1 DFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
Qy 82 QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEYL 141
Db 61 QLLLTVIERTIGSLNITGAKMLQNDAIKKNLESFGLAQSYFNOATLNQAVAGLKEEYL 120
Qy 142 GRGKLNIIQITPKVTKLARNVDIDITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 201
Db 121 GRGKLNIIQITPKVTKLARNVDIDITIDEKSAKITDIEFEGNQVYSDRKLMRQMSLTEG 180
Qy 202 GIWTLTRS 210
Db 181 GIWTLTRS 189

Search completed: July 6, 2005, 16:02:16
Job time : 177 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 49.968 Seconds
(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMMLGISPLAF.....RNRVDITIDECKSAKIDT 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*

3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*

6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*

7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*

8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep.*

9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*

10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep.*

11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep.*

12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*

13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep.*

14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep.*

15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep.*

16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep.*

17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pep.*

18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*

19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pep.*

20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*

21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*

22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	792	14	US-10-181-660-7
2	885	100.0	792	16	US-10-181-660-7
3	885	100.0	797	9	US-09-994-192-4
4	885	100.0	797	17	US-10-606-618-4
5	879	99.3	797	14	US-10-181-660-3
6	879	99.3	797	15	US-10-320-800-6
7	879	99.3	797	16	US-10-181-660-3
8	875	98.9	797	14	US-10-181-660-11
9	875	98.9	797	16	US-10-181-660-11
10	863	97.5	792	9	US-09-994-192-2
11	863	97.5	792	16	US-10-467-534-92

12	863	97.5	792	17	US-10-606-618-2	Sequence 2, Appli
13	788	89.0	771	14	US-10-181-660-9	Sequence 9, Appli
14	788	89.0	771	16	US-10-181-660-9	Sequence 9, Appli
15	788	89.0	776	14	US-10-181-660-5	Sequence 5, Appli
16	788	89.0	776	14	US-10-181-660-13	Sequence 13, Appli
17	788	89.0	776	16	US-10-181-660-5	Sequence 5, Appli
18	788	89.0	776	16	US-10-181-660-13	Sequence 13, Appli
19	286	32.3	813	16	US-10-896-725-2	Sequence 2, Appli
20	286	32.3	813	16	US-10-896-725-4	Sequence 4, Appli
21	193	21.8	252	16	US-10-437-963-114029	Sequence 114029,
22	151	17.1	896	14	US-10-210-296-5	Sequence 5, Appli
23	151	17.1	896	15	US-10-449-462-5	Sequence 5, Appli
24	100	11.3	792	16	US-10-467-534-25	Sequence 25, Appli
25	98	11.1	792	17	US-10-498-327-55	Sequence 55, Appli
26	97	11.0	21	14	US-10-181-660-8	Sequence 8, Appli
27	97	11.0	21	16	US-10-181-660-8	Sequence 8, Appli
28	95	10.7	614	15	US-10-335-977-4918	Sequence 4918, Ap
29	95	10.7	847	10	US-09-988-067B-8	Sequence 8, Appli
30	95	10.7	925	15	US-10-335-977-4919	Sequence 4919, Ap
31	94.5	10.7	665	16	US-10-437-963-126949	Sequence 126949,
32	94	10.6	299	15	US-10-335-977-4917	Sequence 4917, Ap
33	93.5	10.6	795	15	US-10-289-762-314	Sequence 314, App
34	92	10.4	865	14	US-10-287-274-354	Sequence 354, App
35	92	10.4	865	15	US-10-282-122A-42646	Sequence 42646, A
36	91.5	10.3	790	15	US-10-312-273-147	Sequence 147, App
37	91	10.3	21	14	US-10-181-660-4	Sequence 4, Appli
38	91	10.3	21	16	US-10-181-660-4	Sequence 4, Appli
39	90.5	10.2	541	15	US-10-282-122A-48825	Sequence 48825, A
40	89.5	10.1	2412	16	US-10-408-765A-214	Sequence 214, App
41	88.5	10.0	731	15	US-10-282-122A-52576	Sequence 52576, A
42	87	9.8	21	14	US-10-181-660-12	Sequence 12, Appli
43	87	9.8	21	16	US-10-181-660-12	Sequence 12, Appli
44	87	9.8	638	15	US-10-282-122A-48112	Sequence 48112, A
45	87	9.8	1427	15	US-10-282-122A-48514	Sequence 48514, A

ALIGNMENTS

RESULT 1

US-10-181-660-7

Sequence 7, Application US/10181660

Publication No. US20030027097A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS

FILE REFERENCE: P023785WO

CURRENT APPLICATION NUMBER: US/10/181,660

CURRENT FILING DATE: 2003-03-31

PRIOR APPLICATION NUMBER: GB-0001067.8

PRIOR FILING DATE: 2000-01-17

PRIOR APPLICATION NUMBER: GB-0005699.4

PRIOR FILING DATE: 2000-03-09

NUMBER OF SEQ ID NOS: 14

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 7

LENGTH: 792

TYPE: PRT

ORGANISM: Neisseria gonorrhoeae

US-10-181-660-7

Query Match	100.0%	Score	885	DB	14	Length	792
Best Local Similarity	100.0%	Pred. No.	3.4e-85				
Matches	178	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
QY	1	MKLKQIASALMMLGISPLAFADFTI	DIRVEGIQRTPESTVFNYPVKVGD	TNDTHGSA	60		
Db	1	MKLKQIASALMMLGISPLAFADFTI	DIRVEGIQRTPESTVFNYPVKVGD	TNDTHGSA	60		
QY	61	IIKSLYATGFFDDVRVETADGQLLT	VIERPTIGSLNITGAKMLQNDAIK	KNLESFGLAQ	120		
Db	61	IIKSLYATGFFDDVRVETADGQLLT	VIERPTIGSLNITGAKMLQNDAIK	KNLESFGLAQ	120		


```
Query Match          99.3%; Score 879; DB 14; Length 797;
Best Local Similarity -99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 6
US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT MENINGOCOCCAL VACCINE
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/320,800
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/GB99/03626
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-320-800-6

Query Match          99.3%; Score 879; DB 15; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 7
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02

Query Match          99.3%; Score 879; DB 15; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 8
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-181-660-11

Query Match          98.9%; Score 875; DB 14; Length 797;
Best Local Similarity 98.9%; Pred. No. 4e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 9
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
```

```
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-3

Query Match          99.3%; Score 879; DB 16; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.5e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 8
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

Query Match          98.9%; Score 875; DB 14; Length 797;
Best Local Similarity 98.9%; Pred. No. 4e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQIASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Qy 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 9
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
```

```
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

Query Match
Best Local Similarity 98.9%; Score 875; DB 16; Length 797;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGIGISPLADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178

RESULT 10
US-09-994-192-2
; Sequence 2, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match
Best Local Similarity 97.5%; Score 863; DB 9; Length 792;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178

RESULT 11
US-10-467-534-92
; Sequence 92, Application US/10467534
; Publication No. US20040131625A1
; GENERAL INFORMATION:
; APPLICANT: Berthet, Francois-Xavier Jacques
```

```
; APPLICANT: Lobet, Yves
; APPLICANT: Poolman, Jan
; APPLICANT: Verlant, Vincent Georges Christian Louis
; TITLE OF INVENTION: Vaccine Composition
; FILE REFERENCE: B45261
; CURRENT APPLICATION NUMBER: US/10/467,534
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: PCT/EP02/01356
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: GB 0103169.9
; PRIOR FILING DATE: 2001-02-08
; NUMBER OF SEQ ID NOS: 108
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 92
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-467-534-92

Query Match
Best Local Similarity 97.5%; Score 863; DB 16; Length 792;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178

RESULT 12
US-10-606-618-2
; Sequence 2, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-606-618-2

Query Match
Best Local Similarity 97.5%; Score 863; DB 17; Length 792;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQTASALMMLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Qy 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSKAKITD 178
```



```
Db      121  SQYFNQATLNQAVAGLKEEYLRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
|||||
RESULT 13
US-10-181-660-9
; Sequence 9, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-660-9

Query Match      89.0%; Score 788; DB 14; Length 771;
Best Local Similarity 100.0%; Pred. No. 7.4e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db      1  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
|||||
QY      82  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 141
Db      61  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 120
|||||
QY      142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db      121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157
|||||
RESULT 14
US-10-181-600-9
; Sequence 9, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 9
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-10-181-600-9

Query Match      89.0%; Score 788; DB 16; Length 771;
Best Local Similarity 100.0%; Pred. No. 7.4e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db      1  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
|||||
QY      82  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 141
Db      61  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 120
|||||
QY      142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db      121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157
|||||
```

```
QY      82  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 141
Db      61  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 120
|||||
QY      142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db      121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157
|||||
RESULT 15
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON Spa
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181.660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match      89.0%; Score 788; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 7.5e-75;
Matches 157; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 81
Db      1  DFTIQDIRVEGLQRTPESTVFNVLPVKVGDYNDTHGSAIIKSLYATGFFDDVRVETADG 60
|||||
QY      82  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 141
Db      61  QLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQYFNQATLNQAVAGLKEEYL 120
|||||
QY      142 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 178
Db      121 GRGKLNQITPKVTKLARNRVDITIDEGKSAKTD 157
|||||
```

Search completed: July 6, 2005, 15:42:20
Job time : 50.968 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 11.5584 Seconds

(without alignments)
1481.738 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMMLGIGSLAP.....RNRVDITIDECKSAK178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	879	99.3	797	2	G81228
2	875	98.9	797	2	D82000
3	346	39.1	784	2	E82731
4	305.5	34.5	803	2	AB0530
5	304.5	34.4	795	2	AC0129
6	295.5	33.4	797	2	H83190
7	295.5	33.4	810	2	A64742
8	295.5	33.4	810	2	C90651
9	295.5	33.4	810	2	C85502
10	292.5	33.1	803	2	B82099
11	239	27.0	768	2	D71726
12	236.5	26.7	797	2	JC4078
13	236.5	26.7	808	2	F64102
14	233	26.3	768	2	B97725
15	221	25.0	769	2	F87486
16	191.5	21.6	774	2	D97527
17	191.5	21.6	774	2	AE2746
18	182.5	20.6	617	2	H84957
19	160	18.1	781	2	AH3355
20	154	17.4	739	2	A81430
21	108.5	12.3	846	2	F75525
22	100	11.3	792	2	B71539
23	96.5	10.9	853	2	A71339
24	96	10.8	792	2	H81693
25	95.5	10.8	861	2	F77409
26	95	10.7	906	2	F71910
27	95	10.7	916	2	G64601
28	92	10.4	865	1	C64737
29	91.5	10.3	790	2	D86528

30 91.5 10.3 790 2 D72094
31 89 10.1 821 2 B70199
32 88 9.9 778 2 C70412
33 87.5 9.9 866 2 G90646
34 85.5 9.7 832 2 G85497
35 85.5 9.7 863 2 AE0525
36 84.5 9.5 507 2 B69316
37 84.5 9.5 639 2 A71008
38 84 9.5 236 2 D84961
39 83.5 9.4 447 2 E69061
40 83.5 9.4 676 2 AB2417
41 83.5 9.4 811 2 S67315
42 82.5 9.3 408 2 AI3296
43 82 9.3 728 2 F97262
44 81.5 9.2 452 2 AE1710
45 81.5 9.2 452 2 AG1339

ALIGNMENTS

RESULT 1

G81228

outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 se;
C;Species: Neisseria meningitidis

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004

C;Accession: G81228

R;Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.; Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.; ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M. Science 287, 1809-1815, 2000

A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver A;Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58. A;Reference number: AB1000; MUID:20175755; PMID:10710307

A;Accession: G81228

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-797 <TET>

A;Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; NID:g7225394; PIDN:AAF4063;

A;Experimental source: serogroup B, strain MC58

C;Genetics:

A;Gene: NMB0182

C;Superfamily: protective surface antigen D-15

Query Match 99.3%; Score 879; DB 2; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.3e-67;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 MKLKQIASALMMLGIGSLAPAFDTIODIRVEGLQRTPEPTVFNLYPVKVGDTYNDTHGSA 60

Db 1 MKLKQIASALMMLGIGSLAPADFTIODIRVEGLQRTPEPTVFNLYPVKVGDTYNDTHGSA 60

OY 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLTVIERPTIGSLNITGAKMLQNDIAKKNLESFGLAQ 120

OY 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDECKSAKITD 178

Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNVDITIDECKSAKITD 178

RESULT 2

D82000

outer membrane protein Omp85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491 se;
C;Species: Neisseria meningitidis

C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004

C;Accession: D82000

R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream, Nature 404, 502-506, 2000

A;Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.

A;Reference number: AB1775; MUID:20222556; PMID:10761919

A;Accession: D82000

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Cross-references: UNIPROT:Q9UX31; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8344
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: omp85; NMA0085
C;Superfamily: protective surface antigen D-15

Query Match 98.9%; Score 875; DB 2; Length 797;
Best Local Similarity 98.9%; Pred. No. 2.9e-67;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLQKIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Db 1 MKLQKIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120

Qy 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178
Db 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178

RESULT 3
E82731

outer membrane antigen XF1046 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82731

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:2036517; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STM>
A;Cross-references: UNIPROT:Q9PEI2; GB:AE003941; GB:AE003849; NID:G9105978; PIDN:AAF8385
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carter, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1046
C;Superfamily: protective surface antigen D-15

Query Match 39.1%; Score 346; DB 2; Length 784;
Best Local Similarity 43.2%; Pred. No. 8.8e-22;
Matches 73; Conservative 30; Mismatches 56; Indels 0; Gaps 0;

Qy 8 SALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIIKSLYA 67
Db 15 AANFSLPVLQAASFVANDIRVDGLQRIASGTFVTLPLPNRGDTPDDAKVADAIRALYR 74

Qy 68 TGFDFDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQSQYFNQA 127
Db 75 TGFDFENRDRDQGNILVVKVKRPAINKLITGNKDIKSELLKGLSEIGLSEGGTFDRLL 134

A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-797 <PAR>
A;Cross-references: UNIPROT:Q9UX31; GB:AL162752; GB:AL157959; NID:G7378778; PIDN:CAB8344
A;Experimental source: serogroup A, strain 22491
C;Genetics:
A;Gene: omp85; NMA0085
C;Superfamily: protective surface antigen D-15

Query Match 98.9%; Score 875; DB 2; Length 797;
Best Local Similarity 98.9%; Pred. No. 2.9e-67;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MKLQKIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60
Db 1 MKLQKIASALMMLGISPLALADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSA 60

Qy 61 IIKSLYATGFFDDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQ 120

Qy 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178
Db 121 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKITD 178

RESULT 3
E82731

outer membrane antigen XF1046 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82731

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:2036517; PMID:10910347
A;Note: for a complete list of authors see reference number A59328 below
A;Accession: E82731
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-784 <STM>
A;Cross-references: UNIPROT:Q9PEI2; GB:AE003941; GB:AE003849; NID:G9105978; PIDN:AAF8385
A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carrato, D.M.; Carter, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Pacincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohm
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasak
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silveir
M.; Tshako, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; Z
A;Reference number: A59328
A;Contents: annotation
C;Genetics:
A;Gene: XF1046
C;Superfamily: protective surface antigen D-15

Query Match 39.1%; Score 346; DB 2; Length 784;
Best Local Similarity 43.2%; Pred. No. 8.8e-22;
Matches 73; Conservative 30; Mismatches 56; Indels 0; Gaps 0;

Qy 8 SALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGSAIIKSLYA 67
Db 15 AANFSLPVLQAASFVANDIRVDGLQRIASGTFVTLPLPNRGDTPDDAKVADAIRALYR 74

Qy 68 TGFDFDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLAQSQYFNQA 127
Db 75 TGFDFENRDRDQGNILVVKVKRPAINKLITGNKDIKSELLKGLSEIGLSEGGTFDRLL 134

Qy 128 TLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKI 176
Db 135 SLDRVTQELKQYNNRKYNVQMTTTPDLDRNRVDVTAIKEGAKI 183

RESULT 4
AB0530

outer membrane protein precursor yaet [imported] - Salmonella enterica subsp. enterica sero
C;Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
C;Accession: AB0530
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
th, T.; Connerton, P.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; MUID:21534947; PMID:11677608
A;Accession: AB0530
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-803 <PAR>
A;Cross-references: GB:AL513382; PIDN:CAD08682.1; PID:G16501505; GSPDB:GN00176
C;Genetics:
A;Gene: yaet
C;Superfamily: protective surface antigen D-15

Query Match 34.5%; Score 305.5; DB 2; Length 803;
Best Local Similarity 38.4%; Pred. No. 2.7e-18;
Matches 68; Conservative 36; Mismatches 72; Indels 1; Gaps 1;

Qy 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGS 59
Db 1 MAMKLLIASLLFSSATVVGAGFVVKDHFEGQQRVAVGAALLSNPVTGDTVNDSDS 60

Qy 60 AIKSLYATGFFDDVRVETAGQLLLTIVERTTGSNLITGAKMLQNDAIKKNLSEFGLA 119
Db 61 NTIRALFATGNFEDVRVLRDGNLTLLVQVKRPTIASITFTSGNKSVDKMLKQLEASGVR 120

Qy 120 SQYFNQATLQNAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAKI 176
Db 121 VGESLDRITLSIDIEKGLDFEYVSGKYSASVRAVTPLPNRNRVDLKLVPQEGSAKI 177

RESULT 5
AC0129

probable surface antigen YPO1052 [imported] - Yersinia pestis (strain CO92)
C;Species: Yersinia pestis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0129
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-farraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, I
Nature 413, 523-527, 2001
A;Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A;Reference number: AB0001; MUID:21470413; PMID:11586360
A;Accession: AC0129
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-795 <KUR>
A;Cross-references: UNIPROT:Q8ZH58; GB:AL590842; PIDN:CAC89894.1; PID:G15979119; GSPDB:GN
C;Genetics:
A;Gene: YPO1052
C;Superfamily: protective surface antigen D-15

Query Match 34.4%; Score 304.5; DB 2; Length 795;
Best Local Similarity 37.9%; Pred. No. 3.3e-18;
Matches 67; Conservative 36; Mismatches 73; Indels 1; Gaps 1;

Qy 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYPVKVGDYNDTHGS 59
Db 1 MAMKLLIASLLFSGSATVVGADGFVVNDHFEGQQRVAVGAALLNNMPVRVGDTVSDDDIG 60

```

Db      1 MAMKKLIATSLFFSSATVYGAEGFVVKDIHFESGLORVAVGAALLSPFVRTGDTVNDSDIS 60
Qy      60 AIIKSLVATGFFDVRVETADGQLLTIVERTPTIGSLNITGAKMLONDAIKKNLESGLA 119
Db      61 NTRPALFATGNFEDVRVLRDGTLLVQVKERTIIASITFSGNKSVDKMLKQMLKASGVR 120
Qy      120 OSQYFNQATLNOQAVAGLKEEYLGRGKLNIQITPKVTKLARNRVDIDITIDEGSKAKI 176
Db      121 VGESLDRTTIADIEKGLDFYYSVGKYSASVAVVTPLPNRVRDLKLIVFOEGVSAEI 177

RESULT 8
C90651
hypothetical protein ECS0179 [imported] - Escherichia coli (strain O157:H7, substrain R1H)
C/Species: Escherichia coli
C/Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 09-Jul-2004
C/Accession: C90651
R:Hayaashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Iehii, K.; Yokoyama, K.; Han, C.G.
gaeswara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A/Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and genome
A/Reference number: A99629; MUID:21156231; PMID:11258796
A/Accession: C90651
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-810 <HAY>
A/Cross-references: UNIPROT:P39170; GB:BA000007; PIDN:BA833602.1; PID:gl3359635; GSPDB:GN
A/Experimental source: strain O157:H7, substrain R1MD 0509952
C/Genetics:
A/Gene: ECS0179

```

[illegible]

```

121 VGESLDRRTTIADIEKGLDFYSGKYSASVKAQVVTPLPRNRVDLKLQFQGVSAEI 177
DB

RESULT 9
C85502
C:\hypothetical protein yaeT [imported] - Escherichia coli (strain O157:H7, substrain EDL933)
C:\Species: Escherichia coli
C:\Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004
C:\Accession: C85502
C:\Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew,
R.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
Nature 409, 529-533, 2001
A:\Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:\Reference number: A85480; MUID:21074935; PMID:11206551
A:\Status: preliminary
A:\Molecule type: DNA
A:\Residues: 1-810 <STO>
A:\Cross-references: UNIPROT:P39170; GB:AE005174; NID:gl32512902; PIDN:AGS54479.1; GSPDB:GN
A:\Experimental source: strain O157:H7, substrain EDL933

```

C;Genetics:
A;Gene: yaeT
C;Superfamily: protective surface antigen D-15

Query Match	33.4%;	Score 295.5;	DB 2;	Length 810;
Best Local Similarity	37.3%;	Pred. NO. 2e-17;		

A;Reference number: A64000; MUID:95350630; PMID:7542800
 A;Accession: F64102
 A;Status: nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-808 <TIGR>
 A;Cross-references: GB:L42023; TIGR:HI0917
 C;Superfamily: protective surface antigen D-15
 C;Keywords: surface antigen

Query Match 26.7%; Score 236.5; DB 2; Length 808;
 Best Local Similarity 30.3%; Pred. No. 2.4e-12;
 Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
 QY 3 LKQIASALMLGIGSPLAF-ADFTQDIRVEGLQRTPESTVFNYLPVKVGYDYNTHGSAI 61
 DB 14 MKLLIASLFGITTTTFAAPFVAKDIRDVGVDGQDLEQQIRASLPVRAGQRTVDNVANI 73
 QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
 DB 74 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIGNSIIPTEALKQNLDANGFKVG 133
 QY 122 QYFNQATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAKI 176
 DB 134 DVLIREKLNFPAKSVKSHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 188

RESULT 14
 B97725
 outer membrane protein omp1 [imported] - Rickettsia conorii (strain Malish 7)
 C;Species: Rickettsia conorii
 C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 09-Jul-2004
 C;Accession: B97725
 R;Ogata, H.; Audic, S.; Renesto-Audiffren, P.; Fournier, P.E.; Barbe, V.; Samson, D.; R
 Science 293, 2093-2098, 2001
 A;Title: Mechanisms of Evolution in Rickettsia conorii and Rickettsia prowazekii.
 A;Reference number: A97700; MUID:21442074; PMID:11557893
 A;Accession: B97725
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-768 <KUR>
 A;Cross-references: UNIPROT:Q92J67; GB:AE006914; PIDN:AAL02740.1; PID:g15619252; GSPDB:G
 C;Genetics:
 A;Gene: omp1
 C;Superfamily: protective surface antigen D-15

Query Match 26.3%; Score 233; DB 2; Length 768;
 Best Local Similarity 33.1%; Pred. No. 4.4e-12;
 Matches 60; Conservative 32; Mismatches 73; Indels 16; Gaps 4;
 QY 3 LKQIASALMLGIGSPLAFADFTQDIRVEGLQRTPESTVFNYLPVKVGYDYNTHGSAI 62
 DB 6 ISKLTILLITIFYHISLADSVIRKITEGHNHRVERSTIESYKLVKVGTYNNSKEDEVI 65
 QY 63 KSLYATGFFDDVRVE-TADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
 DB 66 KRLYATSLFRNNHITNDGNLIVNTTPTFFISWFSF-----NSKIKTN-----LAKE 116
 QY 122 QY-----FNOATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAK 175
 DB 117 IYTWSGESLSQAKIELDVKKILEYKSGRFAITVTPKLENLNNRVKVFIDIAEGPKTG 176
 QY 176 I 176
 DB 177 I 177

RESULT 15
 F87486
 outer membrane protein CC1915 [imported] - Caulobacter crescentus
 C;Species: Caulobacter crescentus
 C;Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 09-Jul-2004
 A;Accession: F87486
 R;Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolona
 n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A;Title: Complete Genome Sequence of Caulobacter crescentus.
 A;Reference number: A87249; MUID:21173698; PMID:11259647
 A;Accession: F87486
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-769 <STO>
 A;Cross-references: UNIPROT:Q9A711; GB:AE005673; MID:g13423368; PIDN:AAK23890.1; GSPDB:G
 C;Genetics:
 A;Gene: CC1915
 C;Superfamily: protective surface antigen D-15

Query Match 25.0%; Score 221; DB 2; Length 769;
 Best Local Similarity 30.9%; Pred. No. 4.8e-11;
 Matches 54; Conservative 36; Mismatches 73; Indels 12; Gaps 3;
 QY 11 MMLGIGSPL-----APADF---TIQDIRVEGLQRTPESTVFNYLPVKVGYDYNTHGSAI 61
 DB 3 LLLGSTALLVAPQQAFAQAQTGVVQRIIVQGNRIEQGTIVLSYLPQPGDTVDSQRLDLA 62
 QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
 DB 63 LKTLARTDLFADVKIEMLGGLIVVKKVENPIINQVVFEGNSSLKEDKLDKDEVQ---IRPR 119
 QY 122 QYFNQATLNOAVAGLKEEYGRGKLNITQITPKVTKLARNRVDIDITIDEKSAKI 176
 DB 120 GIFTRAKVQADVQRIIETELVRRSGRISATVTPKVVELPQKRVDLVFEINEGAKSGV 174

Search completed: July 6, 2005, 15:19:13
 Job time : 12.5584 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 7.68831 Seconds

(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745

Perfect score: 140

Sequence: 1 GKTYDDNSSSATGGRVQNIYAGNTH 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: Geneseq1980s:*
- 2: Geneseq1950s:*
- 3: Geneseq2000s:*
- 4: Geneseq2001s:*
- 5: Geneseq2002s:*
- 6: Geneseq2003as:*
- 7: Geneseq2003bs:*
- 8: Geneseq2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	797	3	AAY84947 Amino aci
2	140	100.0	797	4	AUU03959 Neisseria
3	140	100.0	797	4	AUU03957 Neisseria
4	140	100.0	797	4	AUU04451 Neisseria
5	140	100.0	797	4	AAB23788 Neisseria
6	140	100.0	797	4	AAB23784 Neisseria
7	140	100.0	797	4	AAB84746 Amino aci
8	140	100.0	797	4	AAB84744 Amino aci
9	140	100.0	797	5	ABF79802 Neisseria
10	94	67.1	25	4	AUU04412 Neisseria
11	55	39.3	351	5	ABG79591 Candida g
12	55	39.3	1504	8	ADN19818 Bacterial
13	53	37.9	10	4	AUU03975 Neisseria
14	53	37.9	1652	8	ADN20570 Bacterial
15	51.5	36.8	172	4	ABG18158 Novel hum
16	51	36.4	366	5	ABG79585 Candida f
17	51	36.4	366	5	ABG79580 Candida f
18	51	36.4	367	5	ABG79587 Candida g
19	51	36.4	367	5	ABG79561 Candida g
20	51	36.4	368	5	ABG79570 Candida m
21	51	36.4	368	5	ABG79582 Candida g
22	51	36.4	385	5	ABG79572 Candida i
23	51	36.4	385	5	ABG79590 Candida g
24	51	36.4	1266	7	ADB70308 C. neofo
25	50	35.7	31	5	ABG80440 Anti-huma

26	50	35.7	358	5	ABG79568	Abg79568	Candida p
27	50	35.7	359	5	ABG79580	Abg79580	Candida g
28	50	35.7	360	5	ABG79585	Abg79585	Candida i
29	50	35.7	360	5	ABG79576	Abg79576	Candida g
30	50	35.7	361	5	ABG79577	Abg79577	Yeast typ
31	50	35.7	361	5	ABG79566	Abg79566	Candida r
32	50	35.7	361	5	ABG79579	Abg79579	Candida g
33	50	35.7	365	5	ABG79567	Abg79567	Candida u
34	50	35.7	365	5	ABG79589	Abg79589	Candida g
35	50	35.7	366	5	ABG79578	Abg79578	Candida g
36	50	35.7	366	5	ABG79573	Abg79573	Candida k
37	50	35.7	367	5	ABG79574	Abg79574	Candida g
38	50	35.7	367	5	ABG79569	Abg79569	Candida f
39	50	35.7	368	5	ABG79583	Abg79583	Candida g
40	50	35.7	368	5	ABG79583	Abg79583	Candida a
41	50	35.7	369	5	ABG79562	Abg79562	Candida t
42	50	35.7	369	5	ABG79584	Abg79584	Candida g
43	50	35.7	386	8	ADJ71673	Adj71673	Human NOV
44	50	35.7	581	7	ADB37538	Adb37538	Neural th
45	50	35.7	1428	6	ABR53041	Abr53041	Protein s

ALIGNMENTS

RESULT 1	
AAY84947	
ID	AAY84947 standard; protein; 797 AA.
XX	
AC	AAY84947;
XX	
DT	21-AUG-2000 (first entry)
XX	
DE	Amino acid sequence of outer membrane protein (omp) 85.
XX	
KW	Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW	meningococcal infection; protective immune response; vaccine.
XX	
OS	Neisseria meningitidis.
XX	
PN	WO200023595-A1.
XX	
PD	27-APR-2000.
XX	
PF	22-OCT-1998; 98WO-US022352.
XX	
PR	22-OCT-1998; 98WO-US022352.
XX	
PA	(UYMO-) UNIV MONTANA.
XX	
PI	Judd RC, Manning SD;
XX	
DR	WPI; 2000-339694/29.
DR	N-PSDB; AAA15156.
XX	
PT	New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT	meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT	for gonococcal or meningococcal infections.
XX	
PS	Claim 41; Page 89-92; 98pp; English.
XX	
CC	The present sequence represents an outer membrane protein (omp) 85 of
CC	Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC	useful in compositions for use in the prevention, treatment and diagnosis
CC	of non-symptomatic gonococcal infection or meningococcal infection and
CC	symptomatic disease. They are also useful for the detection of
CC	hybridisation complexes. Antigens and antibodies specific omp proteins
CC	also provide diagnostic, therapeutic and prophylactic compositions for
CC	the treatment or prevention of the infections described above. The
CC	antibodies are useful for inducing a protective immune response in humans
CC	or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC	species. The proteins, antibodies and polynucleotide sequences of the
CC	present invention may also be used in the screening and development of

CC chemical compounds such as drugs or vaccines

XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 3; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26

|||||

Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 2

AAU03959

ID AAU03959 standard; protein; 797 AA.

XX

AC AAU03959;

XX 23-OCT-2001 (first entry)

XX Neisseria gonorrhoeae antigenic protein.

XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.

XX Neisseria gonorrhoeae.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "Signal peptide"

FT Protein 22..797

FT /note= "Mature N. gonorrhoeae antigen"

XX WO200138350-A2.

XX 31-MAY-2001.

XX 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

XX 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

XX (STAT-) STATENS INST FOLKEHELSE.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

XX WPI; 2001-381289/40.

XX N-PSDB; AAS07279.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.

XX Claim 1; Page 37-39; 92pp; English.

XX The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.
CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the
CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
CC of meningitis. This antigenic protein is useful in the manufacture of a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria, such as meningitis and septicaemia. It is also useful as a
CC diagnostic reagent for detecting the presence of Neisseria bacteria or
CC antibodies raised against Neisseria, and as a reagent for raising the
CC antibodies. The Neisserial nucleotide sequences can be expressed in a
CC variety of different expression systems, for example, mammalian cells,
CC baculoviruses, plants, bacteria and yeast

XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26

|||||

Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 3

AAU03957

ID AAU03957 standard; protein; 797 AA.

XX

AC AAU03957;

XX 23-OCT-2001 (first entry)

XX Neisseria meningitidis serogroup B antigenic protein.

XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.

XX Neisseria meningitidis.

XX Key Location/Qualifiers

FT Peptide 1..21

FT /note= "Signal peptide"

FT Protein 22..797

FT /note= "Mature N. meningitidis serogroup B antigen"

FT Binding-site 715..722

FT /note= "ATP/GTP-binding site motif A (P-loop)"

XX WO200138350-A2.

XX 31-MAY-2001.

XX 28-NOV-2000; 2000WO-IB001851.

XX 29-NOV-1999; 99GB-00028197.

XX 09-MAR-2000; 2000GB-00005698.

XX (CHIR-) CHIRON SPA.

XX (STAT-) STATENS INST FOLKEHELSE.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;

XX WPI; 2001-381289/40.

XX N-PSDB; AAS07277.

XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.

XX Claim 1; Fig 1; 92pp; English.

XX The sequence represents a Neisseria meningitidis serogroup B 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast

XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;

Best Local Similarity 100.0%; Pred. No. 4.3e-11;

Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26

|||||

Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 4
AAU04451
ID AAU04451 standard; protein; 797 AA.

AC AAU04451;
XX
XX 23-OCT-2001 (first entry)
XX
XX Neisseria meningitidis serogroup A antigenic protein #2.
DE
XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
KW
XX Neisseria meningitidis.
OS

XX Key Location/Qualifiers
FH Peptide 1..21
FT /note= "Signal peptide"
FT Protein 22..797
FT /note= "Mature N. meningitidis serogroup A antigen"
XX
XX WO200138350-A2.
PN
XX 31-MAY-2001.
PD
XX
XX 28-NOV-2000; 2000WO-IB001851.
PF
XX 29-NOV-1999; 99GB-00028197.
PR
XX 09-MAR-2000; 2000GB-00005698.
PR
XX (CHIR-) CHIRON SPA.
PA
XX (STAT-) STATENS INST FOLKEHELSE.
PA
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
PI
XX WPI; 2001-381289/40.
DR
XX
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
PT
XX Claim 1; Page 39-40; 92pp; English.
PS
XX The sequence represents a Neisseria meningitidis serogroup A 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast. Note: There are two versions of this sequence
CC displayed in the specification (see AAU03958)
XX
XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
|||||
Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 5
AAB23788
ID AAB23788 standard; protein; 797 AA.

XX AAB23788;
AC
XX 12-JAN-2001 (first entry)
DT
XX Neisseria meningitidis serogroup A amino acid sequence.
DE
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
XX Neisseria meningitidis.
OS
XX WO200050075-A2.
PN
XX 31-AUG-2000.
PD
XX 09-FEB-2000; 2000WO-IB000176.
PF
XX 26-FEB-1999; 99US-0121792P.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
PI
XX WPI; 2001-015529/02.
DR
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
PT
XX Claim 22; Page 33; 39pp; English.
PS
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (i) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup A amino
CC acid sequence disclosed in GB-928197.4, which is given in the present
CC invention
XX
XX Sequence 797 AA;

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.3e-11;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
|||||
Db 720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 6
AAB23784
ID AAB23784 standard; protein; 797 AA.

XX AAB23784;
AC
XX 12-JAN-2001 (first entry)
DT
XX Neisseria meningitidis serogroup B amino acid sequence.
DE
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KW Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW

KW immune response.
XX Neisseria meningitidis.
XX WO200050075-A2.
XX 31-AUG-2000.
XX 09-FEB-2000; 2000WO-IB000176.
XX 26-FEB-1999; 99US-0121792P.
XX (CHIR-) CHIRON SPA.
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX WPI; 2001-015529/02.
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX Claim 22; Page 32; 39pp; English.
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC adjuvant composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
XX invention
XX Sequence 797 AA;
XX
XX Query Match 100.0%; Score 140; DB 4; Length 797;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-11;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db |||||
17-SEP-2001 (first entry)
Amino acid sequence of a Neisseria serogroup A protein.
Serogroup A protein; outer membrane protein; Neisserial infection;
vaccine.
Neisseria meningitidis.
Key Location/Qualifiers
Peptide 1..21 /note= "signal peptide"
Protein 22..797 /note= "mature protein"
WO200152885-A1.
26-JUL-2001.
17-JAN-2001; 2001WO-IB000166.
XX

PD 26-JUL-2001.
XX 17-JAN-2001; 2001WO-IB000166.
XX 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX (CHIR-) CHIRON SPA.
XX Pizza M, Rappuoli R, Giuliani M;
XX WPI; 2001-451895/48.
DR N-PSDB; AAH42130.
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX Disclosure; Page 71-74; 83pp; English.
XX The present sequence represents a Neisseria serogroup A protein. The
XX protein is used to produce the compositions of the invention. The
XX specification describes a composition, comprising a Neisseria
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component. The immunogenic component is protein disclosed in WO99/57280,
XX WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
XX WO99/31132, WO99/58683, WO95/55873, and/or N. meningitidis protein PorA,
XX TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
XX medicament for treating or preventing infection due to Neisserial
XX bacteria; a diagnostic reagent for detecting the presence of Neisserial
XX bacteria or of antibodies raised against Neisserial bacteria; and/or a
XX reagent which can raise antibodies against Neisserial bacteria. It may
XX also be used as a vaccine
XX Sequence 797 AA;
SQ
XX Query Match 100.0%; Score 140; DB 4; Length 797;
XX Best Local Similarity 100.0%; Pred. No. 4.3e-11;
XX Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db |||||
17-SEP-2001 (first entry)
Amino acid sequence of a Neisseria serogroup B protein.
Serogroup B protein; outer membrane protein; Neisserial infection;
vaccine.
Neisseria meningitidis.
Key Location/Qualifiers
Peptide 1..21 /note= "signal peptide"
Protein 22..797 /note= "mature protein"
WO200152885-A1.
26-JUL-2001.
17-JAN-2001; 2001WO-IB000166.
XX

PR 17-JAN-2000; 2000GB-00001067.
 .PR 09-MAR-2000; 2000GB-00005699.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Pizza M, Rappuoli R, Giuliani M;
 XX WPI; 2001-451895/48.
 DR N-PSDB; AAH42128.
 XX
 XX Composition for treating or preventing infection to, detecting, or for
 PT raising antibodies against Neisserial bacteria, comprises an N.
 PT meningitidis serogroup B outer membrane preparation and an immunogenic
 PT component.
 XX
 XX Disclosure; Page 59-61; 83pp; English.
 XX
 CC The present sequence represents a Neisseria serogroup B protein. The
 CC protein is used to produce the compositions of the invention. The
 CC specification describes a composition, comprising a Neisseria
 CC meningitidis serogroup B outer membrane preparation and an immunogenic
 CC component. The immunogenic component is protein disclosed in WO99/57280,
 CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
 CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
 CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
 CC medicament for treating or preventing infection due to Neisserial
 CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
 CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
 CC reagent which can raise antibodies against Neisserial bacteria. It may
 CC also be used as a vaccine
 XX
 XX Sequence 797 AA;
 SQ
 Query Match 100.0%; Score 140; DB 4; Length 797;
 Best Local Similarity 100.0%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
 DB 720 GKYDDNSSATGGRVQNIYAGNTH 745
 RESULT 9
 ABB79802
 ID ABB79802 standard; protein; 797 AA.
 XX
 AC ABB79802;
 XX
 DT 15-NOV-2002 (first entry)
 XX
 DE Neisseria meningitidis outer membrane protein Omp85.
 KW Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
 KW antibacterial.
 XX
 OS Neisseria meningitidis.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..21
 FT /label= Signal_peptide
 FT Protein 22..797
 FT /label= Mature_protein
 XX
 PN US2002086028-A1.
 XX
 PD 04-JUL-2002.
 XX
 PF 26-NOV-2001; 2001US-00994192.
 XX
 PR 22-OCT-1998; 98US-00177039.
 XX
 PA (JUDD/) JUDD R C.
 PA (MANN/) MANNING D S.

XX Judd RC, Manning DS;
 XX WPI; 2002-642234/69.
 XX
 PT Novel immunogenic composition for vaccinating against meningococcal or
 PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
 PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
 XX
 XX Claim 13; Fig 5; 30pp; English.
 XX
 CC The present sequence is that of the Neisseria meningitidis strain HH
 CC outer membrane protein 85 (Omp85), as predicted from a gene that was
 CC obtained from a genomic DNA by PCR amplification using primers based on
 CC the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
 CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
 CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
 CC fusion proteins including the Omp85, or nucleic acids encoding them,
 CC which induce a protective immune response in a subject. The immunogenic
 CC compositions may also include an antigen from a heterologous or
 CC homologous pathogen, or a nucleic acid encoding it. They are used in a
 CC claimed method of vaccinating a human or animal against non-symptomatic
 CC meningococcal infection or symptomatic disease. A kit for diagnosing
 CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
 CC The Omp85 polypeptides and polynucleotides are also useful in drug
 CC screening and development
 XX
 XX Sequence 797 AA;
 SQ
 Query Match 100.0%; Score 140; DB 5; Length 797;
 Best Local Similarity 100.0%; Pred. No. 4.3e-11;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GKYDDNSSATGGRVQNIYAGNTH 26
 DB 720 GKYDDNSSATGGRVQNIYAGNTH 745
 RESULT 10
 AAU04412
 ID AAU04412 standard; peptide; 25 AA.
 XX
 AC AAU04412;
 XX
 DT 23-OCT-2001 (first entry)
 XX
 DE Neisseria meningitidis serogroup B antigenic oligopeptide #34.
 KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
 KW bacterial infection; baculovirus; yeast.
 XX
 OS Neisseria meningitidis.
 XX
 PN WO200138350-A2.
 XX
 PD 31-MAY-2001.
 XX
 PF 28-NOV-2000; 2000WO-IB001851.
 XX
 PR 29-NOV-1999; 99GB-00028197.
 PR 09-MAR-2000; 2000GB-00005698.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (STAT-) STATENS INST FOLKEHELSE.
 XX
 PI Giuliani MM, Pizza M, Rappuoli R, Holst J;
 XX WPI; 2001-381289/40.
 DR
 XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
 PT gonorrhoeae, useful in the manufacture of a medicament for treating and
 PT preventing Neisserial bacteria infection.
 XX

CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.

XX SQ Sequence 1504 AA;
Query Match 39.3%; Score 55; DB 8; Length 1504;
Best Local Similarity 63.2%; Pred. No. 1.2e+02;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDSSSSATGRVQNIYGA 22
||||| ||||| |||||
Db 215 YDSSSSATGRVQNIYGA 231

RESULT 13
AAU03975
ID AAU03975 standard; peptide; 10 AA.
XX AC AAU03975;
XX XX
XX 23-OCT-2001 (first entry)
XX Neisseria meningitidis serogroup B antigenic protein AMPHI region #16.
XX Serogroup B antigen; pharynx; meningitis; septicemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; AMPHI region.
XX Neisseria meningitidis.
XX OS
XX WO200138350-A2.
XX 31-MAY-2001.
XX 28-NOV-2000; 2000WO-IB001851.
XX 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX (CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.

XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
PI WPI; 2001-381289/40.
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
XX gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX Claim 1; Page 79; 92pp; English.
XX The sequence represents a Neisseria meningitidis serogroup B antigenic
CC oligopeptide. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic peptide is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast.
XX Sequence 10 AA;

Query Match 37.9%; Score 53; DB 4; Length 10;
Best Local Similarity 100.0%; Pred. No. 0.84;
Matches 10; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GRVQNIYAG 23
|||||

Db 1 GRVQNIYAG 10
RESULT 14
ADN20570
ID ADN20570 standard; protein; 1652 AA.
XX AC ADN20570;
XX 02-DEC-2004 (first entry)
XX Bacterial polypeptide #3223.
XX Recombinant DNA construct; transformed plant; improved plant property;
KW cold tolerance; heat tolerance; drought tolerance; herbicide; osmosis;
KW pathogen tolerance; pest tolerance; plant growth regulator;
KW cell cycle pathway modification; seed oil yield; protein yield; carbohydrate;
KW homologous recombination; photosynthesis; lignin; galactomannan;
KW bacterial polypeptide.
XX Bacteria.
XX OS
XX US2003233675-A1.
XX 18-DEC-2003.
XX 20-FEB-2003; 2003US-00369493.
XX 21-FEB-2002; 2002US-0360039P.
XX (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;
PI WPI; 2004-061375/06.
XX New recombinant DNA construct comprising a promoter positioned to provide
PT for expression of a polynucleotide encoding a polypeptide from a
PT microbial source, useful for producing plants with improved properties.
XX Claim 1; SEQ ID NO 3223; 122pp; English.
XX The invention relates to a recombinant DNA construct comprising a
CC promoter functional in a plant cell, where the promoter is positioned to
CC provide for expression of a polynucleotide encoding a polypeptide from a
CC microbial source. The invention also relates to a transformed plant
CC comprising the recombinant DNA construct and a method of producing a
CC transformed plant having an improved property. The plant is a crop plant
CC such as maize or soybean. The method of producing a transformed plant
CC having an improved property comprises transforming a plant with the
CC recombinant DNA construct and growing the transformed plant, where the
CC polynucleotide or polypeptide is useful for improving plant properties.
CC The recombinant DNA construct is useful for producing plants with
CC improved plant properties, e.g. improved cold, heat or drought tolerance,
CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,
CC increased resistance to plant disease, better growth rate by modification
CC of the cell cycle pathway with plant growth regulators, increased rate of
CC homologous recombination, modified seed oil or protein yield and/or
CC content, improved yield by modification of carbohydrate, nitrogen or
CC phosphorus use and/or uptake, by modification of photosynthesis or by
CC providing improved plant growth and development under at least one stress
CC condition, improved lignin production or improved galactomannan
CC production. This sequence represents a bacterial polypeptide used in the
CC scope of the invention. Note: The sequence data for this patent did not
CC form part of the printed specification but was obtained in electronic
CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX Sequence 1652 AA;
SQ

Query Match 37.9%; Score 53; DB 8; Length 1652;
Best Local Similarity 46.2%; Pred. No. 2.5e+02;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;

QY 1 GKTYDDNSSSAGRVQNIYGAGNTH 26
| : ||| ||| : ||| :
Db 184 GSNFDDNEKTVGGR--NGYGAKLTN 207

RESULT 15

ABG18158
ID ABG18158 standard; protein; 172 AA.

XX AC ABG18158;

XX 18-FEB-2002 (first entry)

XX DE Novel human diagnostic protein #18149.

XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.

XX OS Homo sapiens.

XX PN WO200175067-A2.

XX PD 11-OCT-2001.

XX PF 30-MAR-2001; 2001WO-US008631.

XX PR 31-MAR-2000; 2000US-00540217.

XX PR 23-AUG-2000; 2000US-00649167.

XX PA (HYSE-) HYSEQ INC.

XX PI Drmanac RT, Liu C, Tang YT;

XX DR WPI; 2001-639362/73.

XX DR N-PSDB; AAS82345.

XX PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.

XX PS Claim 20; SEQ ID NO 48517; 103pp; English.

XX CC The invention relates to isolated polynucleotide (I) and polypeptide (II)
CC sequences. (I) is useful as hybridisation probes, polymerase chain
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
CC and in recombinant production of (II). The polynucleotides are also used
CC in diagnostics as expressed sequence tags for identifying expressed
CC genes. (I) is useful in gene therapy techniques to restore normal
CC activity of (II) or to treat disease states involving (II). (II) is
CC useful for generating antibodies against it, detecting or quantitating a
CC polypeptide in tissue, as molecular weight markers and as a food
CC supplement. (II) and its binding partners are useful in medical imaging
CC of sites expressing (II). (I) and (II) are useful for treating disorders
CC involving aberrant protein expression or biological activities. The
CC polypeptide and polynucleotide sequences have application in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human diagnostic
CC amino acid sequences of the invention. Note: The sequence data for this
CC patent did not appear in the printed specification, but was obtained in
CC electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 172 AA;

Query Match 36.8%; Score 51.5; DB 4; Length 172;

Best Local Similarity 52.4%; Pred. No. 33;
Matches 11; Conservative 1; Mismatches 8; Indels 1; Gaps 1;

QY 6 DNSSSATGGRVONIYGAGNTH 26
| : ||| ||| : ||| :
Db 3 DNPSGTDGGR-NRAFGAGNIH 22

Search completed: July 6, 2005, 15:13:15
Job time : 8.68831 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 : Search time 2 Seconds
(without alignments)
970.438 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKTYDDNSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pcp.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pcp.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pcp.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pcp.*
5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pcp.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	140	100.0	797	4	US-09-994-192-4
2	50	35.7	1531	4	US-09-976-594-203
3	49	35.0	550	4	US-09-107-532A-5564
4	47	33.6	172	4	US-09-252-991A-22814
5	47	33.6	354	4	US-09-198-452A-504
6	47	33.6	354	4	US-09-438-185A-471
7	47	33.6	409	4	US-09-949-016-11141
8	47	33.6	428	3	US-08-301-162-18
9	47	33.6	428	3	US-09-461-240-18
10	47	33.6	428	4	US-09-968-927-18
11	47	33.6	437	3	US-08-961-083-70
12	47	33.6	437	4	US-09-536-784-70
13	47	33.6	627	4	US-09-583-110-5137
14	47	33.6	637	4	US-09-107-433-4391
15	47	33.6	667	3	US-09-303-064-55
16	47	33.6	667	3	US-09-086-503-55
17	46	32.9	350	4	US-09-489-039A-13959
18	46	32.9	457	4	US-09-248-796A-19185
19	45.5	32.5	501	4	US-09-107-433-2872
20	45.5	32.5	2213	1	US-08-727-034-3
21	45	32.1	94	4	US-09-489-039A-8163
22	45	32.1	1070	2	US-08-633-770A-2
23	45	32.1	1070	4	US-09-280-197-6
24	44.5	31.8	543	4	US-09-583-110-4669
25	44.5	31.8	825	4	US-09-328-352-5974
26	44.5	31.8	1216	4	US-09-134-000C-5130
27	44	31.4	79	4	US-09-489-039A-14024

28 44. 31.4 91 1 US-08-480-604A-8 Sequence 8, Appli
29 44 31.4 91 2 US-08-405-496A-8 Sequence 8, Appli
30 44 31.4 91 3 US-08-915-136-8 Sequence 8, Appli
31 44 31.4 91 3 US-08-957-310-8 Sequence 8, Appli
32 44 31.4 91 4 US-10-011-366-8 Sequence 8, Appli
33 44 31.4 91 4 US-09-084-517-8 Sequence 37, Appl
34 44 31.4 353 2 US-08-687-702-37 Sequence 16634, A
35 44 31.4 518 4 US-09-248-796A-16634 Sequence 15457, A
36 44 31.4 581 4 US-09-248-796A-15457 Sequence 7, Appli
37 44 31.4 811 1 US-08-480-604A-7 Sequence 7, Appli
38 44 31.4 811 2 US-08-405-496A-7 Sequence 7, Appli
39 44 31.4 811 3 US-08-915-136-7 Sequence 7, Appli
40 44 31.4 811 3 US-08-957-310-7 Sequence 7, Appli
41 44 31.4 811 4 US-10-011-366-7 Sequence 7, Appli
42 44 31.4 811 4 US-09-084-517-7 Sequence 7, Appli
43 44 31.4 812 1 US-08-480-604A-29 Sequence 29, Appl
44 44 31.4 812 3 US-08-915-136-29 Sequence 29, Appl
45 44 31.4 812 4 US-09-084-517-29 Sequence 29, Appl

ALIGNMENTS

RESULT 1

US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UNSC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match 100.0%; Score 140; DB 4; Length 797;
Best Local Similarity 100.0%; Pred. No. 4.5e-12;

Mismatches 0; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

QY 1 GKTYDDNSSATGGRVQNIYGAGNTH 26
DB 720 GKTYDDNSSATGGRVQNIYGAGNTH 745

RESULT 2

US-09-976-594-203
; Sequence 203, Application US/09976594
; Patent No. 6673549
; GENERAL INFORMATION:
; APPLICANT: Furness, Michael
; APPLICANT: Buchbinder, Jenny
; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
; FILE REFERENCE: PA-0041 US
; CURRENT APPLICATION NUMBER: US/09/976,594
; CURRENT FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240,409
; PRIOR FILING DATE: 2000-10-12
; NUMBER OF SEQ ID NOS: 1143
; SOFTWARE: PERL Program
; SEQ ID NO 203
; LENGTH: 1531
; TYPE: PRT
; ORGANISM: Homo sapiens

```
;
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. 6673549 1867417CD1
US-09-976-594-203

Query Match          35.7%; Score 50; DB 4; Length 1531;
Best Local Similarity 57.9%; Pred. No. 1.3e+02;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY      4 YDDNSSSATGGRRVQNIYGA 22
      |||: |||| |||| ||||
Db      151 YDDDEKVTGGR--NGVGA 167

RESULT 3
US-09-107-532A-5564
; Sequence 5564, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 5564:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 550 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Enterococcus faecium
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (B) LOCATION 1...550
; SEQUENCE DESCRIPTION: SEQ ID NO: 5564:
US-09-107-532A-5564

Query Match          35.0%; Score 49; DB 4; Length 550;
Best Local Similarity 47.6%; Pred. No. 55;
Matches 10; Conservative 3; Mismatches 8; Indels 8; Gaps 0;

QY      4 YDDNSSSATGGRRVQNIYAGN 24
      |||: |||| |||| ||||
Db      360 YEGNSSVTYKGRLSGFGGAPN 380
```

```
RESULT 4
US-09-252-991A-22814
; Sequence 22814, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 22814
; LENGTH: 172
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-22814

Query Match          33.6%; Score 47; DB 4; Length 172;
Best Local Similarity 57.1%; Pred. No. 28;
Matches 8; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      13 GGRVQNIYAGNTH 26
      |||: |||| |||| ||||
Db      135 GGRQRLHGAGGVH 148

RESULT 5
US-09-198-452A-504
; Sequence 504, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Grifffais, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: thereof and uses thereof, and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 504
; LENGTH: 354
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-504

Query Match          33.6%; Score 47; DB 4; Length 354;
Best Local Similarity 40.0%; Pred. No. 65;
Matches 10; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY      1 GKTYDDNSSSATGGRRVQNIYAGNT 25
      |||: |||| |||| ||||
Db      86 GPTAFINNSATSGGALINLSGIGST 110

RESULT 6
US-09-438-185A-471
; Sequence 471, Application US/09438185A
; Patent No. 6822071
; GENERAL INFORMATION:
; APPLICANT: Stephens, Richard
; APPLICANT: Mitchell, Wayne
; APPLICANT: Kalman, Sue
; APPLICANT: Davis, Ronald
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: Chlamydia pneumoniae Genome Sequence
; FILE REFERENCE: 018941-000411US
; CURRENT APPLICATION NUMBER: US/09/438,185A
```

```
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/108,279
; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: US 60/128,606
; PRIOR FILING DATE: 1999-04-08
; NUMBER OF SEQ ID NOS: 1074
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 471
; LENGTH: 354
; TYPE: PRN
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; OTHER INFORMATION: CPN0469
US-09-438-185A-471

Query Match      33.6%; Score 47; DB 4; Length 354;
Best Local Similarity 40.0%; Pred. No. 65;
Matches 10; Conservative 6; Mismatches 9; Indels 9; Gaps 0;

QY 1 GKTYDDNSSATGGRVNIYAGNT 25
Db 86 GPTAFINNSATGGALINLSGIGT 110

RESULT 7
US-09-949-016-11141
; Sequence 11141, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11141
; LENGTH: 409
; TYPE: PRN
; ORGANISM: Human
US-09-949-016-11141

Query Match      33.6%; Score 47; DB 4; Length 409;
Best Local Similarity 38.1%; Pred. No. 77;
Matches 8; Conservative 7; Mismatches 6; Indels 6; Gaps 0;

QY 3 TYDDNSSATGGRVNIYAG 23
Db 333 TMDDLTALGNRVNFGSG 353

RESULT 8
US-08-301-162-18
; Sequence 18, Application US/08301162
; Patent No. 6022546
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; APPLICANT: Ziegelmaier, Robert
; APPLICANT: Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION NUMBER: US/09/461,240
; FILING DATE: 16-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,162
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/167,128
; FILING DATE:
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleschner, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-301-162-18

Query Match      33.6%; Score 47; DB 3; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVNIYAGNT 25
Db 386 AAGGRVDAFGAGLT 400

RESULT 9
US-09-461-240-18
; Sequence 18, Application US/09461240
; Patent No. 6326008
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; APPLICANT: Ziegelmaier, Robert
; APPLICANT: Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/461,240
; FILING DATE: 16-Dec-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
```

```
; APPLICATION NUMBER: US/08/301,162
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/167,128
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleisher, Raz E.
; REGISTRATION NUMBER: 34,331
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-461-240-18

Query Match 33.6%; Score 47; DB 3; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVQNIYGAGNT 25
Db 386 AAGRVDAFGAGLT 400

RESULT 10
US-09-968-927-18
; Sequence 18, Application US/09968927
; Patent No. 6419525
; GENERAL INFORMATION:
; APPLICANT: Knapp, Stefan
; Kuegelmaier, Robert
; Kupper, Hans
; TITLE OF INVENTION: Toxoplasma Gondii Antigens, The
; Preparation Thereof and the Use Thereof
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
; Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/968,927
; FILING DATE: 03-Oct-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/301,162
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US/08/167,128
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 07/623,086
; FILING DATE: 06-DEC-1990
; APPLICATION NUMBER: DE P3940598.2
; FILING DATE: 08-DEC-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Fleisher, Raz E.
; REGISTRATION NUMBER: 34,331
```

```
; REFERENCE/DOCKET NUMBER: 02481.1005-00000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 428 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-968-927-18

Query Match 33.6%; Score 47; DB 4; Length 428;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 ATGGRVQNIYGAGNT 25
Db 386 AAGRVDAFGAGLT 400

RESULT 11
US-08-961-083-70
; Sequence 70, Application US/08961083
; Patent No. 6159469
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,083
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-961-083-70

Query Match 33.6%; Score 47; DB 3; Length 437;
Best Local Similarity 33.3%; Pred. No. 83;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KYDONSSEA-----TGGRVQNIYGA 22
Db 182 KIWDNSNLSISVKVNGKKIYLGGLDNVHGA 214
```

RESULT 12
US-09-536-784-70
; Sequence 70, Application US/09536784
; Patent No. 6573082
; GENERAL INFORMATION:
; APPLICANT: Choi et. al.
; TITLE OF INVENTION: Streptococcus pneumoniae Antigens and Vaccines
; NUMBER OF SEQUENCES: 452
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/536,784
; FILING DATE: 30-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/961,083
; FILING DATE: OCT-30-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Michelle S. Marks
; REGISTRATION NUMBER: 41,971
; REFERENCE/DOCKET NUMBER: PB340P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 70:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 70:
US-09-536-784-70

Query Match 33.6%; Score 47; DB 4; Length 437;
Best Local Similarity 33.3%; Pred. No. 83;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : ||||| :
Db 182 KIWDNSNSLSIVKVGKKIYLGGLDNVHGA 214
| : ||||| :

RESULT 13
US-09-583-110-5137
; Sequence 5137, Application US/09583110
; Patent No. 6699703
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al.
; TITLE OF INVENTION: Nucleic Acid and Amino Acid Sequences Relating to Streptococcus
; FILE REFERENCE: PATH00-07A
; CURRENT APPLICATION NUMBER: US/09/583,110
; CURRENT FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/107,433
; PRIOR FILING DATE: 1998-06-30
; PRIOR APPLICATION NUMBER: US 60/085,131
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: US 60/051,553
; PRIOR FILING DATE: 1997-07-02
; NUMBER OF SEQ ID NOS: 5322
; SEQ ID NO 5137

; LENGTH: 627
; TYPE: PRT
; ORGANISM: Streptococcus pneumoniae
US-09-583-110-5137

Query Match 33.6%; Score 47; DB 4; Length 627;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : ||||| :
Db 203 KIWDNSNSLSIVKVGKKIYLGGLDNVHGA 235
| : ||||| :

RESULT 14
US-09-107-433-4391
; Sequence 4391, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD-ROM ISO9660
; COMPUTER: <Unknown>
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: <Unknown>
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,433
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/ 085131
; FILING DATE: May 12, 1998
; APPLICATION NUMBER: 60/051553
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Ariniello, Pamela Deneke
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-011
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-5007
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 4391:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 637 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: YES
; ORIGINAL SOURCE:
; ORGANISM: Streptococcus pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (B) LOCATION 1...637
; SEQUENCE DESCRIPTION: SEQ ID NO: 4391:
US-09-107-433-4391

Query Match 33.6%; Score 47; DB 4; Length 637;
Best Local Similarity 33.3%; Pred. No. 1.3e+02;
Matches 11; Conservative 5; Mismatches 5; Indels 12; Gaps 1;

QY 2 KTYDDNSSA-----TGGRVQNIYGA 22
| : ||||| :
Db 213 KIWDNSNSLSIVKVGKKIYLGGLDNVHGA 245
| : ||||| :

RESULT 15
US-09-303-064-55
; Sequence 55, Application US/09303064
; Patent No. 6221619
; GENERAL INFORMATION:
; APPLICANT: MAINE, Gregory T.
; APPLICANT: HUNT, Jeffery C.
; APPLICANT: BROJANAC, Susan
; APPLICANT: JYH-TSING SHEU, Michael
; APPLICANT: CHOVAN, Linda E.
; APPLICANT: TYNER, Joan D.
; APPLICANT: HOWARD, Lawrence V.
; APPLICANT: PARMLEY, Stephen F.
; APPLICANT: REMINGTON, Jack S.
; APPLICANT: ARAUJO, Fausto
; APPLICANT: SUZUKI, Yashuhiro
; APPLICANT: LI, Shuli
; TITLE OF INVENTION: ANTIGEN COCKTAILS, P35 AND USES THEREOF
; FILE REFERENCE: 6361.US.P1
; CURRENT APPLICATION NUMBER: US/09/303,064
; CURRENT FILING DATE: 1999-04-30
; EARLIER APPLICATION NUMBER: 09/086,503
; EARLIER FILING DATE: 1998-05-28
; NUMBER OF SEQ ID NOS: 55
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 667
; TYPE: PRT
; ORGANISM: Toxoplasma gondii
US-09-303-064-55

Query Match 33.6% Score 47; DB 3; Length 667;
Best Local Similarity 60.0%; Pred. No. 1.3e+02;
Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 11 ATGGRVQNIYCGAGNT 25
| | | | | : | | | | |
Db 533 AAGGRVDFAGAGLT 547

Search completed: July 6, 2005, 15:20:41
Job time : 3 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:57:40 ; Search time 1.68831 Seconds

(without alignments)

1481.738 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745

Perfect score: 140

Sequence: 1 GKTYYDNNSSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 79:*

1: Pir1:*

2: Pir2:*

3: Pir3:*

4: Pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	797	2 D82000	outer membrane pro
2	140	100.0	797	2 G81228	outer membrane pro
3	60	42.9	588	2 T51154	probable transmemb
4	55	39.3	1485	1 ISZPT2	DNA topoisomerase
5	54	38.6	1462	2 T06819	DNA topoisomerase
6	54	38.6	1473	2 S53599	DNA topoisomerase
7	50	35.7	260	2 T08463	carbonate dehydrat
8	50	35.7	314	1 JCA066	ADPglyceromanno-he
9	50	35.7	1428	1 ISBYT2	DNA topoisomerase
10	50	35.7	1526	2 JN0598	DNA topoisomerase
11	50	35.7	1526	2 A44406	DNA topoisomerase
12	50	35.7	1528	2 JS0703	DNA topoisomerase
13	50	35.7	1530	2 A40493	DNA topoisomerase
14	50	35.7	1612	2 S59969	DNA topoisomerase
15	50	35.7	1626	2 A39242	DNA topoisomerase
16	48.5	34.6	147	1 S24310	flavodoxin - Desul
17	48	34.3	763	2 D86326	hypothetical prote
18	47	33.6	243	2 T28802	hypothetical prote
19	47	33.6	347	2 A86549	polymorphic outer
20	47	33.6	367	2 T24058	hypothetical prote
21	47	33.6	396	1 A58938	surface protein th
22	47	33.6	493	2 A55092	catalase [EC 1.11.
23	47	33.6	572	2 T34273	hypothetical prote
24	47	33.6	627	2 E95107	choline binding pr
25	47	33.6	627	2 G97975	hypothetical prote
26	46.5	33.2	432	2 S51474	hypothetical prote
27	46	32.9	544	2 AB1178	transport protein
28	46	32.9	1083	1 S53048	alpha-mannosidase
29	46	32.9	1103	2 T13590	distal tail fiber

30	-46	32.9	1230	2 T17187	CL3AB protein - ra
31	46	32.9	1231	2 T18390	latrophilin-3, spl
32	46	32.9	1240	2 T18393	latrophilin-3, spl
33	46	32.9	1273	2 T17188	CL3AC protein - ra
34	46	32.9	1274	2 T18391	latrophilin-3, spl
35	46	32.9	1283	2 T18394	latrophilin-3, spl
36	46	32.9	1298	2 T17199	CL3BB protein - ra
37	46	32.9	1299	2 T18398	latrophilin-3, spl
38	46	32.9	1308	2 T18408	latrophilin-3, spl
39	46	32.9	1341	2 T17200	CL3BC protein - ra
40	46	32.9	1342	2 T18405	latrophilin-3, spl
41	46	32.9	1351	2 T18409	latrophilin-3, spl
42	46	32.9	1459	2 T17186	CL3AA protein - ra
43	46	32.9	1503	2 T18389	latrophilin-3, spl
44	46	32.9	1512	2 T18392	latrophilin-3, spl
45	46	32.9	1527	2 T17198	CL3BA protein - ra

ALIGNMENTS

RESULT 1

outer membrane protein OMP85 NMA0085 [imported] - Neisseria meningitidis (strain Z2491 se
DB2000
C:Species: Neisseria meningitidis
C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 09-Jul-2004
C:Accession: DB2000
R:Parkhill, J.; Achtman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morell
; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Mungall, K.; Quail, M.A.; Rajandream,
Nature 404, 502-506, 2000
A:Title: Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491.
A:Reference number: A81775; MUID:2022556; PMID:10761919
A:Accession: DB2000
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-797 <PAR>
A:Cross-references: UNIPROT:Q9JX31; GB:AL162752; GB:AL157959; NID:g7378778; PIDN:CA883401
A:Experimental source: serogroup A, strain Z2491
C:Genetics:
A:Gene: omp85; NMA0085
C:Superfamily: protective surface antigen D-15

Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 3e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0

QY 1 GKTYYDNNSSSATGGRVQNIYGAGNTH 26

Db 720 GKTYYDNNSSSATGGRVQNIYGAGNTH 745

RESULT 2

outer membrane protein Omp85 NMB0182 [imported] - Neisseria meningitidis (strain MC58 se
G81228
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 09-Jul-2004
C:Accession: G81228
R:Tetzelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Maignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ver
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: A81000; MUID:20175755; PMID:10710307
A:Accession: G81228
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-797 <TET>
A:Cross-references: UNIPROT:Q9K1H0; GB:AE002375; GB:AE002098; NID:g7225394; PIDN:AAF4063;
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0182
C:Superfamily: protective surface antigen D-15

Query Match 100.0%; Score 140; DB 2; Length 797;
 Best Local Similarity 100.0%; Pred. No. 3e-12;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSSATGGRVQNIYGANTH 26
 |||||
 Db 720 GKYDDNSSSATGGRVQNIYGANTH 745

RESULT 3
 T51154
 probable transmembrane protein G5p [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 09-Jul-2004
 R:Comella, P.; Wu, H.J.; Laudie, M.; Berger, C.; Cooke, R.; Delseny, M.; Grellet, F.
 Plant Mol. Biol. 41, 687-700, 1999
 A:Title: Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on
 A:Reference number: Z24835; MUID:20108326; PMID:10645728
 A:Accession: T51154
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-588 <COM>
 A:Cross-references: UNIPROT:Q96328; EMBL:AF049236; PIDN:AAC14410.1
 R:Grellet, F.; Gaubier, P.; Wu, H.J.; Laudie, M.; Berger, C.; Delseny, M.
 submitted to the EMBL Data Library, September 1996
 A:Description: Structure of the Arabidopsis thaliana Em1 locus.
 A:Reference number: Z25319
 A:Accession: T51164
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-588 <GRE>
 A:Cross-references: EMBL:U72504; PIDN:AA818128.1
 A:Experimental source: cultivar Columbia
 C:Genetics: AtG5
 A:Gene: AtG5
 A:Map position: 3
 A:Introns: 51/1; 76/1; 118/3; 149/2; 168/3; 187/3; 195/1; 226/1; 261/3; 290/3; 316/3; 336/3

Query Match 42.9%; Score 60; DB 2; Length 588;
 Best Local Similarity 50.0%; Pred. No. 0.94;
 Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

QY 2 KTYDDNSSSATGGRVQNIYGANT 25
 |||||
 Db 47 KPIDENASSGSPRVSTIYGVGCT 70

RESULT 4
 IS2PT2
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - fission yeast (Schizosaccharomyces pombe)
 N:Alternate names: DNA-lyase; type II DNA topoisomerase
 C:Species: Schizosaccharomyces pombe
 C>Date: 30-Sep-1992 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
 C:Accession: T39851; A24897
 R:Wood, V.; Rajandream, M.A.; Barrell, B.G.; Volckaert, G.
 submitted to the EMBL Data Library, July 1998
 A:Reference number: Z21885
 A:Accession: T39851
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: DNA
 A:Residues: 1-1485 <WOO>
 A:Cross-references: UNIPROT:P08096; EMBL:AL031174; PIDN:CAA20107.1; GSPDB:GN00067
 R:Uemura, T.; Morikawa, K.; Yanagida, M.
 EMO J. 5, 2355-2361, 1986
 A:Title: The nucleotide sequence of the fission yeast DNA topoisomerase II gene: structure
 A:Reference number: A24897; MUID:870533875; PMID:3023070
 A:Accession: A24897
 A:Molecule type: DNA
 A:Residues: 55-993; 'I', 995-1485 <UEM>
 A:Cross-references: GB:X04326; NID:G5120; PIDN:CAA27857.1; PID:G5121

C:Comment: Type II DNA topoisomerase catalyzes the ATP-dependent transient breakage, pass
 C:Genetics:
 A:Gene: top2
 A:Map position: 2
 A:Introns: 28/3
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
 C:Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase

Query Match 39.3%; Score 55; DB 1; Length 1485;
 Best Local Similarity 63.2%; Pred. No. 14;
 Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGA 22
 |||||
 Db 196 YDDNQKKTGGR--NGYGA 212

RESULT 5
 T06819
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - garden pea
 C:Species: Pisum sativum (garden pea)
 C>Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
 C:Accession: T06819
 R:Reddy, M.K.; Nair, S.; Tewari, K.K.
 submitted to the EMBL Data Library, August 1997
 A:Reference number: Z15832
 A:Accession: T06819
 A>Status: preliminary; translated from GB/EMBL/DDBJ
 A:Molecule type: mRNA
 A:Residues: 1-1462 <RED>
 A:Cross-references: UNIPROT:O24308; EMBL:Y14559; PIDN:CAA74891.1
 C:Genetics:
 A:Note: TOP11
 C:Function:
 A:Description: involved in DNA replication and chromosome condensation
 C:Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd
 C:Keywords: ATP; DNA binding; isomerase

Query Match 38.6%; Score 54; DB 2; Length 1462;
 Best Local Similarity 56.5%; Pred. No. 19;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDDNSSSATGGRVQNIYGANTH 26
 |||||
 Db 139 YDDNVKKTGGR--NGYGAKLTN 159

RESULT 6
 S53599
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - Arabidopsis thaliana
 N:Alternate names: DNA-lyase; type II DNA topoisomerase
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 15-Jul-1995 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C:Accession: S53598; S53599; S53600
 R:Xie, S.; Lam, E.
 Nucleic Acids Res. 22, 5729-5736, 1994
 A:Title: Abundance of nuclear DNA topoisomerase II is correlated with proliferation in A
 A:Reference number: S53598; MUID:95140639; PMID:7838729
 A:Accession: S53598
 A:Molecule type: mRNA
 A:Residues: 1-1473 <XIE>
 A:Cross-references: UNIPROT:P30182; EMBL:L21015; NID:G474889; PIDN:AAA65448.1; PID:G4748
 A:Experimental source: ecotype Columbia
 A:Accession: S53599
 A:Molecule type: DNA
 A:Residues: 1202-1304 <XIW>
 A:Cross-references: EMBL:U12284; NID:G520557; PIDN:AAC48999.1; PID:G520558
 A:Experimental source: ecotype Columbia
 A:Accession: S53600
 A>Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1202-1212, 'N', 1214-1244, 'G', 1246-1298, 'G', 1300-1304 <XIF>
 A:Cross-references: EMBL:U12285; NID:G520559; PIDN:AAC49000.1; PID:G520560

A;Experimental source: ecotype Kashmir
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C;Genetics:
 A;Gene: TOP11
 A;Introns: 1234/1; 1269/1; 1293/3
 A;Note: list of introns is incomplete
 C;Function:
 A;Description: involved in DNA replication and chromosome condensation
 C;Superfamily: eukaryotic type II DNA topoisomerase (ATP-hydrolyzing)
 C;Keywords: ATP; DNA binding; isomerase; nucleus
 F;673-905/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4>

Query Match 38.6%; Score 54; DB 2; Length 1473;
 Best Local Similarity 56.5%; Pred. No. 19;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDNNSSATGGRVONIYGAGNTH 26
 ||||| ||||| ||||| |||||
 Db 151 YDDNVKKTGG-NGYGAKLTN 171

RESULT 7
 T08463
 carbonate dehydratase (EC 4.2.1.1) - zebra fish
 C;Species: Brachydanio rerio (zebra fish)
 C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
 C;Accession: T08463
 R;Peterson, R.E.; Tu, C.; Linser, P.J.
 J. Mol. Evol. 44, 432-439, 1997
 A;Title: Isolation and characterization of a carbonic anhydrase homologue from the zebra fish
 A;Reference number: Z16422; MUID:97250269; PMID:9089083
 A;Accession: T08463
 A;Status: preliminary; translated from GB/EMBL/DDBU
 A;Molecule type: mRNA
 A;Residues: 1-260 <PET>
 A;Cross-references: UNIPROT:Q92051; EMBL:U55177; NID:g2576334; PID:g2576335
 C;Superfamily: carbonate dehydratase; carbonic anhydrase homology
 C;Keywords: carbon-oxygen lyase; hydro-lyase; zinc
 F;5-259/Domain: carbonic anhydrase homology <CAH>

Query Match 35.7%; Score 50; DB 2; Length 260;
 Best Local Similarity 45.5%; Pred. No. 11;
 Matches 10; Conservative 2; Mismatches 10; Indels 0; Gaps 0;

QY 5 DNSSSATGGRVONIYGAGNTH 26
 ||||| ||||| ||||| |||||
 Db 73 DNSSSLAGPITGIVRLRQFH 94

RESULT 8
 JC4066
 ADPglyceromanno-heptose 6-epimerase (EC 5.1.3.20) rfad VC0240 [similarity] - Vibrio cholerae
 A;Alternate names: ADP-L-glycero-D-mannoheptose-6-epimerase; rfad protein
 C;Species: Vibrio cholerae
 C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C;Accession: JC4066; S70952; G82345; S28467
 R;Stroeher, U.H.; Karageorgios, L.E.; Morona, R.; Manning, P.A.
 Gene 155, 67-72, 1995
 A;Title: In Vibrio cholerae serogroup O1, rfad is closely linked to the rfb operon.
 A;Reference number: JC4066; MUID:95212931; PMID:7698669
 A;Contents: Inaba and Ogawa serotypes, 569B and O17
 A;Accession: JC4066
 A;Molecule type: DNA
 A;Residues: 1-314 <STR>
 A;Cross-references: UNIPROT:Q06963; EMBL:X59554; NID:g48381; PIDN:CAA42133.1; PID:g48382
 R;Bik, E.M.; Bunschoten, A.E.; Willems, R.J.L.; Chang, A.C.Y.; Mooi, F.R.
 Mol. Microbiol. 20, 799-811, 1996
 A;Title: Genetic organization and functional analysis of the otn DNA essential for cell-division in Vibrio cholerae
 A;Reference number: S70952; MUID:96386047; PMID:8793876
 A;Accession: S70952
 A;Status: preliminary; nucleic acid sequence not shown; translation not shown
 A;Molecule type: DNA
 A;Residues: 1-67, 'S', 69-314

A;Cross-references: EMBL:X90547; NID:g1469276; PIDN:CAA62134.1; PID:g1107917
 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1995
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P. 1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: G82345
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-314 <HEI>
 A;Cross-references: GB:AE004113; GB:AE003852; NID:g9654648; PIDN:AAF93416.1; GSPDB:GN001:
 A;Experimental source: serogroup O1; strain N61961; biotype El Tor
 C;Comment: This enzyme is required for the biosynthesis of the lipopolysaccharide precursor
 C;Genetics:
 A;Gene: rfad; VC0240
 A;Map position: 1
 C;Superfamily: ADPglyceromanno-heptose 6-epimerase; UDPglucose 4-epimerase homology
 C;Keywords: isomerase
 F;7-12/Region: helix-turn-helix

Query Match 35.7%; Score 50; DB 1; Length 314;
 Best Local Similarity 40.0%; Pred. No. 14;
 Matches 10; Conservative 3; Mismatches 12; Indels 0; Gaps 0;

QY 2 KYDNNSSATGGRVONIYGAGNTH 26
 ||||| ||||| ||||| |||||
 Db 158 KQHDETLSQLTGFVFNVYGPREQH 182

RESULT 9
 ISBYT2
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) - yeast (Saccharomyces cerevisiae)
 A;Alternate names: DNA gyrase; DNA topoisomerase II; protein N2244; protein YNL088w
 C;Species: Saccharomyces cerevisiae
 C;Date: 30-Sep-1992 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
 C;Accession: S57534; A25630; S63027; S30866; S65093
 R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
 submitted to the EMBL Data Library, June 1995
 A;Reference number: S57533
 A;Accession: S57534
 A;Molecule type: DNA
 A;Residues: 1-1428 <SOL>
 A;Cross-references: UNIPROT:P06786; EMBL:X89016; NID:g887621; PIDN:CAA61422.1; PID:g88762;
 R;Glaever, G.; Lynn, R.; Goto, T.; Wang, J.C.
 J. Biol. Chem. 261, 12448-12454, 1986
 A;Title: The complete nucleotide sequence of the structural gene TOP2 of yeast DNA topoisomerase II
 A;Reference number: A25630; MUID:86304413; PMID:3017975
 A;Accession: A25630
 A;Molecule type: DNA
 A;Residues: 1-74, 'N', 75-546, 'L', 548-836, 'R', 838-1428 <GIA>
 A;Cross-references: GB:M13814; NID:g172997; PIDN:AAB36610.1; PID:g172998
 R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
 submitted to the Protein Sequence Database, April 1996
 A;Reference number: S63018
 A;Accession: S63027
 A;Molecule type: DNA
 A;Residues: 1-1428 <SOW>
 A;Cross-references: EMBL:271364; NID:g1301988; PIDN:CAA95964.1; PID:g1301989; GSPDB:GN000
 A;Experimental source: strain S288C
 R;Jannatipour, M.; Liu, Y.X.; Nitiss, J.L.
 submitted to the EMBL Data Library, January 1993
 A;Description: The top2-5 mutant of yeast topoisomerase II encodes an enzyme resistant to camptothecin
 A;Reference number: S30866
 A;Accession: S30866
 A;Molecule type: DNA
 A;Residues: 812-836, 'R', 838-882, 'P', 884, 'II', 887-977 <JAN>
 A;Cross-references: EMBL:L08968; NID:g172999; PIDN:AAB59328.1; PID:g173000
 R;Soler-Mira, A.; Saiz, J.E.; Ballesta, J.P.G.; Remacha, M.
 Yeast 12, 485-491, 1996
 A;Title: The sequence of a 17 933 bp segment of Saccharomyces cerevisiae chromosome XIV
 A;Reference number: S65092; MUID:96310628; PMID:8740422

A;Accession: S65093
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1428 <SOF>
A;Cross-references: EMBL:X89016; NID:g887621; PIDN:CAA61422.1; PID:g887623
C;Comment: Type II DNA topoisomerase catalyzes the ATP-dependent transient breakage, pass
C;Genetics:
A;Gene: SGD:TOP2; TOR3; TRF3; TOP2-5; MIPS:YNL088W
A;Cross-references: SGD:S0005032; MIPS:YNL088W
A;Map position: 14L
C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd-
C;Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase; phosphoprotein

Query Match 35.7%; Score 50; DB 1; Length 1428;
Best Local Similarity 57.9%; Pred. No. 71;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 YDNSSSATGGRVQNIYGA 22
|||: |||| | |||
Db 130 YDDDEKKVTGGR--NGYGA 146

RESULT 10

JN0598
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.13) - rat
N;Alternate names: DNA topoisomerase II
C;Species: Rattus norvegicus (Norway rat)
C;Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C;Accession: JN0598; S32012
R;Park, S.H.; Yoon, J.H.; Kwon, Y.D.; Park, S.D.
Biochem. Biophys. Res. Commun. 193, 787-793, 1993
A;Title: Nucleotide sequence analysis of the cDNA for rat DNA topoisomerase II.
A;Reference number: JN0598; MUID:93290677; PMID:8390253
A;Accession: JN0598
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
A;Residues: 1-1526 <PAR>
A;Cross-references: EMBL:Z19552; NID:g57963; PIDN:CAA79611.1; PID:g57964
A;Experimental source: testis
A;Note: the authors translated the codon GTG for residue 3 as Leu
C;Comment: This enzyme is required for the segregation of circular DNA molecules after r
C;Genetics:
A;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd-
C;Keywords: ATP; DNA recombination; DNA repair; DNA replication; isomerase
F;689-916/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1526;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 YDNSSSATGGRVQNIYGA 22
|||: |||| | |||
Db 149 YDDDEKKVTGGR--NGYGA 165

RESULT 11

A44406
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.13) - Chinese hamster
N;Alternate names: DNA-tyrase; type II DNA topoisomerase
C;Species: Cricetus griseus (Chinese hamster)
C;Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C;Accession: A44406
R;Chan, V.T.; Ng, S.W.; Eder, J.P.; Schnipper, L.E.
J. Biol. Chem. 268, 2160-2165, 1993
A;Title: Molecular cloning and identification of a point mutation in the topoisomerase I
A;Reference number: A44406; MUID:93131977; PMID:8380592
A;Accession: A44406
A;Molecule type: nucleic acid
A;Residues: 1-1526 <CHA>
A;Cross-references: UNIPROT:P41515; GB:L04607; NID:g191217; PIDN:AAA37023.1; PID:g191218
A;Experimental source: ovary
A;Note: sequence extracted from NCBI backbone (NCBIP:123211)

C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd)
C;Keywords: ATP; DNA binding; DNA replication; heterotetramer; isomerase

Query Match 35.7%; Score 50; DB 2; Length 1526;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 YDDNSSATGGRVQNIYGA 22
|||: |||| |
Db 150 YDDDEKKVTGGR--NGYGA 166

RESULT 12

JS0703
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) II - mouse
C;Species: Mus musculus (house mouse)
C;Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
C;Accession: JS0703; S35483
R;Adachi, N.; Miyaake, M.; Ikeda, H.; Kikuchi, A.
submitted to JIPID, July 1992
A;Reference number: JS0703
A;Accession: JS0703
A;Status: translation not shown
A;Molecule type: mRNA
A;Residues: 1-1528 <ADA>
A;Cross-references: UNIPROT:Q01320; DDBJ:D12513; NID:g220615; PIDN:BAA02076.1; PID:g220616
R;Adachi, N.; Miyaake, M.; Ikeda, H.; Kikuchi, A.
Nucleic Acids Res 20, 5297-5303, 1992
A;Title: Characterization of cDNA encoding the mouse DNA topoisomerase II that can complete
A;Reference number: S35483; MUID:93065194; PMID:1331984
A;Accession: S35483
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1528 <ADA>
A;Cross-references: EMBL:D12513; NID:g220615; PIDN:BAA02076.1; PID:g220616
C;Superfamily: eukaryotic type II DNA topoisomerase; phage T4 DNA topoisomerase (ATP-hyd)
C;Keywords: ATP; DNA binding; isomerase; leucine zipper; nucleus
F;994-1015/Region: leucine zipper motif
F;804/Active site: Tyr #status predicted

Query Match 35.7%; Score 50; DB 2; Length 1528;
Best Local Similarity 57.9%; Pred. No. 76;
Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

Qy 4 YDDNSSATGGRVQNIYGA 22
|||: |||| |
Db 150 YDDDEKKVTGGR--NGYGA 166

RESULT 13

A40493
DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) alpha - human
C;Species: Homo sapiens (man)
C;Date: 07-Feb-1992 #sequence_revision 03-Apr-1992 #text_change 19-Dec-1998
C;Accession: A40493; A41278
R;Tsai-Pflugfelder, M.; Liu, L.F.; Liu, A.A.; Tewey, K.M.; Whang-Peng, J.; Knutsen, T.; F
Proc. Natl. Acad. Sci. U.S.A. 85, 7177-7181, 1988
A;Title: Cloning and sequencing of cDNA encoding human DNA topoisomerase II and localizat
A;Reference number: A40493; MUID:89017161; PMID:2845399
A;Accession: A40493
A;Molecule type: mRNA
A;Residues: 1-1530 <TSA>
A;Cross-references: GB:J04088
R;Buggy, B.Y.; Danks, M.K.; Beck, W.T.; Suttle, D.P.
Proc. Natl. Acad. Sci. U.S.A. 88, 7654-7658, 1991
A;Title: Expression of a mutant DNA topoisomerase II in CCRF-CEM human leukemic cells sel
A;Reference number: A41278; MUID:91352047; PMID:1652758
A;Accession: A41278
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 442-521 <BUG>
A;Note: a mutant with residue 449-Arg replaced by Gln was resistant to teniposide
C;Genetics:

A;Gene: GDB:TOP2A; TOP2
 A;Cross-references: GDB:I18884; OMIM:126430
 A;Map position: 17q21-17q22
 C;Superfamily: eukaryotic type II DNA topoisomerase (ATP-hyd
 C;Keywords: ATP; DNA binding; isomerase; nucleus

Query Match 35.7%; Score 50; DB 2; Length 1530;
 Best Local Similarity 57.9%; Pred. No. 76;
 Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSATGGRVQNIYGA 22
 |||||
 Db 150 YDDDEKKTGGR--NGYGA 166

RESULT 14
 S59969
 N;Alternate names: DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) isoform beta - Chinese hamster
 N;Alternate names: DNA topoisomerase II isoform beta; DNA-gyrase
 C;Species: Crictetus griseus (Chinese hamster)
 C;Date: 15-Feb-1996 #sequence_revision 13-Mar-1997 #text_change 16-Jul-1999
 C;Accession: S59969; S54154
 R;Dereudre, S.; Frey, S.; Delaporte, C.; Jacquemin-Sablon, A.
 Biochim. Biophys. Acta 1264, 178-182, 1995
 A;Title: Cloning and characterization of full-length cDNAs coding for the DNA topoisom
 A;Reference number: S59969; MUID:96085121; PMID:7495861
 A;Accession: S59969
 A;Status: translation not shown
 A;Molecule type: mRNA
 A;Residues: 1-1612 <DER>
 A;Cross-references: EMBL:X66455; NID:g790987; PIDN:CAA60173.1; PID:g790988
 A;Experimental source: lung
 C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
 C;Keywords: ATP; DNA binding; DNA replication; isomerase; nucleus
 F;697-927/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1612;
 Best Local Similarity 57.9%; Pred. No. 81;
 Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSATGGRVQNIYGA 22
 |||||
 Db 160 YDDDEKKTGGR--NGYGA 176

RESULT 15
 A39242
 DNA topoisomerase (ATP-hydrolyzing) (EC 5.99.1.3) beta, splice form 2 - human
 N;Alternate names: DNA topoisomerase II isoform beta-2
 N;Contains: DNA topoisomerase II isoform beta-1
 C;Species: Homo sapiens (man)
 C;Date: 04-Oct-1991 #sequence_revision 03-May-1996 #text_change 09-Jul-2004
 C;Accession: S26730; A39242; S10710; S33970; S30191; S41641; S30190
 R;Jenkins, J.R.; Ayton, P.; Jones, T.; Davies, S.L.; Simmons, D.L.; Harris, A.L.; Sheer,
 Nucleic Acids Res. 20, 5587-5592, 1992
 A;Title: Isolation of cDNA clones encoding the beta isozyme of human DNA topoisomerase I
 A;Reference number: S26730; MUID:93087165; PMID:1333583
 A;Accession: S26730
 A;Molecule type: mRNA
 A;Residues: 1-23,29-1626 <JEN>
 A;Cross-references: UNIPROT:Q02880; EMBL:X68060; NID:g37230; PIDN:CAA48197.1; PID:g37231
 R;Chung, T.D.Y.; Drake, F.H.; Tan, K.B.; Per, S.R.; Crooke, S.T.; Mirabelli, C.K.
 Proc. Natl. Acad. Sci. U.S.A. 86, 9431-9435, 1989
 A;Title: Characterization and immunological identification of cDNA clones encoding two h
 A;Reference number: A39242; MUID:90083281; PMID:2556712
 A;Accession: A39242
 A;Molecule type: mRNA
 A;Residues: 149-1043 <CHU>
 A;Cross-references: GB:M27504
 R;Austin, C.A.; Fisher, L.M.
 FEBS Lett. 266, 115-117, 1990
 A;Title: Isolation and characterization of a human cDNA clone encoding a novel DNA topoi
 A;Reference number: S10710; MUID:90306333; PMID:2163884

A;Accession: S10710
 A;Molecule type: mRNA
 A;Residues: 1043-1276 <AUS>
 A;Cross-references: GB:X53662; GB:S56813; NID:g38324; PIDN:CAA37706.1; PID:g38325
 R;Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M.
 Biochim. Biophys. Acta 1172, 283-291, 1993
 A;Title: Novel HeLa topoisomerase II is the II-beta isoform: complete coding sequence an
 A;Reference number: S30190; MUID:93192319; PMID:8383537
 A;Accession: S33970
 A;Molecule type: mRNA
 A;Residues: 1-23,29-1610,'A',1612-1626 <AU2>
 A;Cross-references: EMBL:Z15111
 R;Austin, C.A.; Sng, J.H.; Patel, S.; Fisher, L.M.
 submitted to the EMBL Data Library, September 1992
 A;Reference number: S30191
 A;Accession: S30191
 A;Molecule type: mRNA
 A;Residues: 596-1430,'S',1432-1610,'A',1612-1626 <AU1>
 A;Cross-references: EMBL:Z15115; NID:g288564; PIDN:CAA78821.1; PID:g288565
 R;Davies, S.L.; Jenkins, J.R.; Hickson, I.D.
 Nucleic Acids Res. 21, 3719-3723, 1993
 A;Title: Human cells express two differentially spliced forms of topoisomerase II-beta m
 A;Reference number: S41641; MUID:93376494; PMID:8396237
 A;Accession: S41641
 A;Molecule type: DNA
 A;Residues: 24-80 <DAV>
 A;Cross-references: EMBL:X71911; NID:g396540; PIDN:CAA50726.1; PID:g3980296
 A;Note: this sequence represents a long minor splice form, designated beta-2
 C;Genetics:
 A;Gene: GDB:TOP2B
 A;Cross-references: GDB:131575; OMIM:126431
 A;Map position: 3p24-3p24
 C;Superfamily: eukaryotic type II DNA topoisomerase; phase T4 DNA topoisomerase (ATP-hyd
 C;Keywords: alternative splicing; ATP; dimer; isomerase; nucleus
 F;1-1626/Product: DNA topoisomerase II beta-2 #status predicted <MINR>
 F;1-23,29-1626/Product: DNA topoisomerase II beta-1 #status predicted <MAJR>
 F;709-939/Domain: phase T4 DNA topoisomerase (ATP-hydrolyzing) medium chain homology <T4

Query Match 35.7%; Score 50; DB 2; Length 1626;
 Best Local Similarity 57.9%; Pred. No. 82;
 Matches 11; Conservative 1; Mismatches 5; Indels 2; Gaps 1;

QY 4 YDDNSSATGGRVQNIYGA 22
 |||||
 Db 172 YDDDEKKTGGR--NGYGA 189

Search completed: July 6, 2005, 15:19:14
 Job time : 2.68831 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:18:21 ; Search time 7.2987 Seconds
(without alignments)
1374.310 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKYDDNSSATGGRVQNIYGAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1722976 seqs, 385795295 residues

Total number of hits satisfying chosen parameters: 1722976

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications AA:*
1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pbp:*
2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pbp:*
3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pbp:*
4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pbp:*
5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pbp:*
6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pbp:*
7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pbp:*
8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pbp:*
9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pbp:*
10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pbp:*
11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pbp:*
12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pbp:*
13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pbp:*
14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pbp:*
15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pbp:*
16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pbp:*
17: /cgn2_6/ptodata/2/pubpaa/US10E_PUBCOMB.pbp:*
18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pbp:*
19: /cgn2_6/ptodata/2/pubpaa/US11A_PUBCOMB.pbp:*
20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pbp:*
21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pbp:*
22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pbp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	776	14 US-10-181-660-5	Sequence 5, Appli
2	140	100.0	776	14 US-10-181-660-13	Sequence 13, Appl
3	140	100.0	776	16 US-10-181-600-5	Sequence 5, Appli
4	140	100.0	776	16 US-10-181-600-13	Sequence 13, Appl
5	140	100.0	797	9 US-09-994-192-4	Sequence 4, Appli
6	140	100.0	797	14 US-10-181-660-3	Sequence 3, Appli
7	140	100.0	797	14 US-10-181-660-11	Sequence 11, Appl
8	140	100.0	797	15 US-10-320-800-6	Sequence 6, Appli
9	140	100.0	797	16 US-10-181-600-3	Sequence 3, Appli
10	140	100.0	797	16 US-10-181-600-11	Sequence 11, Appl
11	140	100.0	797	17 US-10-606-618-4	Sequence 4, Appli

12	60	42.9	588	16	US-10-739-930-6705	Sequence 6705, Ap
13	59	42.1	315	14	US-10-156-761-10028	Sequence 10028, A
14	55	39.3	1504	15	US-10-369-493-2471	Sequence 2471, Ap
15	54	38.6	196	16	US-10-425-115-232640	Sequence 232640,
16	54	38.6	1487	16	US-10-437-963-161300	Sequence 161300,
17	53	37.9	1652	15	US-10-369-493-3223	Sequence 3223, Ap
18	51	36.4	193	16	US-10-425-115-288133	Sequence 288133,
19	51	36.4	219	15	US-10-425-114-64250	Sequence 64250, A
20	51	36.4	1266	15	US-10-320-797-3352	Sequence 3352, Ap
21	50.5	36.1	355	15	US-10-425-114-54797	Sequence 54797, A
22	50.5	36.1	589	15	US-10-424-599-164871	Sequence 164871,
23	50	35.7	260	17	US-10-732-923-19028	Sequence 19028, A
24	50	35.7	386	17	US-10-635-398-74	Sequence 74, Appl
25	50	35.7	581	14	US-10-198-070-20	Sequence 20, Appl
26	50	35.7	1428	15	US-10-369-493-1980	Sequence 1980, Ap
27	50	35.7	1429	15	US-10-448-871A-2	Sequence 2, Appli
28	50	35.7	1526	16	US-10-471-758-2	Sequence 347, App
29	50	35.7	1531	9	US-09-876-889-347	Sequence 2593, Ap
30	50	35.7	1531	9	US-09-998-598-2593	Sequence 222, App
31	50	35.7	1531	14	US-10-171-311-222	Sequence 211, App
32	50	35.7	1531	14	US-10-301-822-211	Sequence 46, Appl
33	50	35.7	1531	15	US-10-435-696-46	Sequence 2100, Ap
34	50	35.7	1531	16	US-10-723-860-2100	Sequence 42, Appl
35	50	35.7	1531	17	US-10-645-756-42	Sequence 1161, Ap
36	50	35.7	1621	15	US-10-296-115-1161	Sequence 3017, Ap
37	50	35.7	1626	16	US-10-408-765A-3017	Sequence 8754, Ap
38	49.5	35.4	1534	17	US-10-732-923-8754	Sequence 25453,
39	49	35.0	291	15	US-10-424-599-25453	Sequence 264378,
40	49	35.0	297	15	US-10-424-599-264378	Sequence 10695, A
41	49	35.0	692	9	US-09-815-242-10695	Sequence 57121, A
42	49	35.0	692	15	US-10-282-122A-57121	Sequence 43730, A
43	49	35.0	1953	15	US-10-282-122A-43730	Sequence 282071,
44	48.5	34.6	96	16	US-10-425-115-282071	Sequence 177136,
45	48	34.3	55	15	US-10-424-599-177136	

ALIGNMENTS

RESULT 1
US-10-181-660-5
; Sequence 5, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-5

Query Match 100.0%; Score 140; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. NO. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKYDDNSSATGGRVQNIYGAGNTH 26

Db 699 GKYDDNSSATGGRVQNIYGAGNTH 724

RESULT 2
US-10-181-660-13
; Sequence 13, Application US/10181660


```
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-13

Query Match      100.0%; Score 140; DB 14; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 3
US-10-181-600-5
; Sequence 5, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 5
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-5

Query Match      100.0%; Score 140; DB 16; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 4
US-10-181-600-13
; Sequence 13, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
```

```
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 13
; LENGTH: 776
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-13

Query Match      100.0%; Score 140; DB 16; Length 776;
Best Local Similarity 100.0%; Pred. No. 3.9e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      699 GKYDDNSSSATGGRVQNIYGAGNTH 724

RESULT 5
US-09-994-192-4
; Sequence 4, Application US/09994192
; Publication No. US20020086028A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; FILE REFERENCE: UMSBC147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match      100.0%; Score 140; DB 9; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GKYDDNSSSATGGRVQNIYGAGNTH 26
Db      720 GKYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 6
US-10-181-660-3
; Sequence 3, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SpA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-660-3

Query Match      100.0%; Score 140; DB 14; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GKTDDNSSSATGGRVQNIYGAGNTH 26
|||
Db 720 GKTDDNSSSATGGRVQNIYGAGNTH 745

```

RESULT 7
US-10-181-660-11
; Sequence 11, Application US/10181660
; Publication No. US20030027097A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785W0
; CURRENT APPLICATION NUMBER: US/10/181,660
; CURRENT FILING DATE: 2003-03-31
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PR1
; ORGANISM: Neisseria meningitidis
US-10-181-660-11

```

```
Query Match      100.0%; Score 140; DB 14; Length 797;
Best Local Similarity 100.0%;
Matches 26; Conservative 0; Mismatches 0; Indels 0;
Pred. No. 4e-12;
```

Qy 1 GKTYDDNSSATGGRVQNIYGAGNTH 26
Db 720 GKTYDDNSSATGGRVQNIYGAGNTH 745

```

RESULT 8
US-10-320-800-6
; Sequence 6, Application US/10320800
; Publication No. US20030215469A1
; GENERAL INFORMATION:
; APPLICANT: ROBINSON, ANDREW
; APPLICANT: GORRINGE, ANDREW
; APPLICANT: HUDSON, MICHAEL
; APPLICANT: REDDIN, KAREN
; TITLE OF INVENTION: MULTICOMPONENT
; FILE REFERENCE: 1581.0790001
; CURRENT APPLICATION NUMBER: US/10/
; CURRENT FILING DATE: 2002-12-17
; PRIOR APPLICATION NUMBER: PCT/G899
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 6
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-320-800-6

```

```
Query Match      100.0%; Score 140; DB 15; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy	1	GKTYDDNSSATGGRVQNIYGANTH	26
Db	720	GKTYDDNSSATGGRVQNIYGANTH	745

RESULT 9
US-10-181-600-3
; Sequence 3, Application US/10181600
; Publication No. US20040249125A1

```

; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P023785WO
; CURRENT APPLICATION NUMBER: US/10/181,600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: SeqWin99, version 1.02
; SEQ ID NO 3
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
; US-10-181-600-3

```

Query Match 100.0%; Score 140; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	GKTYDDNSSATGGRVQNIYGANTH	26
Db	720	GKTYDDNSSATGGRVQNIYGANTH	745

```

RESULT 10
US-10-181-600-11
; Sequence 11, Application US/10181600
; Publication No. US20040249125A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: SUPPLEMENTED OMV VACCINE AGAINST MENINGOCOCCUS
; FILE REFERENCE: P02378SWO
; CURRENT APPLICATION NUMBER: US/10/181.600
; CURRENT FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: GB-0001067.8
; PRIOR FILING DATE: 2000-01-17
; PRIOR APPLICATION NUMBER: GB-0005699.4
; PRIOR FILING DATE: 2000-03-09
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 11
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-10-181-600-11

```

```
Query Match      100.0%; Score 140; DB 16; Length 797;
Best Local Similarity 100.0%; Pred. No. 4e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

Qy 1 GKTYDDNSSSATGGRVQNIYGAGNTH 26
|||
Db 720 GKTYDDNSSSATGGRVQNIYGAGNTH 745

RESULT 11
US-10-606-618-4
; Sequence 4, Application US/10606618
; Publication No. US20050074458A1
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; APPLICANT: Manning, Scott D.
; TITLE OF INVENTION: Omp85 Proteins of *Neisseria gonorrhoeae* and *Neisseria meningitidis*
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: USMBC147AUSA
; CURRENT APPLICATION NUMBER: US/10/606,618
; CURRENT FILING DATE: 2003-06-26
; PRIOR APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039

0
4
0
0
4

4
2
、

0
0
4

0
4

0
0

```

    taps 1;

```

Oy 4 YDDNSSSATGGRVONIYGA 22
| | | | |
Db 148 YDDNERKTYGGR--NGYGA 164

Search completed: July 6, 2005, 15:42:21
Job time : 8.2987 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:56:39 ; Search time 7.27273 Seconds
(without alignments)
1830.683 Million cell updates/sec

Title: US-10-606-618-4_COPY_720_745
Perfect score: 140
Sequence: 1 GKYTDNNSSSATGGRVQNIYAGNTH 26

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot 03:.*
1: uniprot_sprot:.*
2: uniprot_trembl:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	140	100.0	797	2 O30912	O30912 neisseria m
2	140	100.0	797	2 O9JX31	O9JX31 neisseria m
3	140	100.0	797	2 O9KH0	O9KH0 neisseria m
4	60	42.9	588	2 O96328	O96328 arabidopsis
5	59	42.1	315	2 O82KB2	O82KB2 streptomyces
6	55	39.3	1077	2 O7NTE3	O7NTE3 chromobacte
7	55	39.3	1427	2 O755V8	O755V8 ashbya goss
8	55	39.3	1485	1 TOP2_SCHPO	P08096 schizosacch
9	54	38.6	1482	1 TOP2_PEA	O24308 pisum sativ
10	54	38.6	1473	1 TOP2_ARATH	F30182 arabidopsis
11	54	38.6	1525	2 O6ZBD9	O6ZBD9 oryza sativ
12	53	37.9	1127	2 O8EUA7	O8EUA7 mycoplasma
13	53	37.9	1923	2 O7S9W8	O7S9W8 neurospora
14	51	36.4	516	2 O8FPU1	O8FPU1 corynebacte
15	51	36.4	782	2 O9HG4	O9HG4 candida dub
16	51	36.4	782	2 O9HG5	O9HG5 candida tro
17	51	36.4	782	2 O9HG6	O9HG6 candida tro
18	51	36.4	1100	2 O8XU2	O8XU2 penicillium
19	50.5	36.1	456	2 O8ECA8	O8ECA8 shewanella
20	50	35.7	68	2 O63BF2	O63BF2 bacillus ce
21	50	35.7	260	1 CAH2_BRARE	Q92051 brachydanio
22	50	35.7	262	2 O81TW9	O81TW9 bacillus an
23	50	35.7	263	2 O6HM55	O6HM55 bacillus th
24	50	35.7	264	2 O9DFB6	O9DFB6 gallus gall
25	50	35.7	295	2 O81AM9	O81AM9 bacillus ce
26	50	35.7	303	2 O637T8	O637T8 bacillus ce
27	50	35.7	303	2 O733W0	O733W0 bacillus ce
28	50	35.7	303	2 O81YG1	O81YG1 bacillus an
29	50	35.7	303	2 O6HFR3	O6HFR3 bacillus th
30	50	35.7	314	1 HLDV_VIBCH	O06963 vibrio chol
31	50	35.7	345	2 O6PET9	O6PET9 mus musculu

32 50 35.7 363 2 Q82UQ3 Q82UQ3 nitrosomona
33 50 35.7 386 1 BCAT_HUMAN P54687 homo sapien
34 50 35.7 507 2 Q8BRY5 Q8BRY5 mus musculu
35 50 35.7 553 2 Q6BYE6 Q6BYE6 debaromyce
36 50 35.7 642 2 Q6LF16 Q6LF16 plasmodium
37 50 35.7 772 2 Q9HGH0 Q9HGH0 kluyveromyc
38 50 35.7 777 2 Q9HGH8 Q9HGH8 pichia guil
39 50 35.7 782 2 Q9HGH1 Q9HGH1 issatchenki
40 50 35.7 804 2 Q9HGH7 Q9HGH7 xenopus lae
41 50 35.7 1132 2 O7ZXS2 O7ZXS2 candida gla
42 50 35.7 1406 1 TOP2_CANGA P06786 saccharomyc
43 50 35.7 1428 1 TOP2_YEAST Q8TF86 saccharomyc
44 50 35.7 1428 2 Q8TF86 Q8TF86 saccharomyc
45 50 35.7 1428 2 Q8TG43 Q8TG43 saccharomyc

ALIGNMENTS

RESULT 1
O30912 PRELIMINARY; PRT; 797 AA.
AC O30912
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85;
OS Neisseria meningitidis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=487;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98379445; PubMed=9705245; DOI=10.1006/mpat.1998.0206;
RA Manning D.S., Reschke D.K., Judd R.C.;
RT "Omp85 proteins of Neisseria gonorrhoeae and Neisseria meningitidis are similar to Haemophilus influenzae D-15-Ag and Pasteurella multocida Omp85";
RL Microb. Pathog. 25:11-21 (1998).
DR EMBL; AF021245; AAC17599.1;
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf_Ag_VNR.
DR Pfam; PF01103; Bac_surfAg_1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
SQ SEQUENCE 797 AA; 88539 MW; CF911B5F70B9999CF CRC64;
Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9,8e-12; Mismatches 0; Indels 0; Gaps 0;
Matches 26; Conservative 0;

OY 1 GKYTDNNSSSATGGRVQNIYAGNTH 26
|||||
Db 720 GKYTDNNSSSATGGRVQNIYAGNTH 745

RESULT 2
O9JX31 PRELIMINARY; PRT; 797 AA.
AC O9JX31
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN Name=omp85; OrderedLocusNames=NMA0085;
OS Neisseria meningitidis (serogroup A).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=65699;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=Z2491 / Serogroup A / Serotype 4A;

```

RX MEDLINE=20222556; PubMed=10761919; DOI=10.1038/35006655;
RA Parkhill J., Achtman M., James K.D., Bentley S.D., Churcher C.M.,
RA Klee S.R., Morelli G., Basham D., Brown D., Chillingworth T.,
RA Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Holroyd S.,
RA Jagels K., Leather S., Moule S., Mungall K.L., Quail M.A.,
RA Rajandream M.A., Rutherford K.M., Simmonds M., Skelton J.,
RA Whitehead S., Spratt B.G., Barrett B.G.;
RT "Complete DNA sequence of a serogroup A strain of Neisseria meningitidis Z2491."
RL Nature 404:502-506(2000).
DR EMBL: ALJ62752; CAB83401.1; -.
DR FIRM; D82000; D82000.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88404 MW; 65DE47E0C9E1D1F CRC64;

Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKTYDDNSSSATGGRVQNIYAGNTH 26
Db 720 GKTYDDNSSSATGGRVQNIYAGNTH 745
|||||
|||||

RESULT 3
Q9K1H0 PRELIMINARY; PRT; 797 AA.
ID Q9K1H0
AC Q9K1H0
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Outer membrane protein Omp85.
GN OrderedLocuNames=NM0182;
OS Neisseria meningitidis (serogroup B).
OC Bacteria; Proteobacteria; Betaproteobacteria; Neisseriales;
OC Neisseriaceae; Neisseria.
OX NCBI_TaxID=491;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MC58 / Serogroup B;
RX MEDLINE=20175755; PubMed=10710307; DOI=10.1126/science.287.5459.1809;
RA Tettelin H., Saunders N.J., Heidelberg J.F., Jeffries A.C.,
RA Nelson K.E., Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F.,
RA Dodson R.J., Nelson W.C., Gwinn M.L., DeBoy R.T., Peterson J.D.,
RA Hickey E.K., Haft D.H., Salzberg S.L., White O., Fleischmann R.D.,
RA Dougherty B.A., Mason T.M., Ciecko A., Parksey D.S., Blair E.,
RA Citterone H., Clark E.B., Cotton M.D., Utterback T.R., Khouri H.M.,
RA Qin H., Vamathevan J.J., Gill J., Scarlato V., Maignani V., Pizza M.,
RA Grandi G., Sun L., Smith H.O., Fraser C.M., Moxon E.R., Rappuoli R.,
RA Venter J.C.;
RT "Complete genome sequence of Neisseria meningitidis serogroup B strain MC58."
RL Science 287:1809-1815(2000).
DR EMBL: AR002375; AAF40639.1; -.
DR FIRM; G81228; G81228.
DR TIGR; NMB0182; -.
DR InterPro; IPR000184; Bac_surfAg_D15.
DR InterPro; IPR010827; Surf Ag VNR.
DR Pfam; PF01103; Bac surface Ag; 1.
DR Pfam; PF07244; Surf_Ag_VNR; 5.
KW Complete proteome.
SQ SEQUENCE 797 AA; 88436 MW; B68BFC5A3D22BE8 CRC64;

Query Match 100.0%; Score 140; DB 2; Length 797;
Best Local Similarity 100.0%; Pred. No. 9.8e-12;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GKTYDDNSSSATGGRVQNIYAGNTH 26
Db 720 GKTYDDNSSSATGGRVQNIYAGNTH 745
|||||
|||||

```

```

Db 720 GKTYDDNSSSATGGRVQNIYAGNTH 745
RESULT 4
Q96328 PRELIMINARY; PRT; 588 AA.
ID Q96328
AC Q96328;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Putative transmembrane protein G5P (SAC domain protein 8).
GN Name=AtG5; Synonyms=At3G51830, SAC8;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Columbia;
RA Grelllet P., Gaubier P., Wu H.-J., Laudie M., Berger C., Delseny M.;
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=20108326; PubMed=10645728; DOI=10.1023/A:1006395324818;
RA Comella P., Wu H.J., Laudie M., Berger C., Cooke R., Delseny M.,
RA Grelllet P.;
RT "Fine sequence analysis of 60 kb around the Arabidopsis thaliana AtEm1 locus on chromosome III."
RL Plant Mol. Biol. 41:687-700(1999).
RN [4]
RP SEQUENCE FROM N.A.
RA Yamada K., Chan M.M., Chang C.H., Dale J.M., Deng J.M., Heuan V.W.,
RA Lee J.M., Quach H.L., Tang C., Toriumi M., Wu H.C., Yu G., Bowser L.,
RA Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T.,
RA Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J.,
RA Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
RA Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
RA Theologis A.;
RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RX MEDLINE=22690165; PubMed=12805586; DOI=10.1104/pp.103.021444;
RA Zhong R., Ye Z.H.;
RT "The SAC domain-containing protein gene family in Arabidopsis."
RL Plant Physiol. 132:544-555(2003).
DR EMBL: U72504; AAB18128.1; -.
DR EMBL: AY080659; AAL86335.1; -.
DR EMBL: AF049236; AAC14410.1; -.
DR EMBL: AY133741; AAM91675.1; -.
DR EMBL: AY227251; AAP49841.1; -.
DR FIRM; T51154; T51154.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR InterPro; IPR002013; Syja_N.
DR Pfam; PF02383; Syja_N; 1.
DR PROSITE; PS0275; SAC; 1.
KW Transmembrane.
SQ SEQUENCE 588 AA; 66463 MW; 6ADC187B7CC3753D CRC64;

Query Match 42.9%; Score 60; DB 2; Length 588;
Best Local Similarity 50.0%; Pred. No. 4.2;
Matches 12; Conservative 3; Mismatches 9; Indels 0; Gaps 0;

```

RA	Alves-Gomes J.A., Andrade E.M., Araripe J., de Araujo M.F.F.,
RA	Atoufi-Filho S., Azevedo V., Baptista A.J., Bataus L.A.M.,
RA	Batista J.S., Belo A., van den Berg C., Bogo M., Bonatto S.,
RA	Bordignon J., Brigido M.M., Brito C.A., Brocchi M., Burify H.A.,
RA	Camargo A.A., Cardoso D.D.P., Carneiro N.P., Carraro D.M.,
RA	Carvalho C.M.B., Cascardo J.C.M., Cavada B.S., Chueire L.M.O.,
RA	Creczynski-Pasa T.B., Cunha-Junior N.C., Fgundes N., Falcao C.L.,
RA	Fantinati F., Farias I.P., Felipe M.S.C., Ferrari L.P., Ferro J.A.,
RA	Ferreira M.T., Franco G.R., Freitas N.S.A., Furlan L.R.,
RA	Gazzinelli R.T., Gomes E.A., Goncalves P.R., Grangeiro T.B.,
RA	Grattapaglia D., Griegard E.C., Hanna E.S., Jardim S.N., Laurino J.,
RA	Leoi L.C.T., Lima L.F.A., Loureiro M.F., Lyra M.C.C.P.,
RA	Madeira H.M.F., Manlio G.P., Maranhao A.Q., Martins W.S.,
RA	di Mauro S.M.Z., de Medeiros S.R.B., Meissner R.V., Moreira M.A.M.,
RA	Nascimento F.Z., Nicolas M.F., Oliveira J.G., Oliveira S.C.,
RA	Paixao R.F.C., Parente J.A., Pedrosa F.O., Pena S.D.J., Pereira J.O.,
RA	Pereira M., Pinto L.S.R.C., Pinto L.S., Porto J.I.R., Potrich D.P.,
RA	Ramalho-Neto C.E., Reis A.M.M., Rigo L.U., Rondinelli E.,
RA	Santos E.B.P., Santos F.R., Schneider M.P.C., Seunaz H.N.,
RA	da Silva A.M.R., da Silva A.L.C., Silva D.W., Silva R., Simoes I.C.,
RA	Simon D., Soares C.M.A., Soares R.B.A., Souza E.M., Souza K.R.L.,
RA	Sauza R.C., Steffens M.B.R., Steindel M., Teixeira S.R., Urmenyi T.,
RA	Vettore A., Waesem R., Zaha A., Simpson A.J.G.
RT	"The complete genome sequence of Chromobacterium violaceum reveals
RT	remarkable and exploitable bacterial adaptability."
RL	Proc. Natl. Acad. Sci. U.S.A. 100:11660-11665(2003).
DR	ENBL; AS016921; AAQ60782.2; -.
DR	InterPro: IPR008985; Cona like lec gl.
DR	InterPro: IPR008707; Neisseria_PilC.
DR	Pfam: PF05567; Neisseria_PilC; 1.
KW	Complete proteome.
SQ	SEQUENCE 1077 AA; 111476 MW; F2DB546DF27279DB CRC64;
Query Match	39.3%; Score 55; DB 2; Length 1077;
Best Local Similarity	50.0%; Pred. No. 45;
Matches 13; Conservative 4; Mismatches 7; Indels 2; Gaps	
Qy	1 GKTYDDNSSATGGGRVQNI--YGAGN 24
Db	179 GGYNDNTSSGPGAKPQNLSRGAGS 204
RESULT 7	
Q755V8	
ID	Q755V8 PRELIMINARY; PRT; 1427 AA.
AC	Q755V8;
DT	03-JUL-2004 (TrEMBLrel. 27, Created)
DT	05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT	05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE	AER410WP.
GN	ORFNames=AER410W;
OS	Ashbya gossypii (Yeast) (Eremothecium gossypii).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Eremothecium.
OX	NCBI_TaxID=33169;
ON	[1];
RP	SEQUENCE FROM N.A.
RC	STRAIN=ATCC 10895;
RC	Gates K., Dietrich F.S., Brachat S., Voegelé S.E., Lerch A.,
RA	Philippson P., Gaffney T.;
RL	Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
CC	-I- FUNCTION: Control of topological states of DNA by transient
CC	breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC	makes double-strand breaks (By similarity).
CC	-I- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC	of double-stranded DNA.
CC	-I- SUBUNIT: Homodimer (By similarity).
CC	-I- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC	negative and positive supercoils, whereas prokaryotic enzymes
CC	relax only negative supercoils (By similarity).
CC	-I- SIMILARITY: Belongs to the type II topoisomerase family.
DR	ENBL; AS016818; RAS53089.1; -.
DR	AGD; AER410W; -.

SQ SEQUENCE 1485 AA; 167891 MW; 6D88F76243361B2F CRC64;
Query Match 39.3%; Score 55; DB 1; Length 1485;
Best Local Similarity 63.2%; Pred. No. 64;
Matches 12; Conservative 0; Mismatches 5; Indels 2; Gaps 1;
QY 4 YDSSSSATGGRVQNIYGA 22
||||| ||||| |||||
Db 196 YDDNQKVTGGR--NGYGA 212

RESULT 9
TOP2_PEA
ID TOP2_PEA STANDARD; PRT; 1462 AA.
AC O24308;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3) (PstTopII).
GN Name=TOP2; Synonyms=TOPII;
OS Pisum sativum (Garden pea);
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae; Pisum.
OX NCBI_TaxID=3888;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Leaf;
RX MEDLINE=20023730; PubMed=10561074; DOI=10.1023/A:1006352820788;
RA Reddy M.K., Nair S., Tewari K.K., Mudgil Y., Yadav B.S., Sopory S.K.;
RT "Cloning and characterization of a cDNA encoding topoisomerase II in
RT pea and analysis of its expression in relation to cell
RT proliferation.";
RL Plant Mol. Biol. 41:125-137(1999).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- TISSUE SPECIFICITY: Abundant in proliferative tissues.
CC -1- INDUCTION: By light and growth factors.
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC ENBL; Y14559; CAA74891.1; --
CC PIR; T06819; T06819.
CC HSSP; P06786; 1BJT.
CC InterPro; IPR003594; ATPbind ATPase.
CC InterPro; IPR003957; CBFA NFYB Topis.
CC InterPro; IPR001241; DNA_TopoisoII.
CC InterPro; IPR002205; DNA_TopoisoIV.
CC Pfam; PF00204; DNA_gyraseB; 1.
CC Pfam; PF00521; DNA_topoisoIV; 1.
CC Pfam; PF02518; HATPase_c; 1.
CC PRINTS; PR00615; CCAATSUBUNTA.
CC PRINTS; PR00418; TPI2FAMILY.
CC ProDom; PD149633; DNA_gyrase_B; 1.
CC ProDom; PD000742; DNA_topoisoIV; 1.
CC SMART; SM00387; HATPase_c; 1.
CC SMART; SM00433; TOP2c; 1.
CC SMART; SM00434; TOP4c; 1.
CC PROSITE; PS00177; TOPOISOMERASE_II; 1.

KW ATP-binding; DNA-binding; Isomerase; Topoisomerase.
FT NP_BIND 149 154 ATP (Potential)
FT ACT_SITE 761 761 DNA cleavage (By similarity).
SQ SEQUENCE 1462 AA; 164205 MW; D9212C54AE0F8B2E CRC64;
Query Match 38.6%; Score 54; DB 1; Length 1462;
Best Local Similarity 56.5%; Pred. No. 88;
Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;
QY 4 YDSSSSATGGRVQNIYGA 26
||||| ||||| ||||| |||||
Db 139 YDDNVKKTGGR--NGYGAKLTN 159

RESULT 10
TOP2_ARATH
ID TOP2_ARATH STANDARD; PRT; 1473 AA.
AC P30182; Q38807;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 32, Last sequence update)
DT 01-NOV-1995 (Rel. 45, Last annotation update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE DNA topoisomerase II (EC 5.99.1.3).
GN Name=TOP2; OrderedLocusNames=At3g23890; ORFNames=F14013.7;
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=95148754; PubMed=7846176; DOI=10.1104/pp.106.4.1701;
RA Xie S., Lam E.;
RT "Characterization of a DNA Topoisomerase II cDNA from Arabidopsis
RT thaliana.";
RL Plant Physiol. 106:1701-1702(1994).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia, and cv. Kas-1;
RX MEDLINE=95140639; PubMed=7838729;
RA Xie S., Lam E.;
RT "Abundance of nuclear DNA topoisomerase II is correlated with
RT proliferation in Arabidopsis thaliana.";
RL Nucleic Acids Res. 22:5729-5736(1994).
RN [3]
RN SEQUENCE FROM N.A.
RC STRAIN=cv. Columbia;
RX MEDLINE=20363099; PubMed=10907853;
RA Kaneko T., Katch T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II.
RT Sequence features of the 4,251,695 bp regions covered by 90 PL, TAC
RT and BAC clones.";
RL DNA Res. 7:217-221(2000).
RN [4]
RN SEQUENCE OF 751-838 FROM N.A.
RA Gerhold D., Parsons A., Hadwiger L.A.;
RT "PCR-assisted cloning of a topoisomerase II gene from Arabidopsis.";
RT Submitted (FEB-1992) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks.
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer.
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils.
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).

CC -----
 DR EMBL; L21015; AAA65448.1; --
 DR EMBL; M84654; AAA32877.1; --
 DR EMBL; AP001297; BAB03006.1; --
 DR EMBL; U12284; AAC48999.1; --
 DR EMBL; U12285; AAC49000.1; --
 DR PIR; S53598; S53599.
 DR HSP; P06786; IBGW.
 DR GeneFarm; 2856; 246.

DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003957; CBFA_NFYB_topis.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR002205; DNA_topoisomIV.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisomIV; 1.
 DR Pfam; PF02518; HATPase_C; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PRINTS; PR00418; TPI2FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR ProDom; PD000742; DNA_topoisomIV; 1.
 DR SMART; SM00387; HATPase_C; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.

DR PROSITE; PS00177; TOPOISOMERASE II; 1.
 DR ATP-binding; DNA-binding; Isomerase; Polymorphism; Topoisomerase.
 FT NP_BIND 161 166 ATP (Potential).
 FT ACT_SITE 794 794 DNA cleavage (By similarity).
 FT VARIANT 1213 1213 K -> N (in cv. Kas-1).
 FT VARIANT 1245 1245 A -> G (in cv. Kas-1).
 FT VARIANT 1299 1299 E -> G (in cv. Kas-1).
 SQ SEQUENCE 1473 AA; 164106 MW; 00B6C4836E381403 CRC64;

Query Match 38.6%; Score 54; DB 1; Length 1473;
 Best Local Similarity 56.5%; Pred. No. 88;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDSSSSATGGRVQNIYGAGNTH 26
 ||||| ||||| ||||| |||||
 Db 151 YDNNVKKTTGGR--NGYGAKLTN 171

RESULT 11
 Q6Z8D9 PRELIMINARY; PRT; 1525 AA.
 AC Q6Z8D9
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Putative DNA topoisomerase II.
 GN NamesP0459B01.29;
 OS Oryza sativa (japonica cultivar-group).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzeae; Oryza.
 OC NCBI_TaxID=39947;
 RN [1]
 RP SEQUENCE FROM N.A.

RA Sasaki T., Matsumoto T., Yamamoto K.;
 RA Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Control of topological states of DNA by transient
 CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
 CC makes double-strand breaks (By similarity).
 CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
 CC of double-stranded DNA.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
 CC negative and positive supercoils, whereas prokaryotic enzymes
 CC relax only negative supercoils (By similarity).
 CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
 DR EMBL; AP004778; BAD07880.1; --

DR GO; GO:0005634; C:nucleus; IEA.
 DR GO; GO:0005524; F:ATP binding; IEA.
 DR GO; GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
 DR GO; GO:0006265; P:DNA topological change; IEA.
 DR InterPro; IPR003594; ATPbind_ATPase.
 DR InterPro; IPR003957; CBFA_NFYB_topis.
 DR InterPro; IPR011558; DNA_gyrase_B.
 DR InterPro; IPR001241; DNA_topoisomII.
 DR InterPro; IPR002205; DNA_topoisomIV.
 DR Pfam; PF00204; DNA_gyraseB; 1.
 DR Pfam; PF00521; DNA_topoisomIV; 1.
 DR Pfam; PF02518; HATPase_C; 1.
 DR PRINTS; PR00615; CCAATSUBUNTA.
 DR PRINTS; PR00418; TPI2FAMILY.
 DR ProDom; PD149633; DNA_gyrase_B; 1.
 DR ProDom; PD000742; DNA_topoisomIV; 1.
 DR SMART; SM00387; HATPase_C; 1.
 DR SMART; SM00433; TOP2c; 1.
 DR SMART; SM00434; TOP4c; 1.
 DR PROSITE; PS00177; TOPOISOMERASE II; 1.
 DR ATP-binding; DNA-binding; Isomerase; Topoisomerase.
 SQ SEQUENCE 1525 AA; 170334 MW; 564C712C68698C3B CRC64;

Query Match 38.6%; Score 54; DB 2; Length 1525;
 Best Local Similarity 56.5%; Pred. No. 92;
 Matches 13; Conservative 1; Mismatches 7; Indels 2; Gaps 1;

QY 4 YDSSSSATGGRVQNIYGAGNTH 26
 ||||| ||||| ||||| |||||
 Db 148 YDNNVKKTTGGR--NGYGAKLTN 168

RESULT 12
 O8EUA7 PRELIMINARY; PRT; 1127 AA.
 ID Q8EUA7
 AC Q8EUA7
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Predicted protein-export membrane protein SecD.
 GN OrderedLocusNames=MYPE10240;
 OS Mycoplasma penetrans.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OC NCBI_TaxID=28227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HF-2;
 RX MEDLINE=22354719; PubMed=1246555; DOI=10.1093/nar/gkf667;
 RA Sasaki Y., Ishikawa J., Yamashita A., Oshima K., Kenri T., Furuya K.,
 RA Yoshino C., Horino A., Shiba T., Sasaki T., Hattori M.;
 RT "The complete genomic sequence of Mycoplasma penetrans, an
 RT intracellular bacterial pathogen in humans.";
 RL Nucleic Acids Res. 30:5293-5300(2002).
 DR EMBL; AP004174; BAC44809.1; --
 KW Complete proteome.
 SQ SEQUENCE 1127 AA; 124216 MW; 81DC036B4479A72E CRC64;

Query Match 37.9%; Score 53; DB 2; Length 1127;
 Best Local Similarity 52.0%; Pred. No. 92;
 Matches 13; Conservative 3; Mismatches 5; Indels 4; Gaps 2;

QY 4 YDNNSSSSATGGRVQNIYGAGNTH 24
 ||||| ||||| ||||| |||||
 Db 146 YDNNFNKNSSTGGYIEDPNYGINN 170

RESULT 13
 Q7S9W8 PRELIMINARY; PRT; 1923 AA.
 ID Q7S9W8
 AC Q7S9W8
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Hypothetical protein.
GN Name=NCU06338.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OR74A;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA Elkins T., Engels S., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd G., Mewes W., Straben C., Marcotte E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gnerre S.,
RA Kamal M., Kamyselis M., Maucelli E., Bielke C., Rudd S., Frishman D.,
RA Kryzstofova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmani S.A.,
RA DeSouza C.C., Glass L., Orbach M.J., Berglund J., Voelker R.,
RA Varden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
RA Natvig D.O., Alex L.A., Mannhaupt G., Ebbole D.J., Freitag M.,
RA Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.;
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RL Nature 0:0-0(2003).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL: AAX01000209; EAA33136.1; -;
DR HSPSP; P06786; 1BUT.
DR GO: GO:0005634; C:nucleus; IEA.
DR GO: GO:0005524; F:ATP binding; IEA.
DR GO: GO:0003918; F:DNA topoisomerase (ATP-hydrolyzing) activity; IEA.
DR GO: GO:0006265; P:DNA topological change; IEA.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR003957; CBFA_NFYB_topis.
DR InterPro: IPR011558; DNA_gyrase_B.
DR InterPro: IPR001241; DNA_topoisomI.
DR InterPro: IPR002205; DNA_topoisomIv.
DR Pfam: PF00204; DNA_gyraseB; 1.
DR Pfam: PF00521; DNA_topoisomIv; 1.
DR Pfam: PF02518; HATPase_c; 1.
DR PRINTS: PR00615; CCAATSUBUNTA.
DR PRINTS: PR00418; TPI2FAMILY.
DR ProDom: PD149633; DNA_gyrase_B; 1.
DR ProDom: PD000742; DNA_topoisomIv; 1.
DR PROSITE: PS00177; TOPOISOMERASE_II; UNKNOWN_1.
KW ATP-binding; DNA-binding; Hypothetical protein; Isomerase;
KW Topoisomerase.
SQ SEQUENCE 1923 AA; 213143 MW; 10663EA61ED142E0 CRC64;
Query Match 37.9%; Score 53; DB 2; Length 1923;
Best Local Similarity 46.2%; Pred. No. 1.7e+02;
Matches 12; Conservative 2; Mismatches 10; Indels 2; Gaps 1;
QY 1 GKTYYDNSSSSATGGRVNIYAGNTH 26
DB 246 GSNFDDNEKKTGVGR--NGYGAKLITN 269
RESULT 14
ID Q8FPUI PRELIMINARY; PRT; 516 AA.

AC Q8FPUI;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Putative NADH dehydrogenase I chain M.
GN OrderedLocusNames=CEI1397;
OS Corynebacterium efficiens.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Corynebacteriaceae; Corynebacteriaceae; Corynebacterium.
OX NCBI_TaxID=152794;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YS-314;
RA MEDLINE=2273752; PubMed=12840036; DOI=10.1101/gr.1285603;
RA Nishio Y., Nakamura Y., Kawarayashi Y., Usuda Y., Kimura E.,
RA Sugimoto S., Matsui K., Yamagishi A., Kikuchi H., Ikeo K.,
RA Gojobori T.;
RT "Comparative complete genome sequence analysis of the amino acid
RT replacements responsible for the thermostability of Corynebacterium
RT efficiens."
RL Genome Res. 13:1572-1579(2003).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC EMBL: AP005218; BAC18207.1; -;
DR GO: GO:0016021; C:integral to membrane; IEA.
DR GO: GO:0008137; F:NADH dehydrogenase (ubiquinone) activity; IEA.
DR GO: GO:0042773; P:ATP synthesis coupled electron transport; IEA.
DR InterPro: IPR003916; NADH_oxred5.
DR InterPro: IPR001750; Oxidored_g1.
DR Pfam: PF00361; Oxidored_g1; 1.
DR PRINTS: PR01434; NADHGHNA5.
KW Complete proteome; Oxidoreductase; Transmembrane.
SQ SEQUENCE 516 AA; 54477 MW; 8B45EA8713F5ECF7 CRC64;
Query Match 36.4%; Score 51; DB 2; Length 516;
Best Local Similarity 58.8%; Pred. No. 77;
Matches 10; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 1 GKTYYDNSSSSATGGRVQ 17
DB 454 GSDADSASSATGGATQ 470
RESULT 15
ID Q9HGHA PRELIMINARY; PRT; 782 AA.
AC Q9HGHA;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Type II DNA topoisomerase (Fragment).
GN Name=top2;
OS Candida dubliniensis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetidae; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=42374;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=16F;
RA MEDLINE=21363449; PubMed=11470534; DOI=10.1016/S0378-1119(01)00526-1;
RA Kato M., Ozeki M., Kikuchi A., Kanbe T.;
RT "Phylogenetic relationship and mode of evolution of yeast DNA
RT topoisomerase II gene in the pathogenic Candida species."
RL Gene 272:275-281(2001).
CC -1- FUNCTION: Control of topological states of DNA by transient
CC breakage and subsequent rejoining of DNA strands. Topoisomerase II
CC makes double-strand breaks (By similarity).
CC -1- CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
CC of double-stranded DNA.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- MISCELLANEOUS: Eukaryotic topoisomerase I and II can relax both
CC negative and positive supercoils, whereas prokaryotic enzymes
CC relax only negative supercoils (By similarity).
CC -1- SIMILARITY: Belongs to the type II topoisomerase family.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 14:53:24 ; Search time 52.6354 Seconds
(without alignments)
1307.930 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178

Perfect score: 885

Sequence: 1 MKLKQIASALMWLIGISPLAF.....RNRVDITITDEGSAKIID 178

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: Geneseqp16Dec04:*
2: Geneseqp1980s:*
3: Geneseqp1990s:*
4: Geneseqp2000s:*
5: Geneseqp2001s:*
6: Geneseqp2002s:*
7: Geneseqp2003as:*
8: Geneseqp2003bs:*
9: Geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	885	100.0	792	4	Aau03958 Neisseria
2	885	100.0	792	4	Aab23786 Neisseria
3	885	100.0	792	4	Aab23786 Neisseria
4	885	100.0	792	6	Abp80499 N. gonorr
5	885	100.0	792	6	Abp79748 N. gonorr
6	885	100.0	797	3	Aay84947 Amino aci
7	885	100.0	797	5	Abb79802 Neisseria
8	879	99.3	797	4	Aau03957 Neisseria
9	879	99.3	797	4	Aab23784 Neisseria
10	879	99.3	797	4	Aab23784 Neisseria
11	875	98.9	797	4	Aau03959 Neisseria
12	875	98.9	797	4	Aau04451 Neisseria
13	875	98.9	797	4	Aab23788 Neisseria
14	875	98.9	797	4	Aab23788 Neisseria
15	863	97.5	792	3	Aay84946 Amino aci
16	863	97.5	792	3	Aay84946 Amino aci
17	863	97.5	792	5	Abb79801 Neisseria
18	297.5	33.6	798	6	Abm67563 Photorhab
19	296.5	33.5	827	7	Adf06140 Bacterial
20	295.5	33.4	821	7	Abp72267 Pseudomon
21	292	33.0	815	7	Abp65952 Klebsiell
22	289	32.7	813	8	Adl05786 M. catarr
23	286	32.3	813	3	Aay44390 M. catarr
24	286	32.3	813	3	Aay44391 M. catarr
25	282	31.9	865	6	Ada36211 Acinetoba

26	276	31.2	825	7	ABO61952	Ab061952 Klebsiell
27	273	30.8	639	4	ABG17654	Abg17654 Novel hum
28	236.5	26.7	797	2	AAR53755	Aar53755 H. influe
29	236.5	26.7	797	2	AAR53754	Aar53754 H. influe
30	236.5	26.7	797	2	AAR53756	Aar53756 H. influe
31	234.5	26.5	792	2	AAR53757	Aar53757 H. influe
32	234.5	26.5	793	2	AAR53758	Aar53758 H. influe
33	201.5	22.8	792	8	ADH12911	Adh12911 Francisel
34	151	17.1	896	4	AG78603	Ag78603 Lawsonia
35	151	17.1	896	4	ABU92009	Abu92009 Omp100 po
36	151	17.1	896	7	ADG33885	Adj33885 L. intrac
37	151	17.1	896	7	ADJ66790	Adj66790 Lawsonia
38	151	17.1	896	8	ADR72942	Adr72942 Lawsonia
39	100	11.3	792	5	ABG91029	Abg91029 Chlamydia
40	100	11.3	792	7	AD43760	Ad43760 Chlamydia
41	97	11.0	21	4	AA523787	Aab23787 Neisseria
42	96.5	10.9	837	2	AA52774	Aay52774 Treponema
43	95.5	10.8	812	2	AA52775	Aay52775 Treponema
44	95	10.7	497	5	ABU52025	Abu52025 Helicobac
45	95	10.7	518	5	ABU51207	Abu51207 Helicobac

ALIGNMENTS

RESULT 1
AAU03958
ID AAU03958 standard; protein; 792 AA.
XX
AC AAU03958;
XX
AC
DT 23-OCT-2001 (first entry)
XX
DE Neisseria meningitidis serogroup A antigenic protein #1.
XX
KW Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast.
XX
OS Neisseria meningitidis.
XX
FH Key Location/Qualifiers
FT Peptide 1..21
FT Protein /note= "Signal peptide"
FT /note= "Mature N. meningitidis serogroup A antigen"
XX
PN WO200138350-A2.
XX
PD 31-MAY-2001.
XX
PF 28-NOV-2000; 2000WO-IB001851.
XX
PR 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX
(CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.
XX
GIuliani MM, Pizza M, Rappuoli R, Holst J;
WPI; 2001-381289/40.
DR N-PSDB; AAS07278.
XX
Novel 85 kDa antigen from Neisseria meningitidis and Neisseria gonorrhoeae, useful in the manufacture of a medicament for treating and preventing Neisserial bacteria infection.
PT
PS Claim 1; Page 66-68; 92pp; English.
XX
The sequence represents a Neisseria meningitidis serogroup A 85 kDa antigenic protein. Neisseria meningitidis colonises the pharynx, causing meningitis and, occasionally, septicaemia in the absence of meningitis. This antigenic protein is useful in the manufacture of a medicament for

CC treating or preventing infection due to *Neisseria* bacteria, such as
CC meningitis and septicemia. It is also useful as a diagnostic reagent for
CC detecting the presence of *Neisseria* bacteria or antibodies raised against
CC *Neisseria*, and as a reagent for raising the antibodies. The *Neisseria*
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast. Note: There are two versions of this sequence
XX displayed in the specification (see AAU04451)

XX SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGQRTPEPTVFVLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGQRTPEPTVFVLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 2

AAB23786
ID AAB23786 standard; protein; 792 AA.

XX AC AAB23786;

DT 11-SEP-2003 (revised)
DT 12-JAN-2001 (first entry)

XX DE *Neisseria* gonorrhoeae amino acid sequence.

XX KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
XX KW *Neisseria* antigen; *Neisseria* meningitidis; *Neisseria* gonorrhoeae;
XX KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
XX KW immune response.

XX OS *Neisseria* gonorrhoeae.

XX PN W0200050075-A2.

XX PD 31-AUG-2000.

XX PF 09-FEB-2000; 2000WO-IB000176.

XX PR 26-FEB-1999; 99US-0121792P.

XX PA (CHIR-) CHIRON SPA.

XX PI Grandi G, Rappuoli R, Giuliani MM, Pizza M;

XX DR WPI; 2001-015529/02.

XX Immunogenic composition useful for stimulating an immune response in a
XX mammal against *Neisseria* infection, comprises *Neisseria* antigen and an
XX adjuvant composition comprising an oligonucleotide with a CG motif.

XX PS Claim 22; Page 32; 39pp; English.

XX The present invention describes an immunogenic composition (I) comprising
XX a *Neisseria* antigen and an adjuvant composition comprising an
XX oligonucleotide comprising at least 1 CG motif. Also described is an
XX adjuvant composition (II) comprising an oligonucleotide which comprises
XX at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
XX oligonucleotide preferably comprises at least one phosphorothioate bond.
XX AAA92359 to AAA92385 represent specifically claimed oligonucleotides of

CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against *Neisseria* infection, preferably
CC *Neisseria* meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed *Neisseria* gonorrhoeae amino acid sequence
CC disclosed in GB-928197.4, which is given in the present invention.
CC (Updated on 11-SEP-2003 to standardise OS field)

XX SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGQRTPEPTVFVLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMLGISPLAFADFTIQDIRVEGQRTPEPTVFVLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 3

AAB84745
ID AAB84745 standard; protein; 792 AA.

XX AC AAB84745;

DT 11-SEP-2003 (revised)
DT 17-SEP-2001 (first entry)

XX DE Amino acid sequence of a *Neisseria* gonorrhoeae protein.

XX KW Serogroup B protein; outer membrane protein; *Neisseria* infection;
XX KW vaccine.

XX OS *Neisseria* gonorrhoeae.

XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT /note= "signal peptide"
XX FT Protein 22..792
XX FT /note= "mature protein"

XX PN W0200152885-A1.

XX PD 26-JUL-2001.

XX PF 17-JAN-2001; 2001WO-IB000166.

XX PR 17-JAN-2000; 2000GB-00001067.

XX PR 09-MAR-2000; 2000GB-00005699.

XX PA (CHIR-) CHIRON SPA.

XX PI Pizza M, Rappuoli R, Giuliani M;

XX DR WPI; 2001-451895/48.

XX DR N-PSDB; AAH42129.

XX Composition for treating or preventing infection to, detecting, or for
XX raising antibodies against *Neisseria* bacteria, comprises an N.
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component.

XX PS Disclosure; Page 65-67; 83pp; English.

XX CC The present sequence represents a *Neisseria* gonorrhoeae protein. The

protein is used to produce the compositions of the invention. The specification describes a composition, comprising a *Neisseria meningitidis* serogroup B outer membrane preparation and an immunogenic component. The immunogenic component is protein disclosed in WO99/57280, WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413, WO99/31132, WO99/58683, WO99/55873, and/or *N. meningitidis* protein PorA, TbpA, TbpB, PilC, OpaB, or Omp85. The composition is used for making a medicament for treating or preventing infection due to *Neisseria* bacteria; a diagnostic reagent for detecting the presence of *Neisseria* bacteria or of antibodies raised against *Neisseria* bacteria; and/or a reagent which can raise antibodies against *Neisseria* bacteria. It may also be used as a vaccine. (Updated on 11-SEP-2003 to standardise OS field)

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
XX
SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 4; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 4
ABP80499
ID ABP80499 standard; protein; 792 AA.
XX
AC ABP80499;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 7528.
XX
KW Antibacterial; infection; vaccine; gene therapy.
XX
OS *Neisseria gonorrhoeae*.

XX WO200279243-A2.
XX 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX
DR WPI; 2003-058415/05.
DR N-PSDB; ABZ41469.
XX
XX New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.
XX
PS Disclosure; Page 736; 815pp; English.

CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
CC Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection, this may be in the form of a vaccine or gene therapy.

CC Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
XX
SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Qy 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Qy 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178
Db 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKITD 178

RESULT 5
ABP79748
ID ABP79748 standard; protein; 792 AA.
XX
AC ABP79748;
XX
DT 07-MAR-2003 (first entry)
XX
DE N. gonorrhoeae amino acid sequence SEQ ID 6026.
XX
KW Antibacterial; infection; vaccine; gene therapy.

XX *Neisseria gonorrhoeae*.
XX WO200279243-A2.
XX 10-OCT-2002.
XX
PF 12-FEB-2002; 2002WO-IB002069.
XX
PR 12-FEB-2001; 2001GB-00003424.
XX
PA (CHIR-) CHIRON SPA.
XX
PI Fontana MR, Pizza M, Massignani V, Monaci E;
XX
DR WPI; 2003-058415/05.
DR N-PSDB; ABZ40718.
XX
XX New protein from *Neisseria gonorrhoeae*, useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection.

XX Disclosure; Page 628; 815pp; English.
XX
CC The present invention relates to proteins from *Neisseria gonorrhoeae*.
CC Also disclosed are the nucleic acid molecules encoding the proteins and antibodies that specifically bind to the proteins. The composition comprising the protein, nucleic acid or antibody is useful for the manufacture of a medicament for treating or preventing *N. gonorrhoeae* infection, this may be in the form of a vaccine or gene therapy.
CC Sequences given in records ABP76736-ABP81046 represent nucleic acid molecules of the invention
XX
SQ Sequence 792 AA;

Query Match 100.0%; Score 885; DB 6; Length 792;
Best Local Similarity 100.0%; Pred. No. 2.5e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLPLVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDIDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 6
ID AAY84947
AC AAY84947
XX AAY84947
DT 21-AUG-2000 (first entry)
DE Amino acid sequence of outer membrane protein (omp) 85.
KW Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
KW meningococcal infection; protective immune response; vaccine.
OS Neisseria meningitidis.
XX WO200023595-A1.
XX 27-APR-2000.
XX 22-OCT-1998; 98WO-US022352.
XX 22-OCT-1998; 98WO-US022352.
XX (UYMO-) UNIV MONTANA.
XX Judd RC, Manning SD;
XX WPI; 2000-339694/29.
XX N-PSDB; AAA15156.
PT New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
PT meningitidis useful for vaccine, therapeutic and diagnostic compositions
PT for gonococcal or meningococcal infections.
XX Claim 41; Page 89-92; 98pp; English.
XX The present sequence represents an outer membrane protein (omp) 85 of
CC Neisseria meningitidis. The omp polypeptides and polynucleotides are
CC useful in compositions for use in the prevention, treatment and diagnosis
CC of non-symptomatic gonococcal infection or meningococcal infection and
CC symptomatic disease. They are also useful for the detection of
CC hybridisation complexes. Antigens and antibodies specific omp proteins
CC also provide diagnostic, therapeutic and prophylactic compositions for
CC the treatment or prevention of the infections described above. The
CC antibodies are useful for inducing a protective immune response in humans
CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines
XX
SQ Sequence 797 AA;
Query Match 100.0%; Score 885; DB 3; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLPLVKVGDYNDTHGSA 60
Db 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLPLVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDIDITIDEGKSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNITQTPKVTKLARNRVDIDITIDEGKSAKITD 178

RESULT 7
ID ABB79802
AC ABB79802
XX ABB79802;
DT 15-NOV-2002 (first entry)
DE Neisseria meningitidis outer membrane protein Omp85.
KW Outer membrane protein; Omp85; meningitis; vaccine; diagnosis;
KW antibacterial.
XX Neisseria meningitidis.
XX Key Location/Qualifiers
FT Peptide 1..21
FT Protein /label= Signal_peptide
FT 22..797 /label= Mature_protein
XX US2002086028-A1.
XX 04-JUL-2002.
XX 26-NOV-2001; 2001US-00994192.
XX 22-OCT-1998; 98US-00177039.
XX (JUDD/) JUDD R C.
XX (MANN/) MANNING D S.
XX Judd RC, Manning DS;
XX WPI; 2002-642234/69.
XX Novel immunogenic composition for vaccinating against meningococcal or
PT gonococcal infection, comprises Omp85 protein of Neisseria meningitidis
PT or Neisseria gonorrhoeae, or nucleic acid encoding the protein.
XX Claim 13; Fig 5; 30pp; English.
XX The present sequence is that of the Neisseria meningitidis strain HH
CC outer membrane protein 85 (Omp85), as predicted from a gene that was
CC obtained from a genomic DNA by PCR amplification using primers based on
CC the gonococcal omp85 gene. The meningococcal Omp85 protein is 95%
CC identical and 98% similar to gonococcal Omp85 (see ABB79801). Claimed
CC immunogenic compositions comprise N. meningitidis Omp85, its fragments,
CC fusion proteins including the Omp85, or nucleic acids encoding them,
CC which induce a protective immune response in a subject. The immunogenic
CC compositions may also include an antigen from a heterologous or
CC homologous pathogen, or a nucleic acid encoding it. They are used in a
CC claimed method of vaccinating a human or animal against non-symptomatic
CC meningococcal infection or symptomatic disease. A kit for diagnosing
CC infection with N. meningitidis comprising labelled Omp85 is also claimed.
CC The Omp85 polypeptides and polynucleotides are also useful in drug
CC screening and development
XX
SQ Sequence 797 AA;
Query Match 100.0%; Score 885; DB 5; Length 797;
Best Local Similarity 100.0%; Pred. No. 2.6e-85;
Matches 178; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFVNLPLVKVGDYNDTHGSA 60

Db 1 MKLKQIASALMMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAK1TD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAK1TD 178

RESULT 8
AAU03957
ID AAU03957 standard; protein; 797 AA.
AC AAU03957;
XX
XX 23-OCT-2001 (first entry)
XX
XX Neisseria meningitidis serogroup B antigenic protein.
XX
XX Serogroup B antigen; pharynx; meningitis; septicaemia; mammalian cell;
XX bacterial infection; baculovirus; yeast.
XX
XX Neisseria meningitidis.
XX
XX Key Location/Qualifiers
FH Peptide 1..21
FT /note= "Signal peptide"
FT Protein 22..797
FT /note= "Mature N. meningitidis serogroup B antigen"
FT Binding-site 715..722
FT /note= "ATP/GTP-binding site motif A (P-loop)"
XX
XX WO200138350-A2.
XX
XX 31-MAY-2001.
XX
XX 28-NOV-2000; 2000WO-IB001851.
XX
XX 29-NOV-1999; 99GB-00028197.
XX 09-MAR-2000; 2000GB-00005698.
XX
XX (CHIR-) CHIRON SPA.
XX (STAT-) STATENS INST FOLKEHELSE.
XX
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI: 2001-381289/40.
XX N-PSDB; AAS07277.
XX

Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX
XX Claim 1; Fig 1; 92pp; English.
XX
XX The sequence represents a Neisseria meningitidis serogroup B 85 kDa
CC antigenic protein. Neisseria meningitidis colonises the pharynx, causing
CC meningitis and, occasionally, septicaemia in the absence of meningitis.
CC This antigenic protein is useful in the manufacture of a medicament for
CC treating or preventing infection due to Neisseria bacteria, such as
CC meningitis and septicaemia. It is also useful as a diagnostic reagent for
CC detecting the presence of Neisseria bacteria or antibodies raised against
CC Neisseria, and as a reagent for raising the antibodies. The Neisserial
CC nucleotide sequences can be expressed in a variety of different
CC expression systems, for example, mammalian cells, baculoviruses, plants,
CC bacteria and yeast
XX

Sequence 797 AA;
Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMMLGISPLAFADFTIODIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFFDDVRVETADGQLLLTVIERPTTGSNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAK1TD 178
Db 121 SOYFNOATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGSAK1TD 178

RESULT 9
AAB23784
ID AAB23784 standard; protein; 797 AA.
XX
XX AAB23784;
XX
XX 12-JAN-2001 (first entry)
XX
XX Neisseria meningitidis serogroup B amino acid sequence.
XX
XX CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
XX Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
XX bactericidal; antibacterial; vaccine; immunostimulatory; infection;
XX immune response.
XX
XX Neisseria meningitidis.
XX
XX WO2000050075-A2.
XX
XX 31-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-IB000176.
XX
XX 26-FEB-1999; 99US-0121792P.
XX
XX (CHIR-) CHIRON SPA.
XX
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
XX WPI: 2001-015529/02.
XX

Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
XX Claim 22; Page 32; 39pp; English.
XX
XX The present invention describes an immunogenic composition (I) comprising
CC a Neisseria antigen and an adjuvant composition comprising an
CC oligonucleotide comprising at least 1 CG motif. Also described is an
CC oligonucleotide composition (II) comprising an oligonucleotide which comprises
CC at least 1 CG motif and a complete Freund's adjuvant (CFA), where the
CC oligonucleotide preferably comprises at least one phosphorothioate bond.
CC AAA92359 to AAA92385 represent specifically claimed oligonucleotides of
CC the present invention. (I) is useful for stimulating an immune response
CC in a mammal, preferably a human, against Neisseria infection, preferably
CC Neisseria meningitidis infection and in the manufacture of a medicament
CC for inducing a protective immune response in a mammal. The present
CC sequence represents the claimed Neisseria meningitidis serogroup B amino
CC acid sequence disclosed in GB-9928197.4, which is given in the present
CC invention
XX
XX Sequence 797 AA;

Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. No. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLALADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETAGQLLLTVIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETAGQLLLTVIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITD 178
RESULT 10
AAB84744
ID AAB84744 standard; protein; 797 AA.
XX AAB84744;
AC AAB84744;
XX 17-SEP-2001 (first entry)
XX Amino acid sequence of a Neisseria serogroup B protein.
XX Serogroup B protein; outer membrane protein; Neisserial infection;
KW vaccine.
XX Neisseria meningitidis.
XX Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "mature protein"
XX WO200152885-A1.
XX 26-JUL-2001.
XX 17-JAN-2001; 2001WO-IB000166.
XX 17-JAN-2000; 2000GB-00001067.
PR 09-MAR-2000; 2000GB-00005699.
XX (CHIR-) CHIRON SPA.
XX Pizza M, Rappuoli R, Giuliani M;
XX WPI; 2001-451895/48.
DR N-PSDB; AAH42128.
XX Composition for treating or preventing infection to, detecting, or for
PT raising antibodies against Neisserial bacteria, comprises an N.
PT meningitidis serogroup B outer membrane preparation and an immunogenic
PT component.
XX Disclosure; Page 59-61; 83pp; English.
PS The present sequence represents a Neisseria serogroup B protein. The
XX protein is used to produce the compositions of the invention. The
CC specification describes a composition, comprising a Neisseria
CC meningitidis serogroup B outer membrane preparation and an immunogenic
CC component. The immunogenic component is protein disclosed in WO99/57280,
CC WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
CC WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
CC TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
CC medicament for treating or preventing infection due to Neisserial
CC bacteria; a diagnostic reagent for detecting the presence of Neisserial
CC bacteria; or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX Sequence 797 AA;
SQ

Query Match 99.3%; Score 879; DB 4; Length 797;
Best Local Similarity 99.4%; Pred. NO. 1.1e-84;
Matches 177; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMLGIGISPLAFADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
Db 1 MKLKQIASALMLGIGISPLALADFTIQDIRVEGLQRTPEPTVFYNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETAGQLLLTVIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
Db 61 IIKSLYATGFFDDVRVETAGQLLLTVIERTTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITD 178
Db 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQITPKVTKLARNRVDIDITIDEGSAKITD 178
RESULT 11
AAU03959
ID AAU03959 standard; protein; 797 AA.
XX AAU03959;
AC AAU03959;
XX 23-OCT-2001 (first entry)
DT Neisseria gonorrhoeae antigenic protein.
XX Antigenic protein; pharynx; meningitis; septicaemia; mammalian cell;
KW bacterial infection; baculovirus; yeast; Neisseria meningitidis.
XX Neisseria gonorrhoeae.
XX Key Location/Qualifiers
FT Peptide 1..21
FT /note= "signal peptide"
FT Protein 22..797
FT /note= "Mature N. gonorrhoeae antigen"
XX WO200138350-A2.
XX 31-MAY-2001.
XX 28-NOV-2000; 2000WO-IB001851.
XX 29-NOV-1999; 99GB-00028197.
PR 09-MAR-2000; 2000GB-00005698.
XX (CHIR-) CHIRON SPA.
PA (STAT-) STATENS INST FOLKEHELSE.
XX Giuliani MM, Pizza M, Rappuoli R, Holst J;
XX WPI; 2001-381289/40.
DR N-PSDB; AAS07279.
XX Novel 85 kDa antigen from Neisseria meningitidis and Neisseria
PT gonorrhoeae, useful in the manufacture of a medicament for treating and
PT preventing Neisserial bacteria infection.
XX Claim 1; Page 37-39; 92pp; English.
XX The sequence represents a Neisseria gonorrhoeae 85 kDa antigenic protein.
CC N. gonorrhoeae is closely related to N. meningitidis, which colonises the
CC pharynx, causing meningitis and, occasionally, septicaemia in the absence
CC of meningitis. This antigenic protein is useful in the manufacture of a
CC medicament for treating or preventing infection due to Neisseria
CC bacteria, such as meningitis and septicaemia. It is also useful as a
CC diagnostic reagent for detecting the presence of Neisseria bacteria or
CC antibodies raised against Neisseria, and as a reagent for raising the
CC antibodies. The Neisserial nucleotide sequences can be expressed in a
CC variety of different expression systems, for example, mammalian cells,
CC baculoviruses, plants, bacteria and yeast
XX

CC displayed in the specification (see AAU03958)
XX
SQ Sequence 797 AA;

Query Match 98.9%; Score 875; DB 4; Length 797;
Best Local Similarity 98.9%; Pred. No. 3e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MKLKQTASALMWLGISPLAFADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYNDTHGSA 60
Db 1 MKLKQTASALMWLGISPLALADFTIQDIRVEGLQRTEPSTVFNYLPVKVGDTYNDTHGSA 60

QY 61 IIKSLVATGFDDVRVETADGQLLLTVIERPTTGSNLITGAKMLQNDAIKKNLESFGLAQ 120
Db 61 IIKSLVATGFDDVRVETADGQLLLTVIERPTTGSNLITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNOAVAGLUKEEVLGRGKLNIQTTPKVTKLARNRVDIDITIDSGKSAKITD 178
Db 121 SQYFNQATLNOAVAGLUKEEVLGRGKLNIQTTPKVTKLARNRVDIDITIDSGKSAKITD 178

RESULT 13
AAB23788
ID AAB23788 standard; protein; 797 AA.
XX
AA B23788;
XX AC
XX AC
DT 12-JAN-2001 (first entry)
XX
DE Neisseria meningitidis serogroup A amino acid sequence.
XX
KW CG motif; complete Freund's adjuvant; phosphorothioate; immunogenic;
KK Neisseria antigen; Neisseria meningitidis; Neisseria gonorrhoeae;
KW bactericidal; antibacterial; vaccine; immunostimulatory; infection;
KW immune response.
XX
OS Neisseria meningitidis.
XX WO2000050075-A2.
PN
XX
PD 31-AUG-2000.
XX
XX 09-FEB-2000; 2000WO-IB000176.
PF
XX 26-FEB-1999; 99US-0121792P.
PR
XX (CHIR-) CHIRON SPA.
PA
XX Grandi G, Rappuoli R, Giuliani MM, Pizza M;
PI WPI; 2001-015529/02.
XX
DR
XX
XX Immunogenic composition useful for stimulating an immune response in a
PT mammal against Neisseria infection, comprises Neisseria antigen and an
PT adjuvant composition comprising an oligonucleotide with a CG motif.
XX
PS Claim 22; Page 33; 39pp; English.

The present invention describes an immunogenic composition (I) comprising a Neisseria antigen and an adjuvant composition comprising an oligonucleotide comprising at least 1 CG motif. Also described is an adjuvant composition (II) comprising an oligonucleotide which comprises at least 1 CG motif and a complete Freund's adjuvant (CFA), where the oligonucleotide preferably comprises at least one phosphorothioate bond. AAA92359 to AAA92385 represent specifically claimed oligonucleotides of the present invention. (I) is useful for stimulating an immune response in a mammal, preferably a human, against Neisseria infection, preferably Neisseria meningitidis infection and in the manufacture of a medicament for inducing a protective immune response in a mammal. The present sequence represents the claimed Neisseria meningitidis serogroup A amino acid sequence disclosed in GB-9928197.4, which is given in the present invention

SQ Sequence 797 AA;
Query Match 98.9%; Score 875; DB 4; Length 797;
Best Local Similarity 98.9%; Pred. No. 3e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMVLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMVLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQTPKVTKLARNRVDIDITIDEGKSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQTPKVTKLARNRVDIDITIDEGKSAKITD 178
RESULT 14
AAB84746
ID AAB84746 standard; protein; 797 AA.
XX AAB84746;
AC AAB84746;
XX 17-SEP-2001 (first entry)
XX Amino acid sequence of a Neisseria serogroup A protein.
XX Serogroup A protein; outer membrane protein; Neisserial infection;
XX vaccine.
XX Neisseria meningitidis.
XX Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
FT Protein 22..797 /note= "mature protein"
XX WO200152885-A1.
XX 26-JUL-2001.
XX 17-JAN-2001; 2001WO-IB000166.
XX 17-JAN-2000; 2000GB-00001067.
XX 09-MAR-2000; 2000GB-00005699.
XX (CHIR-) CHIRON SPA.
XX Pizza M, Rappuoli R, Giuliani M;
XX WPI; 2001-451895/48.
XX N-PSDB; AAH42130.
XX Composition for treating or preventing infection to, detecting, or for
XX raising antibodies against Neisserial bacteria, comprises an N.
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component.
XX Disclosure; Page 71-74; 83pp; English.
XX The present sequence represents a Neisseria serogroup A protein. The
XX protein is used to produce the compositions of the invention. The
XX specification describes a composition, comprising a Neisseria
XX meningitidis serogroup B outer membrane preparation and an immunogenic
XX component. The immunogenic component is protein disclosed in WO99/57280,
XX WO99/36544, WO99/24578, WO99/66791, WO97/28273, WO96/29412, WO95/03413,
XX WO99/31132, WO99/58683, WO99/55873, and/or N. meningitidis protein PorA,
XX TbpA, TbpB, PilC, Opa, or Omp85. The composition is used for making a
XX medicament for treating or preventing infection due to Neisserial
XX bacteria; a diagnostic reagent for detecting the presence of Neisserial

CC bacteria or of antibodies raised against Neisserial bacteria; and/or a
CC reagent which can raise antibodies against Neisserial bacteria. It may
CC also be used as a vaccine
XX Sequence 797 AA;
SQ Query Match 98.9%; Score 875; DB 4; Length 797;
Best Local Similarity 98.9%; Pred. No. 3e-84;
Matches 176; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLKQIASALMVLGIGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMVLGIGISPLALADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
QY 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
QY 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQTPKVTKLARNRVDIDITIDEGKSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKLNIIQTPKVTKLARNRVDIDITIDEGKSAKITD 178
RESULT 15
AAY84946
ID AAY84946 standard; protein; 792 AA.
XX AAY84946;
AC AAY84946;
XX 12-SEP-2003 (revised)
XX 21-AUG-2000 (first entry)
XX Amino acid sequence of outer membrane protein (omp) 85.
XX Outer membrane protein; omp85; gonococcal infection; symptomatic disease;
XX meningococcal infection; protective immune response; vaccine.
XX Neisseria gonorrhoeae.
XX Key Location/Qualifiers
FT Peptide 1..21 /note= "signal peptide"
XX WO200023595-A1.
XX 27-APR-2000.
XX 22-OCT-1998; 98WO-US022352.
XX 22-OCT-1998; 98WO-US022352.
XX (UYMO-) UNIV MONTANA.
XX Judd RC, Manning SD;
XX WPI; 2000-339694/29.
XX N-PSDB; AAA15155.
XX New isolated outer membrane protein 85 of Neisseria gonorrhoeae and N.
XX meningitidis useful for vaccine, therapeutic and diagnostic compositions
XX for gonococcal or meningococcal infections.
XX Claim 1; Fig 2; 98pp; English.
XX The present sequence represents an outer membrane protein (omp) 85 of
XX Neisseria gonorrhoeae. The omp polypeptides and polynucleotides are
XX useful in compositions for use in the prevention, treatment and diagnosis
XX of non-symptomatic gonococcal infection or meningococcal infection and
XX symptomatic disease. They are also useful for the detection of
XX hybridization complexes. Antigens and antibodies specific omp proteins
XX also provide diagnostic, therapeutic and prophylactic compositions for
XX the treatment or prevention of the infections described above. The
XX antibodies are useful for inducing a protective immune response in humans

CC or animals with N. gonorrhoeae, N. meningitidis, or other Neisseria
CC species. The proteins, antibodies and polynucleotide sequences of the
CC present invention may also be used in the screening and development of
CC chemical compounds such as drugs or vaccines. (Updated on 12-SEP-2003 to
CC standardise OS field)
XX
SQ

Sequence 792 AA;

Query Match 97.5%; Score 863; DB 3; Length 792;
Best Local Similarity 98.3%; Pred. No. 5.8e-83;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
|||
Db 1 MKLKQIASALMWLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
61 IIKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
|||
Db 61 IIKSLYATGFFDDVRVETADGQLLTIVIVCPTIGSLNITGAKMLONDAIKKNLESFGLAQ 120
QY 121 SQYFNOATLNQAVAGLKEEYVLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178
|||
Db 121 SQYFNOATLNQAVAGLKEEYVLRGKLNIIQITPKVTKLARNRVDITIDEGKSAKITD 178

Search completed: July 6, 2005, 15:13:14
Job time : 53.6354 secs

THIS PAGE BLANK (USPTO)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 6, 2005, 15:05:39 ; Search time 13.6923 Seconds
(without alignments)
970.438 Million cell updates/sec

Title: US-10-606-618-4_COPY_1_178
Perfect score: 885
Sequence: 1 MKLKQIASALMMLGISPLAF.....RNRVDITIDEGKSAKIDT 178

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/6C COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	885	100.0	797	4	US-09-994-192-4
2	863	97.5	792	4	US-09-994-192-2
3	296.5	33.5	827	4	US-09-543-681A-6425
4	295.5	33.4	821	4	US-09-252-991A-21013
5	292	33.0	815	4	US-09-489-039A-12469
6	289	32.7	813	4	US-09-540-236-3472
7	286	32.3	813	4	US-09-701-711-2
8	286	32.3	813	4	US-09-701-711-4
9	282	31.9	865	4	US-09-328-352-7498
10	276	31.2	825	4	US-09-489-039A-8469
11	236.5	26.7	797	3	US-08-433-522A-2
12	236.5	26.7	797	3	US-08-433-522A-6
13	236.5	26.7	797	3	US-08-433-522A-8
14	236.5	26.7	797	3	US-09-135-166-2
15	236.5	26.7	797	3	US-09-135-166-4
16	236.5	26.7	797	3	US-09-135-166-6
17	236.5	26.7	797	3	US-08-942-046-2
18	236.5	26.7	797	3	US-08-942-046-4
19	236.5	26.7	797	3	US-08-942-046-6
20	234.5	26.5	792	3	US-08-433-522A-8
21	234.5	26.5	792	3	US-09-135-166-8
22	234.5	26.5	792	3	US-08-942-046-8
23	234.5	26.5	793	3	US-08-433-522A-10
24	234.5	26.5	793	3	US-09-135-166-10
25	234.5	26.5	793	3	US-08-942-046-10
26	151	17.1	896	4	US-09-689-065B-5
27	93.5	10.6	795	4	US-09-198-452A-314

28	93.5	10.6	795	4	US-09-438-185A-302	Sequence 302, App
29	92	10.4	865	4	US-09-711-164-354	Sequence 354, App
30	89.5	10.1	944	4	US-09-328-352-4401	Sequence 4401, Ap
31	86.5	9.8	443	4	US-09-489-039A-8591	Sequence 8591, App
32	84	9.5	365	4	US-10-101-464A-510	Sequence 510, App
33	83.5	9.4	313	3	US-08-480-640A-192	Sequence 192, App
34	83.5	9.4	313	3	US-08-686-968C-192	Sequence 192, App
35	83.5	9.4	313	3	US-08-488-237A-192	Sequence 192, App
36	83.5	9.4	313	3	US-08-375-992A-192	Sequence 192, App
37	83.5	9.4	313	4	US-08-472-679H-192	Sequence 192, App
38	83	9.4	850	4	US-09-489-039A-13490	Sequence 13490, A
39	82.5	9.3	424	4	US-09-543-681A-5349	Sequence 5349, Ap
40	80	9.0	257	4	US-09-328-352-6621	Sequence 6621, Ap
41	78	8.8	267	4	US-09-252-991A-17521	Sequence 17521, A
42	77	8.7	838	4	US-09-489-039A-9864	Sequence 9864, Ap
43	76	8.6	192	4	US-09-902-540-9869	Sequence 9869, Ap
44	76	8.6	1132	4	US-09-198-452A-466	Sequence 466, App
45	76	8.6	1414	4	US-09-438-185A-446	Sequence 446, App

ALIGNMENTS

RESULT 1
US-09-994-192-4
; Sequence 4, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UM8C147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 4
; LENGTH: 797
; TYPE: PRT
; ORGANISM: Neisseria meningitidis
US-09-994-192-4

Query Match	100.0%	Score	885	DB	4	Length	797
Best Local Similarity	100.0%	Pred. No.	1.7e-93				
Matches	178	Conservative	0	Mismatches	0	Indels	0
						Gaps	0
Qy	1	MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60				
Db	1	MKLKQIASALMMLGISPLAFADFTTQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA	60				
Qy	61	IKLSLYATCFDDVRVETADGQLLTIVIERPTIGSNITGAKMLQNDAIKKNLESFGLAQ	120				
Db	61	IKLSLYATCFDDVRVETADGQLLTIVIERPTIGSNITGAKMLQNDAIKKNLESFGLAQ	120				
Qy	121	SOYFNQATLNQAVAGLKEEYLGRGKLNIIQITPKVTKLARNVDITIDEGKSAKIDT	178				
Db	121	SOYFNQATLNQAVAGLKEEYLGRGKLNIIQITPKVTKLARNVDITIDEGKSAKIDT	178				

RESULT 2
US-09-994-192-2
; Sequence 2, Application US/09994192
; Patent No. 6610306
; GENERAL INFORMATION:
; APPLICANT: Judd, Ralph C.
; TITLE OF INVENTION: Omp85 Proteins of Neisseria gonorrhoeae and Neisseria meningitidis
; TITLE OF INVENTION: Compositions Containing Same and Methods of Use Thereof
; FILE REFERENCE: UM8C147AUSA
; CURRENT APPLICATION NUMBER: US/09/994,192


```
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: US 09/177,039
; PRIOR FILING DATE: 1998-10-22
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 792
; TYPE: PRT
; ORGANISM: Neisseria gonorrhoeae
US-09-994-192-2

Query Match          97.5%; Score 863; DB 4; Length 792;
Best Local Similarity 98.3%; Pred. No. 5.9e-91;
Matches 175; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60
DB 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSA 60

QY 61 IIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120
DB 61 IIKSLYATGFFDDVRVETADGQLLLTVIVCPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

QY 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITD 178
DB 121 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITD 178

RESULT 3
US-09-543-681A-6425
; Sequence 6425, Application US/09543681A
; Patent No. 6605709
; GENERAL INFORMATION:
; APPLICANT: GARY BRETON
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS
; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.1002-001
; CURRENT APPLICATION NUMBER: US/09/543,681A
; CURRENT FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/128,706
; PRIOR FILING DATE: 1999-04-09
; NUMBER OF SEQ ID NOS: 8344
; SEQ ID NO 6425
; LENGTH: 827
; TYPE: PRT
; ORGANISM: Proteus mirabilis
US-09-543-681A-6425

Query Match          33.5%; Score 296.5; DB 4; Length 827;
Best Local Similarity 38.4%; Pred. No. 2.9e-25;
Matches 68; Conservative 34; Mismatches 74; Indels 1; Gaps 1;

QY 1 MKLKQIASALMMLGISPLAFAD-FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGS 59
DB 27 MAMKKLLIASLLGSATYAGSDGFVVDIQFEGQLQRVAVGAALLNMPVRGDSVDDSDIS 86

QY 60 AIKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLA 119
DB 87 RTIRSLFATGNFDDVRVLRDGNVLIIVQKERTPIASITFGSKAIKEDMLKQNLDSNIR 146

QY 120 SQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKITD 176
DB 147 IGETLDRTMLANIEKGLDFYYSVGKYNATVKVVTPLPRNRVDLKLVPFAGVGSATI 203

RESULT 4
US-09-252-991A-21013
; Sequence 21013, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
```

```
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 21013
; LENGTH: 821
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-21013

Query Match          33.4%; Score 295.5; DB 4; Length 821;
Best Local Similarity 37.7%; Pred. No. 3.8e-25;
Matches 66; Conservative 36; Mismatches 70; Indels 3; Gaps 1;

QY 3 LKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTHGSAII 62
DB 33 LPALLSALM---IAEVHAESFTVSDIRVNGLQKVSAGSVFAALPLNVGSETIDDDQALVQAT 89

QY 63 KSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQSQ 122
DB 90 RSLFKTGFQDIQLGRDGNLVVTVVERPSISIEGKAIKSKEDLLKGLKQSGLAEGE 149

QY 123 YFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKIT 177
DB 150 IFQRTATLEGVRNELQRYVQAQGRYSAEINAENVIPQPRNRVALKININEGTVAIS 204

RESULT 5
US-09-489-039A-12469
; Sequence 12469, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 12469
; LENGTH: 815
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-12469

Query Match          33.0%; Score 292; DB 4; Length 815;
Best Local Similarity 38.0%; Pred. No. 9.5e-25;
Matches 68; Conservative 31; Mismatches 72; Indels 8; Gaps 1;

QY 6 IASALMMLGISPLAFAD-----FTIQDIRVEGLQRTPESTVFNYLPVKVGDYNDTH 57
DB 5 ITWAMKKLLIASLLFSATVYGAEGFVVKDHFEGQLQRVAVGAALLSMPVRGDTVTDDD 64

QY 58 GSAITKSLYATGFFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFG 117
DB 65 ISNTIRALPATGNFDDVRVLRDGTLLVQVKERTPIASITFGSKNSVKDDMLKQNLASG 124

QY 118 LAQSQYFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDEGSAKIT 176
DB 125 VRVGESLDRITTIADIEKGLDFYYSVGKYSASVKAIVTPLPRNRVDLKLVPFQEGVSAKI 183

RESULT 6
US-09-540-236-3472
; Sequence 3472, Application US/09540236
; Patent No. 6673910
; GENERAL INFORMATION:
```

APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA

; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS

; FILE REFERENCE: 2709.2004001

; CURRENT APPLICATION NUMBER: US/09/489,039A

; CURRENT FILING DATE: 2000-01-27

; PRIOR APPLICATION NUMBER: US 60/117,747

; PRIOR FILING DATE: 1999-01-29

; NUMBER OF SEQ ID NOS: 14342

; SEQ ID NO 8469

; LENGTH: 825

; TYPE: PRT

; ORGANISM: Klebsiella pneumoniae

; US-09-489-039A-8469

Query Match 31.2%; Score 276; DB 4; Length 825;

Best Local Similarity 34.1%; Pred. No. 6.9e-23;

Matches 60; Conservative 40; Mismatches 76; Indels 0; Gaps 0;

QY 1 MKLKQIASALMMLGISPLAFADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSA 60

Db 20 LKTHITISGLIAPLTLYAATSYQVDDIRFEGLRQRTVIGAGLLSMPLHAGDAVTPEDVSE 79

QY 61 IIKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 120

Db 80 AVRALYASGNFVQIURDGKTLVVQKERTTASVSFGNKAVKDDALKENITAGSISA 139

QY 121 SQVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKI 176

Db 140 GSALDRNSLSEIEKGLQDFYYSAGKSAQVHAVVTPLPRNRVDTLTFVFGSISAKI 195

RESULT 11

US-08-433-522A-2

; Sequence 2, Application US/08433522A

; Patent No. 6013514

; GENERAL INFORMATION:

; APPLICANT: CHONG, Pele

; APPLICANT: THOMAS, Wayne

; APPLICANT: YANG, Yan Ping

; APPLICANT: LOOSMORE, Sheena

; APPLICANT: SIA, Dwo Yuan Charles

; APPLICANT: KLEIN, Michel

; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN

; NUMBER OF SEQUENCES: 55

; ADDRESSEE: Sim & McBurney

; STREET: 6TH Floor, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,522A

; FILING DATE: 12-SEP-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEWART, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 797 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-433-522A-2

Query Match

Best Local Similarity 26.7%; Score 236.5; DB 3; Length 797;

Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;

QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61

Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGQDLEQQIRASLPVRAGQRTDNDVANI 60

QY 62 IKSLEYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 121

Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNDLNGFKVKG 120

QY 122 QVFNQATLNQAVAGLKEEYLGKGLNIQITPKVTKLARNRVDITIDEGKSAKI 176

Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAEILIQINEDDKAKL 175

RESULT 12

US-08-433-522A-4

; Sequence 4, Application US/08433522A

; Patent No. 6013514

; GENERAL INFORMATION:

; APPLICANT: CHONG, Pele

; APPLICANT: THOMAS, Wayne

; APPLICANT: YANG, Yan Ping

; APPLICANT: LOOSMORE, Sheena

; APPLICANT: SIA, Dwo Yuan Charles

; APPLICANT: KLEIN, Michel

; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN

; NUMBER OF SEQUENCES: 55

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Sim & McBurney

; STREET: 6TH Floor, 330 University Avenue

; CITY: Toronto

; STATE: Ontario

; COUNTRY: Canada

; ZIP: M5G 1R7

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/433,522A

; FILING DATE: 12-SEP-1995

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: STEWART, Michael I

; REGISTRATION NUMBER: 24,973

; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (416) 595-1155

; TELEFAX: (416) 595-1163

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 797 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-433-522A-4

Query Match

Best Local Similarity 26.7%; Score 236.5; DB 3; Length 797;

Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;

QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61

Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGQDLEQQIRASLPVRAGQRTDNDVANI 60

QY 62 IKSLEYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQ 121

Db 61 VRSLFVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVIPTALKQNDLNGFKVKG 120

QY 122 QYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDECKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKL 175

RESULT 13

US-08-433-522A-6
; Sequence 6, Application US/08433522A
; Patent No. 6013514
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/433,522A
; FILING DATE: 12-SEP-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-434 MIS:jb
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-433-522A-6

Query Match 26.7%; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;

QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
Db 61 VRSFLVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVPTALKQNLDANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDECKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKL 175

RESULT 14

US-09-135-166-2
; Sequence 2, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele

; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sim & McBurney
; STREET: 6TH Floor, 330 University Avenue
; CITY: Toronto
; STATE: Ontario
; COUNTRY: Canada
; ZIP: M5G 1R7
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/135,166
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/433,522
; FILING DATE: 12-SEP-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: STEWART, Michael I
; REGISTRATION NUMBER: 24,973
; REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (416) 595-1155
; TELEFAX: (416) 595-1163
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 797 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-135-166-2

Query Match 26.7%; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.3%; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;

QY 3 LKQIASALMMLGISPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQDLEQQIRASLPVRAGQRTDNDVANI 60
QY 62 IKSLYATGFFDDVRVETADGQLLTIVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
Db 61 VRSFLVSGRFDVKAHQEGDVLVSVVAKSIISDVKIKGNSVPTALKQNLDANGFKVG 120
QY 122 QYFNQATLNOAVAGLKEEYLGKGLNIQITPKVTKLARNRVDIDITIDECKSAKI 176
Db 121 DVLIREKLNFAKSVKEHYASVGRYNATVEPIVNTLPNNRAELIQINEDDKAKL 175

RESULT 15

US-09-135-166-4
; Sequence 4, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:

RESULT 16

US-09-135-166-6
; Sequence 6, Application US/09135166
; Patent No. 6083743
; GENERAL INFORMATION:
; APPLICANT: CHONG, Pele
; APPLICANT: THOMAS, Wayne
; APPLICANT: YANG, Yan Ping
; APPLICANT: LOOSMORE, Sheena
; APPLICANT: SIA, Dwo Yuan Charles
; APPLICANT: KLEIN, Michel
; TITLE OF INVENTION: HAEMOPHILUS OUTER MEMBRANE PROTEIN
; NUMBER OF SEQUENCES: 55
; CORRESPONDENCE ADDRESS:

ADDRESSEE: Sim & McBurney
STREET: 6TH Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/09/135,166
APPLICATION NUMBER: US/09/135,166
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/433,522
FILING DATE: 12-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-829 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 797 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-135-166-4

Query Match 26.78; Score 236.5; DB 3; Length 797;
Best Local Similarity 30.34; Pred. No. 2.5e-18;
Matches 53; Conservative 38; Mismatches 83; Indels 1; Gaps 1;
Qy 3 LKQIASALMMLGIGSPLAF-ADFTIQDIRVEGLQRTPESTVFNYLPVKVGDTYNDTHGSAI 61
Db 1 MKKLLIASLLFGTTTTFVFAAPFVAKDIRVDGVQGDLEQQIRASLPVRAGORVTDNDVANI 60
Qy 62 IKSLYATGFDDVRVETADGQLLLTVIERPTIGSLNITGAKMLQNDAIKKNLESFGLAQS 121
Db 61 VRSILFVSGREDDVKAHQEGDVLVVSVVAKSIIISDKIKGNSVIPTKALQNLDAANGFKVG 120
Qy 122 QYFNQATLNOAVAGLKEEYLGKLNIIQITPKYTKLARNRVDIDITIDECKSAKI 176
Db 121 DVLIREKLINEFAKSVKEHYASVGRYNATVEFIVNTLPNNRABILIQINEDDKAKL 175

Search completed: July 6, 2005, 15:20:40
Job time : 14.6923 secs